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	- 4 C O C C O A A A A A A C C C C C C C C C	44444444444444	44444 801444
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3.2 69.5 11380 3.2 69.5 12687 3.2 69.5 12687 3.2 69.5 12687 3.2 69.5 15363 3.2 69.5 16056 3.2 69.5 16056 3.2 69.5 20513 3.2 69.5 20513 3.2 69.5 22120 69.5 22120 3.2 69.5 22120 69.5 22120	3.2. 69.5. 4589.3 3.2. 69.5. 3800.7 3.2. 69.5. 42398.4 3.2. 69.5. 42398.4 3.2. 69.5. 45398.4 3.2. 69.5. 45398.4 3.2. 69.5. 4589.3 3.2. 69.5. 4589.3 3.2. 69.5. 5175.4 3.2. 69.5. 5175.4 3.3. 69.5. 5175.4 3.4. 69.5. 5175.4 3.5. 69.5. 5175.4	13.2 69.5 55675 13.2 69.5 62311 13.2 69.5 72742 13.2 69.5 77772 13.2 69.5 80858 13.2 69.5 80858 13.2 69.5 80858 13.2 69.5 80858 13.2 69.5 98864 13.2 69.5 98864 13.2 69.5 102738 13.2 69.5 102738 13.2 69.5 10218 13.2 69.5 11214 13.2 69.5 12188 13.2 69.5 12188 13.2 69.5 12188 13.2 69.5 12188 13.2 69.5 12254 13.2 69.5 12254 13.2 69.5 12254 13.2 69.5 12254 13.2 69.5 12254 13.2 69.5 12254 13.2 69.5 12254	3.2 69.5 187916 3.2 69.5 194790 3.2 69.5 194933 3.2 69.5 194933 3.2 69.5 209210 3.2 69.5 209631 3.2 69.5 209632
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                                                                                                                                                                                                                Preparation of heterodimeric PDGF-AB using a bicistronic vector system in mammalian cells
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628 nt of the 5' non-translated region of
poliovirus Typ 1 (Mahoney)"
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                                                                                                                                                                                                          TITLE OF INVENTION: Preparation of heterodimeric PDGF-AB TITLE OF INVENTION: bicistronic vector system in mammalia NUMBER OF SEQUENCES: 16
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPA)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/387,845
FILING DATE:
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CLONE: pGEM 3-5'Polio (M) (4708 bp), (Sarnow, 1989)
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ORIGINAL SOURCE:
ORGANISM: Poliovirus Typ 1 (Mahoney strain)
                                                                                                                sequence 5, Application US/08387845
Patent No. 5665567
GENERAL INFORMATION:
APPLICANT:
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Patent No. 5935819
GENERAL INFORMATION:
APPLICANT:
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CCCCTGAATGCGGCTAATC 19
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SEQUENCE CHARACTERISTICS:
LENGTH: 628 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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Best Local Similarity 100.
Matches 19; Conservative
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OTHER INFORMATION: /nc
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OTHER INFORMATION: at
PUBLICATION INFORMATION:
AUTHORS: Sarnow, P.
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J. Virol.
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LOCATION: 1..628
OTHER INFORMATION:
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FEATURE:
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US-08-387-845-5
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Gaps
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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628 nt of the 5' non-translated region of
poliovirus Typ 1 (Mahoney)"
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Pred. No. 1.1;
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                                     SOFTWARE: Patentin Release #1.0, Version #1.25 (EPA)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/778,275
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/867,352
                                                                                                                                                                                                                                                                                                                                                                                                             (4708 bp), (Sarnow, 1989)
                                                                                                                                                                                                                                                                                                                                        ORIGINAL SOURCE:
ORGANISM: Poliovirus Typ 1 (Mahoney strain)
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                    FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/387,845
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/387,847
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 5, Application US/08867352; Patrent No. 6060273; GENERAL INFORMATION:
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100.0%;
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INFORMATION POR SEQ ID NO: 5
SEQUENCE CHARACTERISTICS:
LENGTH: 628 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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INFORMATION FOR EQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 628 base pairs
TYPE: nucleic acid
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Best Local Similarity 100.
Matches 19; Conservative
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OTHER INPORMATION: /no
OTHER INFORMATION: du
OTHER INFORMATION: at
PUBLICATION INFORMATION: A
AUTHORS: Sarnow, P
JOURNAL: J. Virol.
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LOCATION: 1..628
OTHER INFORMATION:
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FEATURE:
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DATE: 1989
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GENERAL INFORMATION:
APPLICANT: Lee, Kang-Hung
APPLICANT: Bair, Chi-Horng
APPLICANT: Bair, Chi-Horng
APPLICANT: Theng, Yang-Yuan
APPLICANT: Wang, Yih-Weng
APPLICANT: Wang, Shing-Hwan
TITLE OF INVENTION: and Probes Therefor
FILE REPERENCE: TAI 316
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 16
SOFTWARE: Patentin version 3.1
SEQ ID NO 16
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100.0%; Score 19; DB 3; Length 1560;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 19; Conservative 0; Mismatches 0; Indels
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US-09-724-678D-16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
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628 nt of the 5' non-translated region of
poliovirus Typ 1 (Mahoney)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                    ORIGINAL SOURCE:
ORGANISM: Poliovirus Typ 1 (Mahoney strain)
IMMEDIATE SOURCE:
CLONE: pGEM3-5'Polio (M) (4708 bp), (Sarnow, 1989)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
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CORGANISM: SWINE VESICULAR DISEASE VIRUS
US-09-116-032-2
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US-09-724-678D-16
; Sequence 16, Application US/09724678D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2, Application US/09116032
Patent No. 6200576
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NAME/KEY:
LOCATION:
LOCATION:
OTHER INFORMATION:
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NAME/KEY:
LOCATION:
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AUTHORN:

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Best Local Similarity 100.(
Matches 19; Conservative
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Best Local Similarity 100.
Matches 19; Conservative
STRANDEDNESS: single
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DATE: 1989
US-08-867-352-5
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US-09-116-032-2
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Gaps

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Sequence 10, Application US/09202904A

Sequence 10, 6395471

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Kang, Sung Key
APPLICANT: Hahn, Bumsuk
TITLE OF INVENTION: Hepatitis C Surrogate Virus for Testing
TITLE OF INVENTION: He Activity of Hepatitis C Virus Protease, a Recombinant
TITLE OF INVENTION: Gene and a Use Thereof
FILE REFERENCE: A32210-PcT-USA 072944.0104
CURRENT APPLICATION NUMBER: US/09/202,904A
CURRENT FILING DATE: 1997-06-25
PRIOR PILING DATE: 1997-06-25
NUMBER OF SEQ ID NOS: 14
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 10
LENGTH: 2320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; OTHER INFORMATION: Genetically engineered virus derived from ; OTHER INFORMATION: poliovirus and hepatitis C virus US-09-202-904A-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1, Application US/09116032
Patent No. 6200576
GENERAL INFORMATION:
APPLICANT: HWONG, CHING LONG
APPLICANT: LOO, CHENG-KAI
APPLICANT: YOU, CHENG-KAI
APPLICANT: YANG, YING-CHUAN
APPLICANT: JENG, KING-SONG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              451 CCCCTGAATGCGGCTAATC 469
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                                                                                                                                     - 3.5 inch, 1.44 Mb storage
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APPLICANT: Glustein, Joseph Z.
APPLICANT: Glustein, Garth D.
APPLICANT: Thang, Yingze
TITLE OF INVENTION: PCR Assay For Bacterial and
TITLE OF INVENTION: Viral Meningitis
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: University of Pittsburgh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 18; DB 3
Pred. No. 2.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: 3-1/2" high density diskette
COMPUTER: IBM PC or compatibles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: University of Pittsburgh
STREET: Office of Technology Transfer
STREET: 911 William Pitt Union
                                                                                                                                                                           OPERATING SYSTEM: MS DOS
SOFWARE: WORD PERÍECE
CURRENT APPLICATION DEATA:
APPLICATION NUMBER: US/09/311,260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/061,273
FILING DATE: 17-APR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: other nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 9, Application US/09061273; Patent No. 6258570
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Best Local Similarity 100.0%; Pi
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                                                                                                                                                                                                                                                                                                                                                                                                                                 REPERENCE/DOCKET NUMBER: VV
TELECOMMUNICATION INFORMATION
TELEPHONE: (970) 668-2050
TELEFAX: (970) 668-2082
                                                                                                                                                                                                                                                                                                                                               FILING DATE: ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MS-DOS
                                                                                                                                                  IBM compatib
                                                                                                                                                                                                                                                                                                                                                                                         NAME: Larson, Marina T
REGISTRATION NUMBER: 3
                                                                                                                                   Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; FRAGMENT TYPE: internal US-09-311-260-105
        Box 5270
                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM: MEDIUM TYPE: 3-1/2"
                                                                                      ZIP: 80443-5270
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Pittsburgh
STATE: Pennsylvania
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          nucleic acid
                                                                                                                                                    COMPUTER: IBM CON OPERATING SYSTEM:
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STREET: P.O. CITY: Frisco
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STRANDEDNESS:
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                                              STATE: C
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                 APPLICANT: DEVELOPMENT CENTER FOR BIOTECHNOLOGY
TITLE OF INVENTION: SWINE VESTICULAR DISEASE VIRUS AND MUTANT STRAINS AND
TITLE OF INVENTION: PREPARATION PROCESS AND USE THEREOF
FILE REFERENCE: 9751.79US01
FULKENT APPLICATION NUMBER: US/09/116,032
CURRENT FILING DATE: 1998-07-15
EARLIER APPLICATION NUMBER: CHINA 86105814
SARLIER APPLICATION NUMBER: CHINA 86105814
SARLIER PILING DATE: 1997-05-01
NUMBER OF SEQ ID NOS: 39
SOFTWARE: PATENTIN Ver. 2.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Yong Soo. Bae
APPLICANT: Yong Soo. Bae
APPLICANT: Jung, Hye Rhan
TITLE OF INVENTION: Replication-Competent Sabin Type 1 Strain
FILE REFERENCE: Docket No. 6696289: 4220-109 US
CURRENT APPLICATION NUMBER: US/09/284,349B
CURRENT FILING DATE: 1999-06-04
PRIOR APPLICATION NUMBER: PCT/KR98/00242
PRIOR FILING DATE: 1998-07-08
PRIOR FILING DATE: 1997-07-08
NUMBER OF SEQ ID NOS: 30
                                                                                                                                                                                                                                                                                                                                                                   Score 19; DB 3; Length 7400;
Pred. No. 1.4;
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                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                            TYPE: DNA
CORGANISM: SWINE VESICULAR DISEASE VIRUS
US-09-116-032-1
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Patent No. 6214555
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sequence 1, Application US/09284349B
Patent No. 6696289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               454 CCCCTGAATGCGGCTAATC 472
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APPLICANT: Hui, May
APPLICANT: Dunn, James M.
APPLICANT: LaCroix, Jean-Michel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            451 CCCCTGAATGCGGCTAATC 469
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Best Local Similarity 100.0%;
Matches 19; Conservative 0
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SEQ ID NO 1
LENGTH: 7441
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US-09-284-349B-1
  EDWARD L
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Oppedahl &
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TITLE OF INVENTION:
TITLE OF INVENTION:
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Best Local Similarity
Matches 19; Conserv
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                                                                                                                                                                                                                                SEQ ID NO 1
LENGTH: 7400
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Gaps

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CORRESPONDENCE ADDRESS:
ADDRESSES: Cooper & Dunham
STREET: 30 Rockefeller Plaza
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-461-503-1; Sequence 1. Application US/08461503
Patent No. 5834302; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 94.7%; So
Best Local Similarity 100.0%; P.
Matches 18; Conservative 0;
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                                                                                                                                                                               Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: NUCLEIC ACID
STRANDEDNESS: single
                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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743..7361
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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LOCATION:
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Sequence 116.6468743

GENERAL INFORMATION:

APPLICANT: Thomas L. Romick (Inventor)

TITLE OF INVENTION:

TITLE OF INVENTION: PCR TECHNIQUES FOR DETECTING MICROBIAL

TITLE OF INVENTION: PCR TECHNIQUES FOR DETECTING MICROBIAL

TITLE OF INVENTION: PCR TECHNIQUES FOR DETECTING MICROBIAL

TITLE OF INVENTION: PCR 1890-05-17

FILE REFERENCE: HUNN A-ND VIRAL

CURRENT APPLICATION NUMBER: US/09/313,221A

CURRENT APPLICATION NUMBER: US 60/086,025

PRIOR PILING DATE: 1998-05-18

NUMBER OF SEQ ID NOS: 145

SOFTWARE: FastSEQ for Windows Version 4.0

LENGTH: 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Racaniello, Vincent
APPLICANT: Tatem, Joanne M.
APPLICANT: Weeks-Levy, Carolyn L.
TITLE OF INVENTION: METHODS FOR PRODUCING RNA VIRUSES FROM
TITLE OF INVENTION: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 3; Length 44; 2.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                      94.7%; Score 18; DB 3; Length 25;
100.0%; Pred. No. 2.5;
ive 0; Mismatches 0; Indels
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: No. 6258570 applicable
FILING DATE: No. 6258570 applicable
FILING DATE: No. 6258570 applicable
ATTORNY AGENT INFORMATION:
NAME: Mary-Elizabeth Buckles
REGISTRATION NUMBER: 31,907
REFERENCE/DOCKT NUMBER: 017917/20132
TELECHMUNICATION INFORMATION:
TELEPHONE: 202/414-9267
TELEPHONE: 202/414/9299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   94.7%; Score 18;
100.0%; Pred. No.
tive 0; Mismatch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1, Application US/07852260 Patent No. 5525715
                                                                                                                                                                                             TELEFAX: 202/41419299
TELEX: 64711
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 nuclectides
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
NOLECULE TYPE: synthetic DNA
US-09-061-273-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 CCCCTGAATGCGGCTAAT 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8 CCCCTGAATGCGGCTAAT 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 CCCCTGAATGCGGCTAAT 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Ouery Match
Best Local Similarity 100.
Matches 18, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-313-221A-114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 13
US-07-852-260-1
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Gaps
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APPLICANT: Tatem, Joanne M.
APPLICANT: Weeks-Levy, Carolyn L.
TITLE OF INVENTION: METHODS FOR PRODUCING RNA VIRUSES
TITLE OF INVENTION: FROM CDNA
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESSE: Cooper & Dunham
STREET: 1185 Avenue of the Americas
COMPUTER: IBM PC COMPATILLS
COMPATIEN: TEMP PC COMPATILLS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/852,260
FILLING DATE: 19920619
CLIASSIFICATION: 435
CLIASSIFICATION: 435
ATTORNEY AGENT INPORMATION:
NAME: White, John P. REGISTRATION NUMBER: 36.678
FELEPHONE: (212) 664-055
TELEPHONE: (212) 664-055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/461,503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 18; DB 2;
Pred. No. 5;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Cooper & Dunham STREET: 1185 Avenue of the Americas CITY: New York COUNTRY: U.S.A.
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Gaps
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                                                                                                                                                                               Length 7432;
                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Miles, Vincent J.
APPLICANT: Mathews, Michael B.
APPLICANT: Katze, Michael G.
APPLICANT: Witherell, Gary
APPLICANT: Watson, Julia C.
TITLE OF INVENTION: METHOD FOR SELECTIVE INACTIVATION
TITLE OF INVENTION: 09 VIRAL REPLICATION
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
                                                                                                                                                                           Query Match 94.7%; Score 18; DB 3;
Best Local Similarity 100.0%; Pred. No. 5;
Matches 18; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. 7.8;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 1155 Avenue of the Americas CITY: New York COUNTRY: USA ZIP: 100.7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPOTER: IBM COMPATIBLE
COMPOTER: IBM COMPATIBLE
OPERATING SYSTEM: DOS
SOFTWARE: FESTESCO VERSION 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/221,816B
FILING DATE: 01-APR-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: COLUZZI, LAUTA A
REGISTRATION NUMBER: 30,742
                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 31, Application US/08221816B
; Patent No. 5738985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                457 CCCCUGAAUGCGGCUAACC 475
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 75
TELECOMMUNICATION INFORMATION:
                      DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (212) 869-8864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 627 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 78.9
Matches 15; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 10036/2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                     743..7361
  linear
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                                       8
                      MOLECULE TYPE:
HYPOTHETICAL: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE:
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                                                             ANTI-SENSE:
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US-08-465-250-1
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US-08-221-816B-31
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                                                                              FEATURE:
NAME/KEY:
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APPLICANT: Recaniello, Vincent
APPLICANT: Tatem, Joanne M.
APPLICANT: Weeks-Levy, Carolyn L.
TITLE OF INVENTION: METHODS FOR PRODUCING RNA VIRUSES FROM
TITLE OF INVENTION: DDNA
NUMBER OF SEQUENCES: 9
CORRESPONDENCE DUNHAM LLP
STREET: 1185 Avenue of the Americas
CITY: New York
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PARENT: Release 1.30
CURRENT APPLICATION NUMBER: US/08/465,250
FILING DATE: 6-UUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 94.7%; Score 18; DB 2; Length 7432; Best Local Similarity 100.0%; Pred. No. 5; Matches 18; Conservative 0; Mismatches 0; Indels
                CLASSIFICATION: 435
ATTONREY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REGISTRATION NUMBER: 36607-D-PCT-US
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 1970-0400
TELEPRA: (212) 391-0525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1, Application US/08465250 Patent No. 6136570
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CLASSIFICATION: 435
ATTORNEY/AGENT INPOMMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 7432 base pairs TYPE: nucleic acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 36
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEFPAX: (212) 391-0525
                                                                                                                                                                                                                                                                                            TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 7432 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
5-JUN-1995
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743..7361
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                                                                                                                                                                                                                                                                                                                                    HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                    ; LOCATION:
US-08-461-503-1
                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY:
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COMPUTER: IEM COMPATIBLE
COMPUTER: IEM COMPATIBLE
OPERATING SYSTEM: DOS
SOFTWARE: PASSESO VERSION 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/112,241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPOTER: IEM. COMPATIBLE
COMPOTER: IEM. COMPATIBLE
COPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/104,611
FILING DATE: 22-Mar-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: RNA
SEQUENCE DESCRIPTION: SEQ ID NO: 31:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864
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INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 627 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 CCCCTGAATGCGGCTAATC 19
                                    STATE: New York
COUNTRY: USA
ZIP: 10036/2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA
ZIP: 10036/2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
    Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie
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Best Local Similarity 78.93
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEOUENCES:
                     CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 19
US-10-104-611-31
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Patent No. 6623961
GENERAL INFORMATION:
Mathews, Wichael B.
Katze, Michael G.
Witherell, Gary
Watson, Julia C.
TITLE OF INVENTION: METHOD FOR SELECTIVE INACTIVATION
                                                                                                                                                                                    SELECTIVE INACTIVATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Indels
            Sequence 31, Application US/10112547

Patent No. 6579674

GENERAL INFORMATION:

APPLICANT: Mathews, Michael B.

Katze, Michael B.

Katze, Michael G.

Witherell, Gary

Watson, Julia C.

TITLE OF INVENTION:

OF VIRAL REPLICATION
                                                                                                                                                                                                                                                                                                                                            COUNTRY: USA
ZIP: 10036/2711
COMPUTER READABLE FORM:
COMPUTER: Diskette
COMPUTER: Diskette
COMPUTER: DISKETTE
COMPUTER: TBM COMPATIBLE
COMPUTER: TBM COMPATIBLE
COMPUTER: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/112,547
FILING DATE: 28-Mar-2002
CLASSIFICATION AUMBER: US/08/221,816B
FILING DATE: 01-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: COLUZZI, LAURA A
REGISTRATION NUMBER: 30,742
REPERENCE/DOCKET NUMBER: 30,742
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OF VIRAL REPLICATION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TOPOLOGY: linear; MOLECULE TYPE: RNA SEQUENCE DESCRIPTION: SEQ ID NO: 31: US-10-112-547-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (212) 790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (212) 869-8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 31:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              457 CCCCUGAAUGCGGCUAACC 475
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 3. CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15; Conservative
                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                  STATE: New York
                                                                                                                                                                                                                                                                                                              CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 15; Conserva
US-10-112-547-31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 31, Application US/10104611
Patent No. 6667152
GENERAL INFORMATION:
APPLICANT: Miles, Vincent J.
Mathews, Michael B.
Katze, Michael G.
Witherell, Gary
Watson, Julia C.
TITLE OF INVENTION: METHOD FOR SELECTIVE INACTIVATION
OF VIRAL REPLICATION
                                                                                                                                                                                                                                                                FILING DATE: 28-MAI-2002
CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/221,816B
FILING DATE: 01-APR-1994
ATTORNEY/AGENT INFORMATION:
NAMB: COTLOZI, LAURA A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7960-030
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 1155 Avenue of the Americas CITY: New York STATE: New York
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Gaps
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                                                                                                                                                                          Score 17.4; DB 3;
Pred. No. 7.8;
                                                                                                                                                                                                                    3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     METHOD FOR SELECTIVE OF VIRAL REPLICATION
                          TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECTLE TYPE: RNA
SEQUENCE DESCRIPTION: SEQ ID NO: 31:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/09/724,380
FILING DATE: 01-APR-1994
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 1155 Avenue of the Americas CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
PRICING NUMBER: 08/221,816
APPLICATION NUMBER: 01-APR-1994
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 31, Application US/09724380; Patent No. 6824976
                                                                                                                                                                                                                                                                                     457 CCCCUGAAUGCGGCUAACC 475
                                                                                                                                                                                                                                                            1 CCCCTGAATGCGGCTAATC 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 796
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pennie & Edmonds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Miles, Vincent J.
APPLICANT: Machews, Michael
APPLICANT: Katze, Michael G.
APPLICANT: Witherell, Gary
APPLICANT: Watson, Julia C.
                                                                                                                                                                        Query Match
Best Local Similarity 78.9%;
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM Compatible OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (212) 869-8864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  : 627 base pairs
nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
ZIP: 10036/2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: ME
TITLE OF INVENTION: OF
NUMBER OF SEQUENCES: 3:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: RNP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE:
                                                                                                                                US-10-109-368-31
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Pred. No. 7.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 31, Application US/10109368
Patent No. 6777179
GENERAL INFORMATION:
APPLICANT: Miles, Vincent J.
Mathews, Michael B.
Katze, Michael G.
Witherell, Gary
Watson, Julia C.
TITLE OF INVENTION: METHOD FOR SELECTIVE INACTIVATION
OF VIRAL REPLICATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READBLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/109,368
FILING DATE: 27-Mar-2002
CLASSIFICATION: CUNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
                                 APPLICATION NUMBER: US/08/221,816B
FILING DATE: 01-APR-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 91.6%; Score 17.4; D
Best Local Similarity 78.9%; Pred. No. 7.8;
Matches 15; Conservative 3; Mismatches
                                                                                                      NAME: Coruzzi, Laura A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7960-030
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Coruzzi, Laura A. REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7960-030
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/221,816
FILING DATE: 01-ARR-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE DESCRIPTION: SEQ ID NO: 31:
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                             TELEX: 66141 PERNIE
INFORMATION FOR SEQ 1D NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 627 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 CCCCTGAATGCGGCTAATC 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEX: 66141 PENNIE INFORMATION FOR SEQ ID NO: 31: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCES: 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 10036/2711
                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF
                                                                                                                                                                                                                                                                                                                                                                                                                              US-10-104-611-31
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US-09-949-016-15436

| Sequence 15436 | Application US/09949016 |
| Sequence 15436 | Application US/09949016 |
| Parent No. 681239 |
| GENERAL INPORMATION: |
| THE NO. 681230 |
| TITLE OF INVENTION: | POLYMORPHISMS IN KNOWN GENES ASSOCIATED |
| TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF |
| TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF |
| TITLE OF INVENTION: WIMBER: US/09/949,016 |
| CURRENT APPLICATION NUMBER: 60/241,755 |
| PRIOR PLING DATE: 2000-10-03 |
| PRIOR PLING DATE: 2000-10-03 |
| PRIOR APPLICATION NUMBER: 60/231,498 |
| PRIOR PLING DATE: 2000-09-08 |
| WUMBER OF SEQ ID NOS: 207012 |
| SOFTHARE: PSESEE FOR Windows Version 4.0 |
| LENGTH: 199945
                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 5242, Application US/09489039A

Sequence 5242, Application US/09489039A

Patent No. 6610836

GENERAL INFORMATION:
PATENTION:
PATENTION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
CURRENT PELLICALION UNMBER: US/09/489, 039A
CURRENT FILING DATE: 1209-01-29
NUMBER OF SEQ ID NOS: 14342

SEQ ID NO 5242

LENGTH: 1269
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 81.1%; Score 15.4; DB 3; Length 1269; Best Local Similarity 94.1%; Pred. No. 1e+02; Matches 16; Conservative 0; Mismatches 1; Indels 0
                                                                                               DB 9; Length 250;
                                                                                                                                                                0; Mismatches
                                                                                               Score 15.8; I
Pred. No. 52;
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                                                                                                                                                                                                                                                                                               202 ccccrcaarcrecraacc 220
                                                                                                                                                                                                                                 1 CCCCTGAATGCGGCTAATC 19
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ORGANISM: Klebsiella pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 CCCTGAATGCGGCTAAT 18
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                                                                                            Query Match
Best Local Similarity 89.5%;
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ) ORGANISM: Human
US-09-949-016-15436
                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-489-039A-5242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-489-039A-5242
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                              5340713-1
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                                                                                                                                            Sequence 1, Application US/08246373
Faceure No. 5550018
GENERAL INFORMATION:
GENERAL INFORMATION:
TENTRAL INFORMATION:
TITLE OF INVENTION:
THE OF INVENTIO
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; Patent No. 5340713
; Patent No. 5340713
; Patent No. 5340713
; Tatle OF INVENTION: PROCESS FOR THE CHARACTERIZATION OF ; HUMAN RHINOVIRUSES
; NUMBER OF SEQUENCES: 5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/541,907
; RILING DATE: 22-JUN-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sense strand PCR primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Gerald M. Murphy, Jr.
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 1173-234P
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 241-1300
TELEPAX: (703) 241-0369
457 CCCCUGAAUGCGGCUAACC 475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (703) 241-0365
TELEX: 248345
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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STRANDEDNESS: singl
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 17; Conserva
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                                                                                               RESULT 22
US-08-246-373-1
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Sequence 34646, Application US/09949016

Sequence 34646, Application US/09949016

Batent No. 6812339

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
FILE REPERENCE: CL001307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

FRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-03

FRIOR FILING DATE: 2000-10-03

FRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: PSESEE for Windows Version 4.0

SEQ ID NO 34646
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                             SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/361,337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 15; DB 2; Lo Pred. No. 1.1e+02; 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     77.9%; Score 14.8; DB 3; 88.9%; Pred. No. 2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 29
US-09-949-016-146512/c
; Sequence 146512, Application US/09949016
; Patent No. 6812339
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: Other nucleic acid
                                                                                                                          FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: PETTYMEN, DEA'LG G.
REGISTRATION NUMBER: 33,438
REFRENCE/DOCKET NUMBER: 1414
TELEPHONE: (404) 688-0770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100.0%;
Matches 15; Conservative 0
                                                                                                                                                                                                                                                                                                       TELEFAX: (404) 688-9880 INFORMATION FOR SEQ ID NO: 3 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 88.9°
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 35 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-949-016-34646
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-949-016-34646
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                             APPLICANT: Levenbook, Inessa S.
APPLICANT: Chumakov, Konstantin M.
APPLICANT: Chumakov, Konstantin M.
APPLICANT: Roninson, 1gor
TITLE OF INVENTION: ASSAY FOR VIRULENT REVERTANTS OF
TITLE OF INVENTION: ATTENUATED LIVE VACCINES
TOWNER OF SEQUENCES: 77
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 38, Application US/08361337
Patent No. 5728519
GENERAL INFORMATION:
APPLICANT: Levenbook, Inessa S.
APPLICANT: Chumakov, Konstantin M.
APPLICANT: Noninson, Igor
TITLE OF INVENTION: ASSAY FOR VIRULENT REVERTANTS OF
TITLE OF INVENTION: ATTENDATED LIVE VACCINES
                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS OSTWARE: PATENTIN Release #1.0, Version #1.25 APPLICATION DATA: APPLICATION NUMBER: US/08/361,337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 2; Le
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  78.9%; Score 15;
100.0%; Pred. No.
:ive 0; Mismatc
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CORRESPONDENCE ADDRESS:
ADDRESSES: NEEDLE & ROSENBERG, P.C.
STREET: 127 Peachtree Street, N.E.
                                                                                                                                                                                                                                                                                NEEDLE & ROSENBERG, P.C.
                                                                                                                                                                                                                                                                           ADDRESSEE: NEEDLE & ROSENBERG, P.C STREET: 127 Peachtree Street, N.E. CITY: Atlanta STATE: Georgia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear MOLECULE TYPE: Other nucleic acid
                                      Sequence 36, Application US/08361337
Patent No. 5728519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Perryman, David G.
REGISTRATION NUMBER: 33,438
REFERENCE/DOCKET NUMBER: 14:
TELECOMMUNICATION: INFORMATION:
TELEPHONE: (404) 688-0770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (404) 688-0770
TELEPAX: (404) 688-9880
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 35 base pairs
                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 30303
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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Best Local Similarity 100.
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 435
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US-08-361-337-38
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RESULT 33
US-09-614-221A-478/C
; Sequence 478, Application US/09614221A
; Patent No. 6723837
; GENERAL INFORMATION:
; APPLICANT: Karunanadaa, Balasulojini
; APPLICANT: Kishore, Ganesh M.
; APPLICANT: Kishore, Ganesh M.
; TITLE OF INVENTION: WITH STEROL SYNTHESIS AND OTHER MOLECULES ASSOCIATED
; TITLE OF INVENTION: WITH STEROL SYNTHESIS AND METABOLISM
; FILE REFERENCE: 16516.075
; CURRENT FILING DATE: 2000-07-12
; PRIOR FILING DATE: 2000-07-12
; PRIOR FILING DATE: 1999-07-12
; NUMBER OF SEQ ID NOS: 626
; SEQ ID NO 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 13244, Application US/09270767
Patent No. 6703491
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster FILE REFERENCE: File Reference: 7326-094.
CURRENT APPLICATION NUMBER: US/09/270, 767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: PatentIn Ver. 2.0
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Pred. No. 2.1e+02;
0; Mismatches 2; Indels
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88.9%; Pred. No. 2.6e+02;
tive 0; Mismatches 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-13244
                                                                                                                                            ; ORGANISM: Drosophila melanogaster
US-09-270-767-13998
                                                                                                                                                                                                                                                                                                                                                                    299 CTCTGAATGTGGCTAATC 282
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CURRENT FILING DATE: 1999-03-17
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               NUMBER OF SEQ ID NOS: 62517
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 13998
LENGTH: 678
TYPE: DNA
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Best Local Similarity 88.9'
Matches 16; Conservative
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Best Local Similarity 88.9
Matches 16; Conservative
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Best Local Similarity
Matches 16; Conserv
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LENGTH: 960
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FACELL NO. SEL2AS;
FACELL NO. SEL2AS;
FACELL NO. SEL2AS;
FACELL NO. SELZAS;
FACELL NO. SELZAS;
FILE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
FILE REFERENCE: CLOO1307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
FRIOR APPLICATION NUMBER: 60/241,755
FRIOR FILING DATE: 2000-10-20
FRIOR FILING DATE: 2000-10-03
FRIOR FILING DATE: 2000-10-03
FRIOR FILING DATE: 2000-09-08
FRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: RESEERE FOR WINDOWS VERSION 4.0
ENDICHMENT: 601
               APPLICANT: VENTER, J. Craig et al.

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REPERENCE: CL001307

CURRENT APPLICATION NUMBER: 080/949,016

CURRENT APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FASICEO FOR WINDOWS VERSION 4.0
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Patent No. 4703491
GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster PILE PERERNCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 14.8; DB 3; Length 601;
Pred. No. 2e+02;
0; Mismatches 2; Indels
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88.9%;
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Best Local Similarity 88.9
Matches 16; Conservative
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Best Local Similarity 88.9
Matches 16; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO 146512
LENGTH: 601
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FILING DATE
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                                                                                                                                                                                                                                                                           TITLE OF INVENTION: No. 6365723el Sequences of R. coli 0157
NUMBER OF SEQUENCES: 265
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: No. 6855814el Sequences of E. coli 0157 NUMBER OF SEQUENCES: 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 9057;
                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:

MEDLIUM TYPE: Diskette, 3.50 inch. 1.44Mb storage COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Word Perfect 8.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/453,702B

FILING DATE: 03-Dec-1999

CLASSIFICATION OFTA:

APPLICATION NUMBER: 60/110,955

FILING DATE: 04-DEC-1998

ATTORNEY/AGENT INVERSE: 66/110,955

FILING DATE: 04-DEC-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 14.8; DB 3;
Pred. No. 2.8e+02;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Seay, Nicholas J.
REGISTRATION NUMBER: 27386
REFERENCE/DOCKET NUMBER: 960296.95017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 194:
                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Quarles & Brady
STREET: 1 South Pinckney Street
CITY: Madison
                                                                                                                                                                     attner, Frederick R.
Irland. Valerie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Blattner, Frederick R. Burland. Valerie
                                                                                                     Sequence 194, Application US/09453702B
Patent No. 6365723
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 194, Application US/10114170 Patent No. 6855814 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                           Perna, Nicole T.
Plunkett, Guy
Welch, Rod
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4504 CACTGATTGCGGCTAATC 4521
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Plunkett, Guy
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408 CCCTGAATGCGGCAGATC 391
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STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 194
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Best Local Similarity . 88.9%;
Matches 16; Conservative
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                                                                                                                                                                                              Burland,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Burland,
                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: US
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                                                                                                                                                                                                                                                                                                                                                                                                         STATE: WI
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                                                                               -09-453-702B-194
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APPLICANT: Grossman, Alex
APPLICANT: Grossman, Alex
APPLICANT: Richardson, Christopher D.
TITLE OF INVENTION: NOVEL GENES ENCODING LSIRF POLYPEPTIDES
WIWHER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen Canada Inc.
                                                                                COUNTRY: US
ZIP: 53701-2113
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch. 1.44Mb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Seay, Nicholas J.
REGISTRATION NUMBER: 27386
REFERENCE/DOCKET NUMBER: 960296.95017
                                                                                                                                                                                                              CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/114,170
FILING DATE: 01-Apr-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION NUMBER: 09/453,702
FILING DATE: 03-DEC-1999
APPLICATION NUMBER: 60/110,955
FILING DATE: 04-DEC-1998
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Amgen Canada Inc.
STREET: 6733 Mississauga Road, Suite 303
CITY: Mississauga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

SEQUENCE DESCRIPTION: SEQ ID NO: 194:
US-10-114-170-194
ADDRESSEE: Quarles & Brady
STREET: 1 South Pinckney Street
                                                                                                                                                                        COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/611,280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
TELEPHONE: (608) 251-5000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (608) 251-9166
INFORMATION FOR SEQ ID NO: 194:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 4, Application US/08611280
Patent No. 5891666
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS
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ATTORNEY/AGENT INFORMATION:
                                            CITY: Madison
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GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence A Application US/09195940
Fatent No. 6258935
GENERAL INFORMATION:
APPLICANT: Matsuyama, Toshifumi
APPLICANT: Richardson, Christopher D.
TITLE OF INVENTION: NOVEL GENES ENCODING LSIRF POLYPEPTIDES
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen Canada Inc.
STREET: 6733 Mississauga Road, Suite 303
CITY: Mississauga
STREET: Graatio
COUNTRY: Canada
CONTRY: Canada
COMPUTER: LSN 6JB
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Pred. No. 3e+02;
0; Mismatches 2; Indels 0;
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APPLICATION NUMBER: US/09/195,940
                                                        A-338A
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/611,280
REGISTRATION NUMBER: 34,688
REFERENCE/DOCKET NUMBER: A-336
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 12537 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
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88.9%;
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Best Local Similarity 88.9
Matches 16; Conservative
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Best Local Similarity 88.9
Matches 16; Conservative
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US-09-195-940-4/c
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RESULT 38

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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLOO1307
CURRENT FILING DATE: 2000-04-14
FRIOR APPLICATION NUMBER: 60/241,755
FRIOR APPLICATION NUMBER: 60/231,768
FRIOR APPLICATION NUMBER: 60/231,498
FRIOR APPLICATION NUMBER: 60/231,498
FRIOR FILING DATE: 2000-10-03
FRIOR APPLICATION NUMBER: 60/231,498
FRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
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                                                                                  Grossman, Alex
Richardson, Christopher D.
TITLE OF INVENTION: NOVEL GENES ENCODING LSIRF POLYPEPTIDES
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                          CITY: Misslesunce
STATE: Ontario
COUNTRY: Canada
LIP: LSW GJB
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRIT APPLICATION NUMBER: US/09/562,466
FILING DATE: 01-May-2000
CLIASSIPICATION NUMBER: 09/195,940
FILING DATE: cuhknown>
PRIOR APPLICATION NUMBER: 09/195,940
FILING DATE: cuhknown>
APPLICATION NUMBER: 09/195,940
FILING DATE: cuhknown>
APPLICATION NUMBER: 34,688
ARTORNEY/AGENT INFORMATION:
NAME: Oleski, Nancy A.
REFERRECE/DOCKET NUMBER: 3-338A
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 12537 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                  ADDRESSEE: Amgen Canada Inc.
STREET: 6733 Mississauga Road, Suite 303
CITY: Mississauga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 14.8; DB 3
Pred. No. 3e+02;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear MOLECULE TYPE: DNA (genomic) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 17245, Application US/09949016 Patent No. 6812339
Sequence 4, Application US/09562466; Patent No. 6369202; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1565 cccrcaarccrccraacc 1548
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Best Local Similarity 88.9%;
Matches 16; Conservative
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LENGTH: 16083
TYPE: DNA
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Sequence 16549, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVERTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVERTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
TITLE OF INVERTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
TITLE OF INVERTION WIMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR PLILNG DATE: 2000-10-20
PRIOR PLILNG DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SEQ ID NOS: 207012
SEQ ID NO 16549
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APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION A
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR PELING DATE: 2000-10-03
PRIOR PLILING DATE: 2000-10-03
PRIOR PLILING DATE: 2000-10-03
PRIOR PELICATION NUMBER: 60/231,498
PRIOR PLILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FasteSEQ for Windows Version 4.0
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Pred. No. 3.5e+02;
0; Mismatches 2;
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Pred. No. 3.5e+02;
0; Mismatches 2;
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Sequence 12598, Application US/09949016
Patent No. 6812339
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Patent No. 6812339
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88.9%;
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1 Similarity 88.9%;
16; Conservative
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Best Local Similarity 88.9
Matches 16; Conservative
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Best Local Similarity
                                                  JS-09-949-016-16549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          , ORGANISM: Human
US-09-949-016-16549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TYPE: DNA
; ORGANISM: Human
US-09-949-016-12598
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APPLICANT: Inoko, Hidetoshi
APPLICANT: Inoko, Hidetoshi
APPLICANT: Inoko, Hidetoshi
TITLE OF INVENTION: METHOD OF TESTING FOR PSORIASIS VULGARIS
FILE REFERENCE: 06501-112US1
CURRENT APPLICATION NUMBER: US/10/164,230
CURRENT FILING DATE: 2002-04
FRIOR APPLICATION NUMBER: PCT/JP00/08624
FRIOR APPLICATION NUMBER: DT 11/346867
FRIOR APPLICATION NUMBER: JP 11/346867
FRIOR RILING DATE: 1999-12-06
NUMBER OF SEQ ID NOS: 63
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 25235
                                                                    Length 16083;
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                                                                                                         Indels
                                                               Score 14.8; DB 3;
Pred. No. 3.1e+02;
0; Mismatches 2;
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88.9%;
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LOCATION: (14244)...(14407)
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LOCATION: (14244)...(14344)
                                                           Query Match
Best Local Similarity 88.9°
Matches 16, Conservative
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; LOCATION: (25190)...(25235)
US-10-164-230-2
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(1282)...(1405)
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Best Local Similarity
-hem 16; Conserval
; ORGANISM: Human
US-09-949-016-17245
                                                                                                                                                                                                                                                                           US-10-164-230-2/c
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Query Match
Best Local Similarity 88.99
Matches 16; Conservative
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US-09-949-016-15858
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ORGANISM: Human
                                                                                                                                                                                                                                                                              ORGANISM: Human
                                                                                                                                                                                                                                                                                                   US-09-949-016-15890
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APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/241,756
PRIOR PILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FASLESQ for Windows Version 4.0
SEQ ID NO 13765
LENGTH: 128470
APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
FILE SEPERENCE: CLOO1307

CURRENT PELICATION NUMBER: US/09/949,016

CURRENT PELICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR PELING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FRASESEQ for Windows Version 4.0

SEQ ID NO 17433

LENGTH: 101349
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Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
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Pred. No. 3.8e+02;
0; Mismatches 2; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         77.9%; Score 14.8; DB 3; Length 128470;
88.9%; Pred. No. 3.9e+02;
iive 0; Mismatches 2; Indels 0;
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; Patent No. 6812339
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88.9%;
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Best Local Similarity 88..
Thes 16; Conservative
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Best Local Similarity 88.9
Matches 16; Conservative
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US-09-949-016-15890/c
                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Human
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US-09-949-016-13765
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ORGANISM: Human
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is Sequence 18858, Application US/09949016
j Batent No. 6812339
j GENERAL INFORMATION:
j PAPLICANT: VENTER, J. Craig et al.
j TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
j FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT APPLICATION NUMBER: 06/241,755
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR PILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR PILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SEQ ID NOS: 207012
SEQ ID NO 15858
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Patent No. 6294328
Patent No. 6294328
Patent No. 6294328
APPLICANT: FLEISCHMAN, Robert D.
APPLICANT: WHITE, Owen R.
APPLICANT: WHITE, Owen R.
APPLICANT: VENERRY Claire M.
APPLICANT: WEASER, John F.
TITLE OF INVENTION: TUBERCULOSIS
TITLE OF INVENTION: US/09/103,840A
FILE REPRENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 77.9%; Score 14.8; DB 3; Length 144922; Best Local Similarity 88.9%; Pred. No. 3.9e+02; Matches 16; Conservative 0; Mismatches 2; Indels 0;
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Pred. No. 3.9e+02;
0; Mismatches 2;
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR PRILCATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-3
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
SPRIOR FILING DATE: 2000-10-03
SOFTWARE: PRESIZE OF WINDER: 6/231,498
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: PRESIZE FOR WINDOWS VERSION 4.0
SEQ ID NO 15890
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88.9%;
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GENERAL INFORMATION:
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US-09-736-457-1724
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APPLICANT:
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                                                                                                                                            OTHER INFORMATION: CDC 1551
OTHER INFORMATION: "n" bases at various positions throughout the sequence
COTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2
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APPLICANT: FRASER, Claire M.
APPLICANT: FRASER, Claire M.
APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
TITLE OF INVENTION: TUBBERCULOSIS
FILE REFERENCE: 24366-22007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PATENTIN VET. 2.1
                                                                                                                                                                                                                                                Query Match 77.9%; Score 14.8; DB 3; Length 4403765; Best Local Similarity 88.9%; Pred. No. 3.2e+02; Matches 16; Conservative 0; Mismatches 2; Indels 0;
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88.9%; Pred. No. 3.1e+02;
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CURRENT FILING DATE: 2000-10-30
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Patent No. 6504010
GENERAL INFORMATION:
APPLICANT: Wang, Tongtong
APPLICANT: Bangur, Chaitanya S.
                                                                                                   ORGANISM: Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Mycobacterium tuberculosis
COTHER INFORMATION: H37Rv
US-09-103-840A-1
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APPLICANT: FLEISCHWAN, Robert D.
APPLICANT: WHITE, Owen R.
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Bangur, Chaitanya S.
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NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2
LENGTH: 4403765
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Carter, Darrick
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 77.9
Best Local Similarity 88.9
Matches 16; Conservative
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LENGTH: 4411529
                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-103-840A-1/C
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US-09-702-705-1724
                                                                                    TYPE: DNA
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APPLICANT:
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CURRENT APPLICATION NUMBER: US/09/736,457
CURRENT FILING DATE: 2000-12-13
NUMBER OF SEQ ID NOS: 1864
SOFTWARE: FastSEQ for Windows Version 3.0
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                                                                                                                                                                                                                     Length 145;
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                                                                                                                                                                                                                 Score 14.4; DB 3;
Pred. No. 2.8e+02;
0; Mismatches 2;
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SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 1724
LENGTH: 145
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Patent No. 6667154
                                                                                                                  ; NAME/KEY: misc_feature
; LCCATION: (1)...(145)
; OTHER INFORMATION: n = A,T,C or G
US-09-702-705-1724
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; LOCATION: (1/...(145)
; OTHER INFORMATION: n = A,T,C or G
US-09-736-457-1724
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88.2%;
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Bangur, Chaitanya
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fanger, Gary
Vedvick, Tom
Carter, Darrick
                                                                                                                                                                                                             Query Match
Best Local Similarity 88.2%
Matches 15; Conservative
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Vedvick, Tom
Carter, Darrick
Retter, Marc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: misc feature
                                                             TYPE: DNA
ORGANISM: Homo sapiens
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APPLICANT:
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FEATURE:
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APPLICANT: Mannion, Jane
APPLICANT: Fan, Liqun
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.478C12
CURRENT APPLICATION NUMBER: US/09/671,325
CURRENT APPLICATION NUMBER: US/09/671,325
CURRENT APPLICATION NUMBER: US/09/671,325
NUMBER OF SEQ ID NOS: 1825
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 1724
LENGTH: 145
TYPE: DNA
ORGANISM: HOMO sapien8
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APPLICANT: Wang, Tongtong
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Lodes, Michael A.
APPLICANT: Lodes, Michael A.
APPLICANT: Vedrick, Tom
APPLICANT: Vedrick, Tom
APPLICANT: Carter, Darrick
APPLICANT: Amnion, Jane
APPLICANT: Mannion, Jane
APPLICANT: Pan, Liqun
TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.479621
CURRENT FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 1788
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 1724
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US-09-658-824-1724
Sequence 1724, Application US/09658824
; Patent No. 6746846
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LOCATION: (1)...(145)
OTHER INFORMATION: n = A,T,C or G
                                                                                                                                                                                                                                                                                                                                                       ; NAME/KEY: misc_feature
; LOCATION: (1)...(145)
; OTHER INFORMATION: n = A,T,C or G
US-09-671-325-1724
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Matches 15; Conservative
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ORGANISM: Homo sapiens
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GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Homburger et al.

TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster FILLE REPERENCE: File Reference: 7326-034
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 27427
LENGTH: 671
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: MCNADD, Andria
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIACNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.478C18
CURRENT APPLICATION NUMBER: US/10/017,754
CURRENT FILING DATE: 2001-10-29
NUMBER OF SEQ ID NOS: 2004
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 1724
LENGTH: 145
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Patent No. 6833447
GENERAL INFORMATION:
APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
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1 LOCATION: 4, 12, 27, 32, 45, 47, 4

2 CTHER INFORMATION: n = A,T,C or G

US-10-017-754-1724
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                                                                                                                                                              Retter, Marc W.
Marnerakis, Margarita
Carter, Darrick
                                                                                                                                                                                                                                                                                    APPLICANT: Fanger, Gary R. APPLICANT: Vedvick, Thomas S. APPLICANT: Bangur, Chaitanya S. HAPPLICANT: McNabh. Profile
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Wang, Tongtong
Watanabe, Yoshihiro
Johnson, Jeffrey C.
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US-10-017-754-1724
; Sequence 1724, Application US/10017754
; Patent No. 6858204
; GENERAL INPORMATION:

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HYPOTHETICAL:
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U. Stater, Steven C.

TITLE OF INVENTION: Wisgand, Roger C.

TITLE OF INVENTION: Waxococcus xanthus Genome Sequences and Uses Thereof

FILE REFERENCE: 38-10(15649)B

CURRENT APPLICATION NUMBER: US/09/902,540

CURRENT APPLICATION NUMBER: 02/01/0

PRIOR APPLICATION NUMBER: 60/217,883

PRIOR FILING DATE: 2000-07-10

NUMBER: OF SEQ ID NOS: 16825

LENGTH: 1494
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APPLICANT: ROBB, Bruce C.
TITLE OF INVENTION: P. GINGIVALIS NUCLEOTIDES AND USES THEREOF NUMBER OF SEQUENCES: 1120
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
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Pred. No. 3.7e+02;
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PAPLICATION NUMBER: US/09/221,017B
FILING DATE: 23-DEC-1998
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PRICATION NUMBER:
PRICATION NUMBER:
PILING DATE:
PRICA APPLICATION DATA:
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STREET: 755 PAGE MILL ROAD
CITY: Palo Alto
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ELECOMMUNICATION INFORMATION:
TELEPHONE: 650-813-5600
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Best Local Similarity 93.8%;
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-8469
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TYPE: nucleic acid
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     650-494-0792
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OPERATING SYSTEM:
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STATE:
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TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: Patentin Ver. 2.0
LENGTH: 2058
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APPLICANT: Glidman, Barry S.
APPLICANT: Alarer, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Alegand, Roger C.
TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof FILE REFRENCE: 38-10(15849) B
CURRENT PAPLICATION NUMBER: US/09/902,540
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: 60/217,883
PRIOR FILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 16825
SEQ ID NO 891
LENGTH: 6380
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Pred. No. 3.9e+02;
0; Mismatches 1; Indels 0;
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                                                                                                                                                                                Score 14.4; DB 3;
Pred. No. 3.8e+02;
); Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; OTHER INFORMATION: n means any nucleotide US-09-270-767-11790
ANTI-SENSE: UNKNOWN
ORIGINAL SOURCE:
ORGANISM: PORYPHYROMONAS GINGIVALIS
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 11790, Application US/09270767
Patent No. 6703491
GENERAL INFORMATION:
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93.8%;
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93.8%;
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                                                                                          ) NAME/KEY: misc feature
; LOCATION: 1...1660
US-09-221-017B-461
                                                                                                                                                                                Query Match 75.8
Best Local Similarity 93.8
Matches 15; Conservative
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Best Local Similarity 93.8
Matches 15, Conservative
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Best Local Similarity
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Sequence 17056, Application US/09949016

Sequence 17056, Application US/09949016

Batent No. 6812339

GENERAL INFORMATION:
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR PILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FESTESEQ for Windows Version 4.0
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; Sequence 30496, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Duclett, J.Y.
; APPLICANT: Glordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REPERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 1999-02-24
; PRIOR PILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SEQ ID NO 30496
; LENGTH: 403
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; LOCATION: (1)...(331814)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-17056
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US-09-513-999C-30496
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  79048 CCTTAATGCGGCTAAT 79033
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ORGANISM: Homo sapiens
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LOCATION: 371
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                                                                         RESULT 61
US-09-949-016-17056/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID NO 17056
LENGTH: 331814
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US-09-949-016-12008/c

Sequence 12008, Application US/09949016

Patent No. 681239

GENERAL INFORMATION:

TITLE OF INVENTION: POLYMORPHISNS IN KNOWN GENES ASSOCIATED

FILE OF INVENTION NUMBER: 60/241, 755

PRIOR PELLORICATION NUMBER: 60/241, 755

PRIOR PELLOR DATE: 2000-10-03

PRIOR PELLOR DATE: 2000-10-03

PRIOR PELLOR DATE: 2000-10-03

PRIOR PELLOR DATE: 2000-09-08

NUMBER: COMPARE: FEBELSCO FOR WINDOWS VERSION 4.0

SOFTWARE: FEBELSCO FOR WINDOWS VERSION 4.0

SOFTWARE: FEBELSCO FOR WINDOWS VERSION 4.0

LENGTH: 331814
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Parent No. 676291

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: INSECT PS3 TUMOR SUPPRESSOR GENES AND PROTEINS
TITLE OF INVENTION: INSECT PS3 TUMOR SUPPRESSOR GENES AND PROTEINS
FILE REFERENCE: EXO0015C FIRST AMENDMENT
CURRENT APPLICATION NUMBER: US 09/268,969
PRIOR PILING DATE: 12099-03-16
PRIOR APPLICATION NUMBER: US 60/184,373
PRIOR FILING DATE: 2000-02-23
NUMBER OF SEQ ID NOS: 35
SOFTWARE: Patentin version 3.2
SEQ ID NO 18
LENGTH: 27425
  Gaps
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  Mismatches
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; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-12008
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; ORGANISM: Drosophila melanogaster
US-09-524-101D-18
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                                                                                                1168 ccccrcaarccccra 1183
                                                    1 CCCCTGAATGCGGCTA 16
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  15; Conservative
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ORGANISM: Human
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DETECTION AND USES THEREOF

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Sequence 185402, Application US/09949016

Sequence 185402, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION

TITLE OF INVENTION: PUTH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TILLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

CURRENT FILING DATE: 2000-04-14

PRIOR PELLING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/231,768

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR PLILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

SPRIOR FILING DATE: 2000-10-03
Sequence 1823.

Sequence 1812339

GENERAL INFORMATION:

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION A

FILE REFERENCE: CLOO1307, 709/949,016

CURRENT APPLICATION NUMBER: 60/241,755

FRIOR FILING DATE: 2000-04-14

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FastSEQ for Windows Version 4.0

LENGTH: 601
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Pred. No. 4.3e+02;
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Patent No. 6902887
GENERAL INFORMATION:
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84.28;
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Best Local Similarity 84.2%;
Matches 16; Conservative
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Best Local Similarity 84.2
Matches 16; Conservative
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US-09-949-016-185401
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US-09-949-016-185402
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
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                                                                                                                                                      Sequence 185399, Application US/09949016

Fatent No. 681239

GENERAL INFORMATION

GENERAL INFORMATION:

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;

CURRENT APPLICATION NUMBER: 60/241,755

FRIOR APPLICATION NUMBER: 60/21,768

FRIOR FILING DATE: 2000-10-03

FRIOR FILING DATE: 2000-10-03

FRIOR FILING DATE: 2000-10-03

FRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOUTHWARE: FREE SEASESO FOR MINDOWS VERSION 4.0
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US-09-949-016-185400/c

Sequence 185400, Application US/09949016

Patent No. 681239

GENERAL INFORMATION:

APPLICANT: VENTER, J.

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT PILING DATE: 2000-04-14
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84.2%; Pred. No. 4.3e+02;
ive 0; Mismatches 3; Indels
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4.3e+02;
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PRIOR FILING DATE: 2000-10-20
PRIOR PILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR PILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 188400
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Pred. No. 4
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Best Local Similarity 84.2<sup>3</sup>
Matches 16; Conservative
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Best Local Similarity
Matches 16; Conserv
                                                                                                                                      US-09-949-016-185399/c
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; ORGANISM: Human
US-09-949-016-185400
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ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO 185399
LENGTH: 601
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ð ద Length 601;

APPLICANT: Randy M. Berka

RESULT 65

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Gaps

Gaps

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## APPLICANT: Trueheart, Josh
### APPLICANT: Zhang, Lixin
### TITLE OF INVENTION: No. 6806082el Regulators of Fungal Gene Expression
### FILE REFERENCE: MIC-004
### CURRENT APPLICATION WIMBER: US/10/029,180
### FILING APPLICATION NUMBER: US 60/257,431
### PRIOR APPLICATION NUMBER: US 60/257,431
### NUMBER OF SEQ ID NOS: 138
### SOFTWARE: FastSEQ for Windows Version 4.0
### SEQ ID NO 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Schroder, Hartwig
APPLICANT: Schroder, Hartwig
APPLICANT: Schroder, Oskar
APPLICANT: Schroder, Oskar
APPLICANT: APPLICANT: Schroder, Oskar
APPLICANT: APPLICANT: Abberharer, Gerger
APPLICANT: Haberharer, Gerger
TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS
TITLE OF INVENTION: INVOLVED IN HOMEOSTASIS AND ADAPTATION
FILE REFREENCE: BGI-128CP
CURRENT APPLICATION NUMBER: US 60/141031
PRIOR APPLICATION NUMBER: US 60/141031
PRIOR APPLICATION NUMBER: DE 1993125.6
PRIOR FILING DATE: 1999-07-09
PRIOR FILING DATE: 1999-07-04
PRIOR PLING DATE: 1999-07-04
PRIOR FILING DATE: 1999-07-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 1095;
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74.7%; Score 14.2; DB 3;
Best Local Similarity 84.2%; Pred. No. 4.6e+02;
Matches 16; Conservative 0; Mismatches 3;
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PRIOR APPLICATION NUMBER: DE 1993292.2
PRIOR PILING DATE: 1999-07-14
PRIOR PELING DATE: 1999-07-14
PRIOR APPLICATION NUMBER: DE 19932924.9
PRIOR APPLICATION NUMBER: DE 19932928.1
PRIOR PILING DATE: 1999-07-14
PRIOR APPLICATION NUMBER: DE 1993293.8
PRIOR PILING DATE: 1999-07-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-602-777A-393/c; Sequence 393, Application US/09602777A; Sequence 393, Application US/09602777A; Patent No. 6831165; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 418 ccrcrcharacecrcarc 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 CCCCTGAATGCGGCTAATC 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; OTHER INFORMATION: fungal gene
US-10-029-180-61
                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA ORGANISM: Artificial Sequence
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APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PREUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERENCE: 2709.2004001
CURRENT PELLING NATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR APPLICATION NUMBER: US 60/117,747
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 5060
LENGTH: 1020
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 14.2; DB 3; Length 608; Pred. No. 4.3e+02;
                                                                                                                APPLICANT: Jeffrey R. Shuster
APPLICANT: Jeffrey R. Shuster
APPLICANT: Sakari Kauppinen
APPLICANT: Bakari Kauppinen
APPLICANT: Borch Clausen
TITLE OF INVENTION: Methods For Monitoring Multiple Gene
TITLE OF INVENTION: Expression
FILE REPERENCE: S849.200-U3
CURRENT FILING DATE: 2000-03-22
CURRENT FILING DATE: 2000-03-22
NUMBER OF SEQ ID NOS: 7860
SOFTWARE: FastSEQ for Windows Version 4.0
SSQ ID NO 1622
LENGTH: AND 1622
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-489-039A-5060
; Sequence 5060, Application US/09489039A
; Patent No. 6610836
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; Sequence 61, Application US/10029180

; Patent No. 6806082

; GENERAL INFORMATION:
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; OTHER INFORMATION: n = A,T,C or G
US-09-533-559-1622
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 CCCCTGAATGCGGCTAATC 19
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Conservative 0;
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ORGANISM: Klebsiella pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Fusarium venenatum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Cali, Brian M.
APPLICANT: Holtzman, Doug
APPLICANT: Madden, Kevin T.
APPLICANT: Milna, G. Todd
APPLICANT: Sherman, Amir
APPLICANT: Silva, Jeffry C.
                                                                                                    APPLICANT: Michael W. Rey
APPLICANT: Jeffrey R.Shuster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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LOCATION: (1)...(608)
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Matches 16; Conserva
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Best Local Similarity
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Length 3344; Indels

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GENERAL INFORMATION:
APPLICANT: Shylan, Andrew W.
APPLICANT: Shylan, Andrew W.
APPLICANT: Shylan, Andrew W.
APPLICANT: Shylan, Andrew W.
TITLE OF INVENTION: OF PROSTATE CANCER THERAPIES AND THE DIAGNOSIS OF PROSTATE CANCE TILE REFERENCE: 07334-074001
CURRENT APPLICATION NUMBER: US 60/079,303
PRIOR APPLICATION NUMBER: US 60/079,303
PRIOR APPLICATION NUMBER: US 60/079,303
PRIOR APPLICATION NUMBER: US 60/068,821
PRIOR APPLICATION NUMBER: US 60/068,821
PRIOR FILING DATE: 1997-12-24
PRIOR FILING DATE: 1997-12-24
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REPERENCE: CLOO1307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT APPLICATION NUMBER: 05/241,755
PRIOR APPLICATION NUMBER: 60/231,768
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-30
PRIOR FILING DATE: 2000-10-31
PRIOR FILING DATE: 2000-10-39
PRIOR FILING DATE: 2000-09-09
                                                                                                                                                                                                                                                                                                            Score 14.2; DB 2;
Pred. No. 5.3e+02;
0; Mismatches 3;
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Pred. No. 5.3e+02;
0; Mismatches 3;
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SOFTWARE: FastSEQ for Windows Version 4.0
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Patent No. 6812339
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18-09-220-132-73
Sequence 73, Application US/09220132
Patent No. 6506607
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                                                                                                                                                                                                                                                                                                               74.78;
84.28;
                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: CDNA to mRNA
FRATURE:
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74.7%;
Best Local Similarity 84.2%;
Matches 16; Conservative (
                                                   3344 base pairs
                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 84.2
Matches 16; Conservative
                          SEQUENCE CHARACTERISTICS:
INFORMATION FOR SEQ ID NO:
                                                                             nucleic acid
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111..3014
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; ORGANISM: Homo sapiens
US-09-220-132-73
                                                                                                   STRANDEDNESS:
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                                                                                                                                                                                                         NAME/KEY:
LOCATION:
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APPLICANT: Schimmel, Paul R.
APPLICANT: Schimmel, Paul R.
APPLICANT: Schimmel, Paul R.
APPLICANT: Sipmaster, Tracy L.
TITLE OF INVENTION: Human Alanyl-tRNA Synthetase Proteins,
TITLE OF INVENTION: Nucleic Acids and Tester Strains Comprising Same
NUMBER OF SEQUENCES:
ADDRESSES: Bamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
CITY: Lexington
STATE: Massachusetts
COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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Pred. No. 4.7e+02;
0; Mismatches 3; Indels 0
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/426,236
                                     FRIOR AFFLICATION NUMBER: DE 19933002.6

PRIOR APPLICATION NUMBER: DE 19933003.4

PRIOR PILING DATE: 1999-07-14

PRIOR PILING DATE: 1999-07-14

PRIOR FILING DATE: 1999-07-14

PRIOR FILING DATE: 1999-07-14

PRIOR PLILNG DATE: 1999-07-14

PRIOR PLILNG DATE: 1999-07-14

PRIOR APPLICATION NUMBER: DE 1993306.9

PRIOR FILING DATE: 1999-08-31

PRIOR PLILNG DATE: 1999-09-31

NUMBER OF SEQ ID NOS: 442

LENGTH: 1218
                          ON NUMBER: DE 19933002.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Corynebacterium glutamicum
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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CLASSIFICATION: 514
ATCINEY/AGENT INFORMATION:
NAME: Brook, David B.
REGISTRATION NUMBER: 22,592
REFERENCE/DOCKET UNBER: CPI
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 84.2%;
Matches 16; Conservative
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CTHER INFORMATION: RXN00136
US-09-602-777A-393
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: CDS
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US-09-949-016-13284/c

Sequence 13284, Application US/09949016

Sequence 13284, Application US/09949016

Sequence 13284, Application US/09949016

Sequence 13284, Application US/09949016

GENERAL INFORMATION:
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CL001307

CURRENT FILING DATE: 2000-04-14

PRIOR FILING DATE: 2000-10-20

PRIOR PELING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOCTIFTANE: PRESERE FOR Windows Version 4.0

SEQ ID NO 13284

LENGTH: 9962
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 9962;
  Indels
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
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                                          1 CCCCTGAATGCGGCTAATC 19
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Matches 16; Conservative
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  16; Conservative
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Best Local Similarity
Matches 16; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; ORGANISM: Human
US-09-949-016-13284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-949-016-13659
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    Matches
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APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REPERENCE: C1001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT PILLING DATE: 2000-04-14
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                                                                                                      Score 14.2; DB 3; Length 3344; Pred. No. 5.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 74.7%; Score 14.2; DB 3; Length 3505; Best Local Similarity 84.2%; Pred. No. 5.4e+02; Matches 16; Conservative 0; Mismatches 3; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Loring, Jeanne F.
APPLICANT: Tingley, Debora W.
APPLICANT: Tingley, Debora W.
APPLICANT: Edwards, Carla M.
TITLE OF INVENTION: GENES EXPRESSED IN ALZHEIMER'S DISEASE
FILE REFERENCE: PA-0024 US
CURRENT APPLICATION NUMBER: US/09/566,921
CURRENT FILING DATE: 2000-05-05
NUMBER OF SEQ ID NOS: 138
SOFTWARE: PERL Program
                                                                                                                                                 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6682888 263336.12
US-09-566-921-63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: 08/09/949,016

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-3

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SEQ ID NO 16816

LENGTH: 8165

LENGTH: 8165
                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 16816, Application US/09949016 Patent No. 6812339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2847 CCCCAGAATGCAGCCAATC 2865
                                                                                                                                                                                                                              2826 ccccacaarccacccaarc 2844
                                                                                                                                                                                                                                                                                                                                Sequence 63, Application US/09566921
Patent No. 6682888
                                                                                                                                                                                       1 CCCCTGAATGCGGCTAATC 19
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84.28;
                                                                                                      74.78;
84.28;
                                                                                                      Query Match 74.7
Best Local Similarity 84.2
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                     ; TYPE: DNA
; ORGANISM: Human
US-09-949-016-4054
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TYPE: DNA
; ORGANISM: Human
US-09-949-016-16816
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO 63
LENGTH: 3505
  LENGTH: 3344
                                                                                                                                                                                                                                                                                           RESULT 74
US-09-566-921-63
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Gaps

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GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CL001307

CURRENT APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/241,756

PRIOR APPLICATION NUMBER: 60/231,768

PRIOR APPLICATION NUMBER: 60/231,768

PRIOR APPLICATION NUMBER: 60/231,498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 17045, Application US/09949016 Patent No. 6812339
                                                                                                                                                                                                                                                                                                                                                                                            13061 CGCTTGAACGCGGCTAATC 13079
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26300 CTCCTGAATGCTGGTAATC 26282
                                                                                                                                                                 MYCOBACTERIUM LEPRAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             , LOCATION: (1)...(49407)
, OTHER INFORMATION: n = A,T,C or G
US-09-949-016-12532
                                                                                                                                                                                                                                                                                                                                      1 CCCCTGAATGCGGCTAATC 19
                                           TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
                                                                                                                                                                                                                                         Query Match
Best Local Similarity 84.2%;
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 84.2
Matches 16; Conservative
                 double
nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-949-016-12532/c
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                                                                                                                   ANTI-SENSE: NO ORIGINAL SOURCE:
               STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Human
                                                                                                                                                                 ; ORGANISM: N
US-08-311-731A-124
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                                                                                                                                                       APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLOO1307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT APPLICATION NUMBER: 02000-04-14

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-09

PRIOR FILING DATE: 2000-10-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 124, Application US/08311731A
Patent No. 658326
GENERAL INFORMATION:
APPLICANT: SMITH, DOUGLAS
APPLICANT: MAO, JEN-I
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
TITLE OF INVENTION: RELATING TO MYCOBACTERIUM TUBERCULOSIS AND LAPRAE FOR TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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Pred. No. 6.8e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/311,731A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                74.7%; bcc. No. c...
84.2%; Pred. No. c...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: WOLF, GREENFIELD & SACKS, P.C. STREET: 600 ATLANTIC AVENUE CITY: BOSTON STATE: MASSACHUSETTS COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 207012
SOFTWARE PESTSEQ for Windows Version 4.0
SEQ ID NO 12582
LENGTH: 23108
                                                                               Sequence 12582, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: GATES, EDWARD R.
REGISTRATION NUMBER: 31,616
REPREBRICE/POCKET NUMBER: C000
TELECOMMUNICATION:
TELEPHONE: 617/720-3500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 CCCCTGAATGCGGCTAATC 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 84.2
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Human
US-09-949-016-12582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
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Sequence 12532, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:
PATENT NO. 6812339

GENERAL INFORMATION:
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
FILE REPERENCE: CLOOK 1307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT PILING DATE: 2000-04-14

PRIOR PILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOCTWARE: PRESENCE FILING DATE: 2000-09-08

LENGTH: 49407
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Score 14.2; DB 3; Length 36033;
Pred. No. 7.1e+02;
0; Mismatches 3; Indels 0;
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84.2%; Pred. No. 7.4e+02;
tive 0; Mismatches 3;
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US-10-270-878-1
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Patent No. 6812339

GENERAL INFORMATION:

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT PILING DATE: 2000-04-14

PRIOR PILING DATE: 2000-10-22

PRIOR PLILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR PLILING DATE: 2000-10-03

PRIOR PLILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-10-03

NUMBER OF SEQ ID NOS: 207012

SOOFWARE: PERSERE OF WINDOWS VERSION 4.0
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74.7%; Score 14.2; DB 3; Length 49408;
Best Local Similarity 84.2%; Pred. No. 7.4e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 79578;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | GENERAL INFORMATION:
| GENERAL INFORMATION:
| APPLICANT: Sigridur Hjorleifsdotter
| APPLICANT: Gudmundur O. Hreggvidsson
| APPLICANT: Olafur H. Fridjonsson
| APPLICANT: Arnthor Aevarsson
| APPLICANT: Arnthor Aevarsson
| TITLE OF INVENTION: Bacteriophage RM378 of a Thermophilic
| TITLE OF INVENTION: Host Organism
| FILE REFERENCE: 2739.1001-001
| CURRENT APPLICATION NUMBER: US/09/585,858
| CURRENT PLLING DATE: 2000-12-18
| PRIOR FILING DATE: 1999-06-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3; Indels
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84.2%; Pred. No. 7.8e+02;
tive 0; Mismatches 3;
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 17045
LENGTH: 49408
                                                                                                                                                                                                                                                                                                                                                                                                                                                            26300 crccrcaarccrccraarc 26282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              45634 ccccrcaarcrcccraacc 45652
                                                                                                                                                                                                                ; LOCATION: (1)....(49408)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-17045
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 83
US-09-585-858-1
; Sequence 1, Application US/09585858
; Sequence No. 6492161
                                                                                                                                                                                                                                                                                                                                                                                                               1 CCCCTGAATGCGGCTAATC 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 CCCCTGAATGCGGCTAATC 19
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Best Local Similarity 84.2
Matches 16; Conservative
                                                                                                                                                                                          NAME/KEY: misc feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: DNA
; ORGANISM: Human
US-09-949-016-16339
                                                                                                                                               ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-949-016-16339
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LENGTH: 79578
                                                                                                                         TYPE: DNA
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Sequence 16476, Application US/09949016
; Sequence 16476, Application US/09949016
; Retent No. 681239
; GENERAL INFORMATION:
    APPLICANT: VENTER, USTOREN J. Craig et al.
    TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
    TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; TURENT PELLICATION NUMBER: 60/241,755
    PRIOR APPLICATION NUMBER: 60/241,755
    PRIOR APPLICATION NUMBER: 60/231,768
    PRIOR FILING DATE: 2000-10-03
    PRIOR FILING DATE: 2000-10-03
    PRIOR FILING DATE: 2000-00-09-08
; NUMBER OF SEQ ID NOS: 207002
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 16476
; TYPE: DNA
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                                                                                                                                                                                                                        Score 14.2; DB 3; Length 129908; Pred. No. 8.1e+02; 0; Mismatches 3; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Sigridur Hjorleifedotter
APPLICANT: Gudmundur O. Hreggvidsson
APPLICANT: Gudmundur O. Hreggvidsson
APPLICANT: Gudmundur O. Hreggvidsson
APPLICANT: Arnthor Aevarsson
APPLICANT: Jakob K. Kristjansson
TITLE OF INVENTION: Bacteriophage RM378 of a Thermophilic
TITLE OF INVENTION: Bacteriophage RM378 of a Thermophilic
TITLE OF INVENTION: Host Organism
FILE REPRENCE: 2739.1001-001
CURRENT APPLICATION NUMBER: US/10/270,878
CURRENT PILING DATE: 2002-10-11
PRIOR PILING DATE: 2000-12-18
NUMBER OF SEQ ID NOS: 73
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 129908
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PastSEQ for Windows Version 4.0
; SSOT NO 1
; LENGTH: 129908
; TYPE: DNA
; TYPE: DNA
US-09-585-858-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1, Application US/10270878; Patent No. 6818425; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                          1 CCCCTGAATGCGGCTAATC 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TYPE: DNA
; ORGANISM: Bacteriophage RM378
US-10-270-878-1
                                                                                                                                                                                                                           Query Match 74.7%;
Best Local Similarity 84.2%;
Matches 16; Conservative
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Best Local Similarity 84.2%;
Matches 16; Conservative
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TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 13
SEQUENCE CHARACTERISTICS:
LENGTH: 11823 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                       FARCHAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLOO1307
CURRENT FILING DATE: 2000-04-14
FRIOR APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/231,768
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR PLING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FREESEQ FOR WINGOWS VETSION 4.0
SEQ ID NO 15868
LENGTH: 374159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Charles Kunsch

Gil H. Choi

Batrick S. Dillon
Craig A. Rosen
Steven C. Barash
Michael R. Fannon

TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                  ö
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                                                                                                                                           Length 141560;
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84.2%; Pred. No. 8.7e+02;
ive 0; Mismatches 3; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
                                                                                                                                                                              Indels
                                                                                                                                       2; DB 3;
8.2e+02;
                                                                                                                                                                              0; Mismatches
                                                                                                                                         Score 14.2;
Pred. No. 8.
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STREET: 9410 Key West Avenue
CITY: Rockville
                                                                                                                                                                                                                                                                                                                                                        Sequence 15868, Application US/09949016
Patent No. 6812339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 136, Application US/08956171B
Patent No. 6593114
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                          42787 CCCCTAAATGTGGCTCATC 42805
                                  1 CCCCTGAATGCGGCTAATC 19
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                                                                                                                                       74.78;
                                                                                                                                       Query Match
Best Local Similarity 84.2
Matches 16; Conservative
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Matches 16; Conservative
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US-08-956-171E-136/c
ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                        US-09-949-016-15868
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ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-949-016-15868
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GENERAL INFORMATION:
APPLICANT: Charles Kunsch
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
TITLE OF INVENTION: 5255
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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100.0%; Pred. No. 8e+02;
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ZIP. 20850
COMPUTE READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS Version 6.2
                                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/956,171E
FILING DATE: 20-0ct-1997
CLASSIFICATION AUNCHOM:
PRIOR APPLICATION DATA:
APPLICATION UNDHER: 60/009,861
FILING DATE: January 5, 1996
APPLICATION NUMBER: 08/781,986
FILING DATE: January 3, 1997
ATTORNEY/AGENT INFORMATION:
NAME: MARK J. HYMAN
OPERATING SYSTEM: MSDOS version 6.2
                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER: 46,789
REFERENCE/DOCKET NUMBER: PB248P1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 136:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/781,986A
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; Patent No. 6737248
                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (240) 314-1224
                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 11823 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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REGISTRATION NUMBER: 30,446
REFERENCE/DOCKET NUMBER: PBZ
TELECOMMUNICATION:
TELEPHONE: (301) 309-8504
                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (301) 309-84
INFORMATION FOR SEQ ID NO: 136:
SEQUENCE CHARACTERISTICS:
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Matches 14; Conservative
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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Page 3.

**AFLICANT: Homburger et al.

TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster

FILE REFERENCE: File Reference: 7326-094

CURRENT FILING DATE: 1999-03-17

CURRENT FILING DATE: 1999-03-17

NUMBER OF SEQ ID NOS: 62517

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 5089

LENGTH: 506

TYPE: DNA

ORGANITATIONAL OF SEQ ID NOS: 62517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 20311, Application US/09270767

Patent No. 6703491

GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: PatentIN Ver. 2.0
SEQ ID NO 20311
LENGTH: 506
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; Sequence 9, Application US/07998289B
; Patent No. 6027896
; GENERAL INFORMATION:
    APPLICANT: Black, Bruce C
    APPLICANT: Taylor, Martin
    APPLICANT: Heckel, David G
    TITLE OF INVENTION: Method for Monitoring Pesticide
    TITLE OF INVENTION: Resistance
    NUMBER OF SEQUENCES: 40
    CORRESPONDENCES: 40
    CORRESPONDENCES: Darby & Darby PC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 72.6%; Score 13.8; DB 3; Best Local Similarity 88.2%; Pred. No. 6.9e+02; Matches 15; Conservative 0; Mismatches 2;
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ORGANISM: Drosophila melanogaster
US-09-270-767-20371
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US-09-270-767-5089
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805 Third Avenue
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Best Local Similarity 88.2%;
Matches 15; Conservative (
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MEDIUM TYPE: Floppy
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Sequence 23542, Application US/09270767

Sequence 23542, Application US/09270767

Sequence 23542, Application US/09270767

Fatent No. 6703491

GENERAL INFORMATION:

APPLICANT: Homburger et al.

TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster;
FILE REFERENCE: File Reference: 7326-094

CURRENT PILING DATE: 1999-03-17

NUMBER OF SEQ ID NOS: 62517

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 23542

LENGTH: 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: FASCERENCE: 1326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 8260
LENGTH: 300
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100.0%; Pred. No. c.
... 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-23542
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                                                                                                                                                                                                                                                                                                                                              5 TGAATGCGGCTAAT 18
                                                                                                                                                                                                                                                                                                 14; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: doubl
TOPOLOGY: linear
                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
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Best Local Similarity
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US-09-270-767-5089
                                                                                                                                                                                   ; TOPOLOGY: ]
US-08-781-986A-136
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Gaps

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US-09-949-016-25349/C

Sequence 25349, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR PELING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-01-03

PRIOR FILING DATE: 2000-01-03
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Fatent No. 6812339
GENERAL INFORMATION:
TATLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REPRENCE: CLO1307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT PILING DATE: 2000-04-14
FRIOR APPLICATION NUMBER: 60/241,755
FRIOR APPLICATION NUMBER: 60/237,768
FRIOR PILING DATE: 2000-10-03
FRIOR PILING DATE: 2000-10-03
FRIOR PILING DATE: 2000-09-06
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FREESEQ for Windows Version 4.0
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                 Length 567;
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             Score 13.8; DB 3;
Pred. No. 7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; DB 3;
7.1e+02;
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Pred. No. 7.1e+
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     283 CCCTGAATGTGTCTAAT 267
                                                                                                                                                                                                             63 cécrécarécedercar 47
          72.6%;
88.2%;
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Best Local Similarity 88.2°
Matches 15; Conservative
                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15; Conservative
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Best Local Similarity
Matches 15; Conserv
                                         Local Similarity
les 15; Conserv
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US-09-949-016-25349
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US-09-949-016-69732
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          Query Match
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                                                                         Matches
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Pred. No. 7e+02;
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COUNTRY: US

ZIP: 10022

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

CORRATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/998,289B

FILING DATE: 30-DEC-1992

FILING AND AND AND AND AND AND AND APPLICATION: APPLICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Black, Bruce C
APPLICANT: Taylor, Martin
APPLICANT: Hackel, David G
TITLE OF INVENTION: Method for Monitoring Pesticide
TITLE OF INVENTION: Resistance
TUTLE OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
   US/07/998,289B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2, Application US/07998289B Patent No. 6027876
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NAME: Robinson, Joseph R
REGISTRATION NUMBER: 33,448
REFERENCE/DOCKET NUMBER: 0646
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-527-7700
                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Robinson, Joseph R
REGIGTRATION NUMBER: 33,448
REFRENCE/DOCKET NUMBER: 064
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-527-7700
TELEFAX: 212-753-6237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Darby & Darby PC
STREET: 805 Third Avenue
CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-07-998-289B-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           72.6%;
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                                                                                                                                                                                                                                                                                                                                    TELEX: 236687
INFORMATION FOR SEQ ID NO: 9: SEQUENCE CHARACTERISTICS: LENGTH: 521 base pairs TYPE: nucleic acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 567 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 88.2
nes 15; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                  CLASSIFICATION:
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Matches
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NAME: Bent, Stephen A. REGISTRATION NUMBER: 29,768
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Doidge
                                                     JS-09-134-000C-3216/c
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                                                                                                                           Sequence 3264, Application US/09902540

Sequence 3264, Application US/09902540

Patent No. 683347

GENERAL INFORMATION:

APPLICANT: Goldman.

APPLICANT: Goldman.

APPLICANT: Hinkle, Gregory J.

APPLICANT: Hinkle, Gregory J.

APPLICANT: Hinkle, Gregory J.

APPLICANT: Hinkle, Gregory J.

TITLE OF INVENTION: Mycococcus xanthus Genome Sequences and Uses Thereof

FILE REFERENCE: 38-10(15849)B

CURRENT APPLICATION NUMBER: US/09/902,540

CURRENT FILING DATE: 2001-07-10

PRIOR APPLICATION NUMBER: 60/217,883

PRIOR FILING DATE: 2000-07-10

NUMBER OF SEQ ID NOS: 16825

SEQ ID NO 3264
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Pred. No. 7.2e+02;
0; Mismatches 2; Indels (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INCORMATION:

APPLICANT: Randy M. Berka
APPLICANT: Michael W. Rey
APPLICANT: Jeffrey R.Shuster
APPLICANT: Jeffrey R.Shuster
APPLICANT: Jefrey R.Shuster
APPLICANT: Deter Bjarke Olsen
APPLICANT: Deter Bjarke Olsen
TITLE OF INVENTION: Methods For Monitoring Multiple Gene
TITLE OF INVENTION: Expression
FILE REFERENCE: 5849.200-US
CURRENT APPLICATION NUMBER: US/09/533,559
CURRENT APPLICATION NUMBER: US/09/533,623
EARLIER PILING DATE: 1999-03-22
NUMBER OF SEQ ID NOS: 7860
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 98
8-09-533-559-6637/c
; Sequence 6637, Application US/09533559
; Patent No. 6902887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; LOCATION: (1)....(672)
; OTHER INFORMATION: n = A,T,C or G
US-09-533-559-6637
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283 CCCTGAATGTGTCTAAT 267
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Best Local Similarity 88.2%;
Matches 15; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
CRGANISM: Myxococcus xanthus
US-09-902-540-3264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15; Conservative
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Best Local Similarity
Matches 15; Conserv
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Query Match 72.6%; Score 13.8; DB 3; Length 1302; Best Local Similarity 88.2%; Pred. No. 7.8e+02; Matches 15; Conservative 0; Mismatches 2; Indels 0;
REFERENCE/DOCKET NUMBER: 017227/0133
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-5300
TELEFRAX: (202) 672-5309
TELEFRAX: (202) 672-5399
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LERGTH: 1302 base pairs
TYPE: nucleic acid
STRANDEDNESS: Single
TYPE: nucleic acid
STRANDEDNESS: Single
OFFICELE TYPE: CDNA
ORIGINAL SOURCE:
ORGANISM: Helicobacter pylori
IMMEDIATE SOURCE:
CLONE: CLONE G3.8
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                           ; NAME/KEY: CDS
; LOCATION: 1..1299
US-08-945-038-5
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Search completed: March 8, 2006, 21:06:49 Job time : 107.126 secs

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Aeb56875 Human pol Aeb56876 Human pol Aeb56873 Human pol Aeb56861 Human ech Aeb56877 Human ech Aeb56871 Human ech Aeb56872 Human pol Aeb56840 Human cox Aeb56840 Human cox Aeb56878 Human cox	uman uman uman uman uman uman uman uman	Aeb56845 Human cox     Aeb56810 Human cox     Aeb56813 Human cox     Aeb56813 Human cox     Aeb56813 Human cox     Aeb56814 Human cox     Aeb56819 Human cox     Aeb5681 Human cox     Aeb5811 Human cox     Abb12451 Coxeackie     Abx12451 Coxeackie     Abx12453 Coxeackie     Abx12453 Coxeackie     Abx12453 Coxeackie     Abx12453 Coxeackie     Abx12452 Coxeackie	Abx1245/ Coxeackie Abx1245 Coxeackie Adag58726 Polioviru Adg58726 Polioviru Adg58726 Polioviru Adg8173 Coxeackie Aec85173 Coxeackie Aec85173 Coxeackie Adg78718 Polioviru Adg78718 Polioviru Adg78719 Polioviru Adg82873 Human cox Adu47469 Enterovir Adh27479 Polioviru Adg82873 Human cox Adu47469 Enterovir Adh2699 Novel bic Adp74701 Novel bic Adp74701 Novel bic Adp74711 Novel bic Adp74710 Novel bic Adp74710 Novel bic
100.0 237 1.00.0 237 1.00.0 237 1.00.0 237 1.00.0 237 1.00.0 237 1.00.0 237 1.00.0 238 1.00.0 20.0 20.0 20.0 20.0 20.0 20.0 20	100.0 238 1.00.0 238 1	100.0 10	20000000000000000000000000000000000000
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GenCore version 5.1.7  Copyright (c) 1993 - 2006 Biocceleration Ltd  - nucleic search, using sw model  March 9, 2006, 00:06:59; Search time 190.369; (without alignments) 665.178 Million cell	US-10-829-474-1 19 1 ccctgaatgcggctaatc 19 e: IDENTITY NUC Gapop 10.0, Gapext 1.0 4996997 seqs, 3332346308 re of hits satisfying chosen para	Maximu Maximu Maximu Maximu Maximu Maximu Maximu N. Gene 11. gene 23. gene 33. gene 65. gene 65. gene 65. gene 66. gene 67. gene	## SUMMARIES  # SUMMARIES  Query  re Match Length DB ID  19 100.0 27 8 ABL53128   19 100.0 27 13 ABL53128   19 100.0 30 6 ABL53128   19 100.0 30 6 ABL53138   10 100.0 30 6 ABL53138    10 100.0 30 6 ABL53138   10 100.0 30 6 ABL53138   10 10 10 10 10 10 10 10 10 10 10 10 10 1
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19 100.0 7235 12 ADP74713 19 100.0 7392 8 ABX12440 19 100.0 7399 2 AAQ11816 19 100.0 7400 3 AAZ28719 19 100.0 7400 3 AAZ28719 19 100.0 7400 3 AAZ28718 19 100.0 7401 3 AAZ28720 19 100.0 7401 3 AAZ28720 19 100.0 7401 3 AAZ28720 19 100.0 7410 1 AAX201042 19 100.0 7411 2 AAX201042 19 100.0 7411 2 AAX201042 19 100.0 7411 2 AAX201042 19 100.0 7943 8 ACC43138 19 100.0 7943 8 ACC43138 19 100.0 7943 8 ACC43139 19 100.0 10633 12 AD007662 19 100.0 11746 12 AD007662 19 100.0 11746 12 AD007662 19 100.0 11746 12 AAX2091 18 94.7 25 3 AAX27426 18 94.7 25 3 AAX27426 18 94.7 25 4 AAX00301 18 94.7 25 4 AAX00301 19 90.0 1174 91.6 627 14 ABB56864 17.4 91.6 627 14 ABB56864 17.4 91.6 627 10 AD084230 17.4 91.6 627 10 AD84230 17.4 91.6 627 10 AD84231 17.4 91.6 627 10 AD84231 17.4 91.6 627 10 AD81923 17.4 91.6 627 11 AAV71616 17.4 91.6 627 11 AAV71616 17.4 91.6 627 11 AAV71616 17.5 86.3 13 2 AAX42931 16.4 86.3 13.2 AAX43139 15.8 83.2 618 1 AARS6545

Abn79827 Fungal ZB Ac126227 Rice abio Adm02816 Human cDN Adr71086 Human ala Aax39683 Renal can Adb31357 Bicalutam Abx7491 Human cDN Adr24775 Breast ca Acn40037 Tumour-as Acn40037 Tumour-as Adp23085 PRO polyp Ady14359 DNA encod	Adi 5943 Human ala Adi 6165 Human cDN Abi 6246 Human cDN Abi 0246 Drosophil Adi 21026 Drosophil Adi 02573 Drosophil Adi 02573 Drosophil Adi 02573 Human bra Adi 02574 Human tra Adi 0528 Human tra Adi 0529 Human tra Adi 0529 Human tra Adi 0539 Human pro Adi 0534 Human pro Adi 05372 Drosophil Adi 05572 Drosophil Adi 0555 Antaqonis	Abl34510 Human met Abl70539 Chemicall Ad899771 Bisulphit Ad899771 Bisulphit Ad899771 Bisulphit Ad899771 Bisulphit Ad72539 Propionib Acf64535 Propionib Ad72509 Human imm Ad112870 Drosophil Ad72539 Human req Ad33416 Muxine ca Ad213427 Murine ca Ad213427 Murine ca Ad234259 Human can Ad23259 Human GDC Ad497795 Mouse can Ad685340 Human Lmo Ad302861 Mouse Ltp Ad302861 Mouse Ltp Ad302861 Mouse Ltp Ad302861 Mouse Ltp Ad402861 Mouse Ltp	Continuation (2 of Continuation (3 of Continuation (17 o Adz42274 Human min Continuation (4 of Continuation (5 of Abd33460 Murine ca Adz5833 R. marinu Adv99887 Nanchangm Adg97410 Mouse can Ad113904 Osteoarth Add20461 Human sof Abd33364 Murine ca Adz13443 Murine ca Adz5346 Rhuman sof Abd53709 ERM picor Abb662210 Rat seque
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6 ABN79827 11 ACL2627 11 ADM02816 2 AAX3068 2 AAX3068 10 ADB31357 10 ABX74491 13 ADX74491 13 ADX74491 14 ADX74359 14 ADX74359	444 0 44 00 W	ABL34510 6 ABL34510 6 ABL36139 14 AASS9666 8 ACF6435 14 ABL1534 4 AAK72509 12 ADJ2871 13 ABB12550 12 ADJ34556 13 ABB33416 14 ADZ13427 6 AAS17820 10 ADB43323 10 ADB43323 10 ADG6870 10 ADG63340 10 ADG63340 10 ADG63340 10 ADG63340	10 ACR65383.1 10 ACR67367_02 14 ADZ42274_0 14 ADZ42274_0 14 ADZ42274_0 13 ADZ9887 13 ADZ9887 14 ADZ13904 10 ADZ13904 11 ADZ1343 12 ADZ0461 12 ADZ0461 13 ADZ1443 14 ADZ1443 15 AAH6829 2 AAGS0709 2 AAGS0709 14 ABZ6824 6 ABZ6824 6 ABZ6824
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c 458 13.8 72.6 889 460 13.8 72.6 889 461 13.8 72.6 993 c 463 13.8 72.6 993 c 464 13.8 72.6 1053 c 464 13.8 72.6 1053 c 464 13.8 72.6 1053 c 467 13.8 72.6 1103 c 467 13.8 72.6 1103 c 470 13.8 72.6 1103 c 471 13.8 72.6 113 c 472 13.8 72.6 138 d 473 13.8 72.6 138 d 474 13.8 72.6 138 d 474 13.8 72.6 138 d 481 13.8 72.6 138 d 482 13.8 72.6 138 d 481 13.8 72.6 1451 d 491 13.8 72.6 1451 d 491 13.8 72.6 1451 d 492 13.8 72.6 1451 d 494 13.8 72.6 1451 d 494 13.8 72.6 1532 d 495 13.8 72.6 1532 d 496 13.8 72.6 1532 d 497 13.8 72.6 1532 d 498 13.8 72.6 1630	03 tic tic  .us. 605 03; 02; MBI
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14 73.7 647 10 ACF66435 14 73.7 966 8 ACAS59313 14 73.7 1566 10 ACR69131 14 73.7 1512 8 ACA74317 14 73.7 1560 10 ADE58863 14 73.7 1660 10 ADE78855 14 73.7 1660 10 ADE78855 14 73.7 1660 10 ADE78855 14 73.7 10000 10 ACF67367 14 73.7 110000 10 ACF67367 14 73.7 110000 10 ACF67380 15 8 72.6 129 10 ADJ37814 13 8 72.6 129 12 ADJ3602 13.8 72.6 295 3 AAA42360 13.8 72.6 295 3 AAA42360 13.8 72.6 493 10 ADJ37814 13.8 72.6 493 10 ADS59328 13.8 72.6 495 10 ADS59328 13.8 72.6 495 10 ADS59328 13.8 72.6 495 10 ADS59338 13.8 72.6 495 10 ADS593338 13.8 72.6 495 10 ADS593333 13.8 72.6 588 10 ADS39331 13.8 72.6 588 10 A	3.8 72.6 660 13 3.8 72.6 660 13 3.8 72.6 672 13 3.8 72.6 672 14 3.8 72.6 673 4 3.8 72.6 673 4 10.8 72.6 673 14 10.8 72.6 694 10 3.8 72.6 694 10 3.8 72.6 73 4 10.8 72.6 73 10 3.8 7

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The invention provides a method and a kit for detecting and differentiating an enterovirus type 71 (EV71)in a sample. The method involves contacting nucleic acids in the sample with a pair of primers to form an amplification product; contacting the amplification product with at least one synthetic nucleoride sequence fixed on a solid substrate and detecting hybridisation. The present sequence is a probe used to detect and differentiate enterovirus type 71 (EV71) in a sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New kit comprising a pair of oligonucleotide primers for nucleic acid amplification, useful in detecting and differentiating an enterovirus
                                                                                                                                                                                                                                                                                                                                                   pl probe used to detect enterovirus type 71 (EV71) in a sample.
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  Length 27;
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100.0%; Score 19; DB
100.0%; Pred. No. 2;
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                                                                                   CCCCTGAATGCGGCTAATC 19
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(first entry)
                                          Conservative
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Matches 19; Conservative
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Query Match
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Matches 19; Conserv
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25-JUN-2002
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                                                                                                                                                                                            The present invention relates to a method of producing cDNA from one or more biological units, comprising preparing an admixture of the biological units, comprising preparing an admixture of the biological unit and the catabolic enzyme. This involves preparing cDNA from one or more biological units by obtaining at least one biological unit and the catabolic enzyme, preparing an admixture of at a temperature where the catabolic enzyme is active and with reverse transcriptase under conditions to allow reverse transcription. The method is useful for detecting a specific sequence of RNA in a crude cell lysate. The kit is useful for producing cDNA in a biological unit. The present sequence is a PCR primer/probe used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention describes the application of nucleotide primer to detecting enterovirus. The detection method and the reagent kit are disclosed. This sequence represents an enterovirus detection method associated primer
                                                                          Producing cDNA from one or more biological units, useful for detecting a specific sequence of RNA in a cell or tissue sample, comprises preparing an admixture of the biological unit and the catabolic enzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Process, primer and probe for detecting and discriminating enterovirus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 19; DB 10; Length 19; 100.0%; Pred. No. 1.9; tive 0; Mismatches 0; Indels
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                                                                                                                                                            Example 1; Page 41; 46pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CCCCTGAATGCGGCTAATC 19
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                                    WPI; 2003-748084/70.
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Lacroix B,

Renaud P, Armand M,

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The present invention relates to a method for monitoring microbiological quality of an aqueous environmental medium that potentially contains many different microorganisms. A reference set of at least three microorganisms is chosen that, separately or collectively. There microbiological quality. The test medium is treated, then any microorganisms, or their fragments, in the treated medium is contacted with a set of at least three probes for specific identification and multiple determination of selected microorganisms. This determination represents the level of microbiological quality. The method is useful for identifying and quantifying microorganisms in water and provides results that are used to control water purification/production processes. The present sequence is a probe which was used to illustrate the invention. (Updated on 29-AUG-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                   Monitoring microbiological quality of water, useful particularly for controlling water purification, uses oligonucleotide probes to detect at least three representative microbes.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 19; DB 6; Length 30; 100.0%; Pred. No. 2;
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                                                                                                                              Vachon C,
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                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 24; Page 79; 85pp; French.
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06-JUL-2000; 2000FR-00008839.
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Laffaire P;
                                                                                                                           Guillot E,
Laffaire P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (revised)
                                                                                                                                                                                                                     WPI; 2002-148021/19.
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                                                                    (INWR ) BIO MERIEUX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200202811-A2.
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25-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10-JAN-2002
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Armand M,
                                                                                                                              Renaud P,
Armand M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABL53130;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 6
      ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention relates to a method for monitoring microbiological quality of an aqueous environmental medium that potentially contains many different microorganisms. A reference set of at least three microorganisms is chosen that, separately or collectively, represent microorganisms is chosen that, separately or collectively, represent microorganisms, or their fragments, in the treated medium is contacted with a set of at least three probes for specific identification and multiple determination of selected microorganisms. This determination represents the level of microbiological quality. The method is useful for identifying and quantifying microorganisms in water and provides results that are used to control water purification/production processes. The present sequence is a probe which was used to illustrate the invention. (Updated on 29-MUG-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Monitoring microbiological quality of water, useful particularly for controlling water purification, uses oligonucleotide probes to detect at least three representative microbes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Vernet G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 19; DB 6; Length 30; 100.0%; Pred. No. 2; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lacroix B,
Probe, microorganism detection; microbiological quality; water purification; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Probe; microorganism detection; microbiological quality;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 30 BP; 5 A; 12 C; 7 G; 6 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Vachon C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Micro-organism detection probe #70.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mabilat C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 24; Page 80; 85pp; French
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11 cccrigariccecriaric 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CCCCTGAATGCGGCTAATC 19
                                                                                                                                                                                                                                                                                      06-JUL-2001; 2001WO-FR002191.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              06-JUL-2001; 2001WO-FR002191.
                                                                                                                                                                                                                                                                                                                                                    06-JUL-2000; 2000FR-00008839
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100.v.
The 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABL53128 standard; DNA; 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (revised)
(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Guillot E,
Laffaire P;
                                                                                                                                                                                                                                                                                                                                                                                                              (INMR ) BIO MERIEUX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2002-148021/19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human poliovirus 2
                                                                                                 Human echovirus 12
                                                                                                                                                           WO200202811-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200202811-A2
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25-JUN-2002
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RESULT 5

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Vernet G;

Lacroix B,

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21-JUL-2005.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 8
     85888888888888888888
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         요
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                   The present invention relates to a method for monitoring microbiological quality of an aqueous environmental medium that potentially contains many different microorganisms. A reference set of at least three microorganisms is chosen that, separately or collectively, represent microorganisms is chosen that, separately or collectively, represent microorganisms, or their fragments, in the treated medium is contacted with a set of at least three probes for specific identification and multiple determination of selected microorganisms. This determination represents the level of microbiological quality. The method is useful for identifiying and quantifying microorganisms in water and provides results that are used to control water purification/production processes. The present sequence is a probe which was used to illustrate the invention. (Updated on 29-AUG-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This sequence represents a primer used in the method of the invention. The method is for classifying an unclassified live poliovirus type 2 vaccine (attenuated by a G to A substitution at nucleotide position 481) as having an acceptable or unacceptable level of neurovirulence, and comprises, prior to vaccine administration: (a) selectively amplifying a region (I) of the poliovirus genome containing nucleotide position 481 using selectively mismatched primers to introduce a site-specific mutation to create a restriction endonuclease (RE) site which includes
                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Determining acceptability of poliovirus vaccines - based on mutation reversion(s) and comparison to World Health Organisation standard.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PCR primer; vaccine classification; poliovirus type 2 vaccine; attenuated poliovirus vaccine; neurovirulence; ss.
                                                                                                                                                                                                                                                                                                                                                                          Score 19; DB 6; Length 30; Pred. No. 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Poliovirus DNA primer 438 used in method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chumakov KM, Levenbook IS, Norwood LP;
                                                                                                                                                                                                                                                                                                                                       Sequence 30 BP; 6 A; 12 C; 6 G; 6 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       USSH ) US DEPT HEALTH & HUMAN SERVICES
least three representative microbes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example; Col 23-24; 38pp; English
                                    Claim 24; Page 79; 85pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 CCCCTGAATGCGGCTAATC 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6 ccccrcaarcccccraarc 24
                                                                                                                                                                                                                                                                                                                                                                            100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAV23434 standard; DNA; 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1998-270433/24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-DEC-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18-MAY-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 06-NOV-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            08-JUL-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US5728519-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17-MAR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Poliovirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAV23434;
                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAV23434/c
                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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nucleotide position 481, (b) digesting an amount of (I) with a RE that specifically cleaves the amplified sequences in revertant viruses which contain an A to G reversion at nucleotide position 481; (c) digesting an amount of (I) with a RE that specifically cleaves the amplified sequences in non-revertant viruses which contain an A at nucleotide position 481; (d) quantifying the percentage of revertant viruses in the unclassified vaccine to the percentage of revertant viruses in the unclassified vaccine to the percentage of revertant viruses in an accepted reference vaccine which can pass the monkey neurovirulence test utilised by the World Health Organisation, an unclassified vaccine with a
                                                                                                                                                                                                                                                                                                                                                                                                          higher percentage of A to G revertant viruses than in the reference vaccine being classified as unacceptable and an unclassified vaccine with an equal or lower percentage of A to G revertant viruses than in the reference vaccine classified as acceptable. The test can also be used to identify cells that are suitable for the culture of attenuated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            selected amplification or detection reaction. Also described: (1) a kit (K1) comprising (1), and one or more container that contains (1); and (2) detecting (M1) an enterovirus target sequence, involving: (a) amplifying the target sequence using first amplification primer having a sequence consisting essentially of target binding sequence of any one of AEB56764 to AEB56771 and optionally a sequence required for selected amplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to an oligonuclectide (I) consisting of: (a) the target binding sequence of an oligonuclectide chosen from any one of the 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for selected amplification or detection reaction. Also described: (1) a kit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             comprising sequences for binding and amplifying or ful for detecting enterovirus nucleic acids.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 19; DB 2; Length 35;
Pred. No. 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 35 BP; 8 A; 8 C; 12 G; 7 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA detection; enteroviral detection; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure, Fig 1A-D; 34pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 CCCCTGAATGCGGCTAATC 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16-JAN-2004; 2004US-00760048
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AEB56836 standard; DNA; 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22-SEP-2005 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       detecting target, useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human coxsackievirus B2
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(PRIC/) PRICE J A.
(HELL/) HELLYER T J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2005-512251/52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 19; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US2005158710-A1.
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Length 173;

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The invention relates to an oligonucleotide (I) consisting of: (a) the target binding sequence of an oligonucleotide chosen from any one of the consequence of ARBS6752 to ARBS6771; and (b) a sequence required for selected amplification or detection. Also described: (1) a kit (XI) comprising (I), and one or more container that contains (I); and (2) detecting (MI) an enterovirus target sequence, involving: (a) amplifying the target sequence using first amplification primer having a sequence consisting essentially of target binding sequence of any one of ARBS6764 consisting essentially of target binding sequence of any one of ARBS6764 consisting absentially a sequence required for selected amplification reaction, and (b) detecting the amplified target sequence. (I) (MI) and (XI) are useful for detecting enterovirus target sequence. (I) specifically and selectively recognizes the enterovirus genome. (I) specifically and rapidly detects fewer than 500 copies of enteroviral genome and allows detection of broad range of enterovirus serotypes. The present sequence represents a viral 5' untranslated polynocleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel oligonucleotide comprising sequences for binding and amplifying or detecting target, useful for detecting enterovirus nucleic acids.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequence given in the exemplification of the present invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human echovirus 5 5' untranslated polynucleotide sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 173 BP; 36 A; 45 C; 45 G; 47 T; 0 U; 0 Other;
                          100.0%; Score 19; DB 14; 100.0%; Pred. No. 2.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA detection; enteroviral detection; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure, Fig 1A-D; 34pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hellyer TJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 CCCCTGAATGCGGCTAATC 19
                                                                                                                                                                CCCCTGAATGCGGCTAATC 65
                                                                                                                                  1 CCCCTGAATGCGGCTAATC 19
                                                                                                                                                                                                                                                                                                                AEB56855 standard; DNA; 173 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16-JAN-2004; 2004US-00760048,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16-JAN-2004; 2004US-00760048
                                                                                                                                                                                                                                                                                                                                                                                                                      22-SEP-2005 (first entry)
                                                                             19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (TSAN/) TSANG S.
(PRIC/) PRICE J A.
(HELL/) HELLYER T J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Price JA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2005-512251/52.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human echovirus 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENBANK; AF188358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US2005158710-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21-JUL-2005
                                                                                                                                                                                                                                                                                                                                                                   AEB56855;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Isang S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   47
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                                                                                                                                                                                                                                                             RESULT 10
AEB56855
ID AEB56
                                                                             Matches
                                                                                                                                                                                                                                                                                                                                           셤
                                                                                                                                                                                   셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to an oligonucleotide (I) consisting of: (a) the target binding sequence of an oligonucleotide chosen from any one of the 10 sequence of AEBS67762 to AEBS6771; and (b) a sequence required for selected amplification or detection reaction. Also described: (I) a kit (KI) comprising (I), and one or more container that contains (I); and (2) detecting (MI) an enterovirus target sequence, involving: (a) amplifying the target sequence using first amplification primer having a sequence consisting essentially of target binding sequence of any one of AEBS6764 to AEBS6771 and optionally a sequence required for selected amplification reaction; and (b) detecting the amplified target sequence. (I), (MI) and (KI) are useful for detecting thereovirus target sequence. (I), (MI) and specifically and selectively recognizes the enterovirus genome. (I)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The
     and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel oligonucleotide comprising sequences for binding and amplifying or detecting target, useful for detecting enterovirus nucleic acids.
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reaction; and (b) detecting the amplified target sequence. (I), (M1) (X1) are useful for detecting enterovirus target sequences. (I) sepecifically and selectively recognizes the enterovirus genome. (I) sensitively and rapidly detects fewer than 500 copies of enteroviral genome and allows detection of broad range of enterovirus serotypes. Present sequence represents a viral 5' untranabated polyuncleotide equence given in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                             100.0%; Score 19; DB 14; Length 119; 100.0%; Pred. No. 2.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human echovirus 5 5' untranslated polynucleotide sequence.
                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                             Sequence 119 BP; 26 A; 28 C; 36 G; 29 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 173 BP; 36 A; 44 C; 45 G; 48 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA detection; enteroviral detection; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Fig 1A-D; 34pp; English.
                                                                                                                                                                                                                                                                                                                                                                   1 CCCCTGAATGCGGCTAATC 19
                                                                                                                                                                                                                                                                                                                                                                                                                      47 CCCCTGAATGCGGCTAATC 65
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AEB56856 standard; DNA; 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (TSAN/) TSANG S.
(PRIC/) PRICE J A.
(HELL/) HELLYER T J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tsang S, Price JA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2005-512251/52
                                                                                                                                                                                                                                                                                Local Similarity
nes 19; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human echovirus 5.
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RESULT 9
ARBS 6856
ARBS 68

AEB56856;

Query Match

8×3333333333

Matches

g

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Gaps

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Indels

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This sequence represents domains V-VI of the internal ribosomal entry size (IRES) of PVI (prr), a recombinant, non-pathogenic oncolytic policyirus that carries the IRES of Policyirus type 1 Mahoney where the terminal loop of regions of domain V and domain VI are substituted with the corresponding fragments of human rhinovirus type 2 (HRV2). PVI (prr) was characterized by a loss of neuropathogenicity, demonstrated by its reduced ability to propagate within cells of neuronal origin and failure to cause neurological disease in Cd155 tymice. Oncolytic potential was chample of novel recombinant policyiruses (I) of the invention in which the IRES of wild-type policyirus is exchanged with the IRES of another region is exchanged with that of Sabin policyirus. (I) are useful for region is exchanged with that of Sabin policyirus. (I) are useful for treathing malignant tumors such as glioblastom multiforme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hepatocellular, bronchial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chimeric recombinant poliovirus useful for treating malignant tumors comprises internal ribosomal entry site derived from picornaviruses.
                                                                                                                                                               Internal ribosomal entry site; IRBS; picornavirus; PVI(prr); tumour; cancer; glioblastoma multiforme; medulloblastoma; mammary carcinoma; prostate carcinoma; colorectal carcinoma; hepatocellular carcinoma; bronchial carcinoma; epidermoid carcinoma; cytostatic; therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              epidermoid carcinomas (claimed). (Updated on 15-SEP-2003 to
                                                                                                                              Recombinant poliovirus PV1(prr) IRES domain V-VI region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 176 BP; 42 A; 43 C; 40 G; 0 T; 51 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               colorectal,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     UYNY ) UNIV NEW YORK STATE RES FOUND.
                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           prostate,
                                                                                                                                                                                                                                                                                                                                                                                                                                                  'note= "domain VI"
                                                                                                                                                                                                                                                                                                                                                                         /*tag= a
/note= "domain V"
138. .176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 6; Fig 7; 99pp; English
AAZ58488 standard; RNA; 176 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99WO-US007839
                                                                                                                                                                                                                                                           Human poliovirus 1.
Human rhinovirus sp; type 2.
                                                                       (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         medulloblastoma, mammary,
                                                                                                                                                                                                                                                                                                                                                        .109
                                                                                                                                                                                                                                                                                                                                                                                                                                   /*tag=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               standardise OS field)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200008166-A1.
                                                                         15-SEP-2003
23-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              09-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  05-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gromeier M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17-FEB-2000
                                                                                                                                                                                                                                                                                                                                                        stem_loop
                                      AAZ58488;
                                                                                                                                                                                                                                                                                                                                                                                                              stem_loop
                                                                                                                                                                                                                                                                                                    Chimeric
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The invention relates to an oligonucleotide (1) consisting of: (a) the target binding sequence of an oligonucleotide chosen from any one of the sequence of ABBS6772 to ABBS6771; and (b) a sequence required for selected amplification or detection reaction. Also described: (1) and (2) selected amplification or detection reaction. Also described: (1); and (2) detecting (M1) an enterovirus target sequence, involving: (a) amplifying the target sequence using first amplification primer having a sequence consisting essentially of target binding sequence of any one of ABBS6764 to ABBS6771 and optionally a sequence required for selected amplification reaction; and (b) detecting the amplified target sequence. (1), (M1) and (M1) are useful for detecting enterovirus target sequence. (1), specifically and selectively recognizes the enterovirus genome. (1) specifically and selectively recognizes the enterovirus genome. (1) sensitively and rapidly detects fewer than 500 copies of enteroviral control of proad range of enterovirus sericipes. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel oligonucleotide comprising sequences for binding and amplifying or detecting target, useful for detecting enterovirus nucleic acids.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             untranslated polynucleotide
                                                                                                                                                                                                                           Human coxsackievirus B1 5' untranslated polynucleotide sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         present sequence represents a viral 5' untranslated polynucleot sequence given in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 19; DB 14; Length 180; Pred. No. 2.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 180 BP; 37 A; 48 C; 47 G; 48 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                  DNA detection; enteroviral detection; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Fig 1A-D; 34pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hellyer TJ;
||||:|||:|||:|||:||:||:||cccugaaugegegeuaaug
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                                                                                                                  AEB56834 standard; DNA; 180 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                  16-JAN-2004; 2004US-00760048.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       16-JAN-2004; 2004US-0076004B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.08;
                                                                                                                                                                                      22-SEP-2005 (first entry)
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                                                                                                                                                                                                                                                                                                       Human coxsackievirus B1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (TSAN/) TSANG S.
(PRIC/) PRICE J A.
(HELL/) HELLYER T J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tsang S, Price JA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2005-512251/52.
GENBANK; 876767.
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                                                                                                                                                   AEB56834;
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                                                                                             AEB56834
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Gaps

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Indels

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4; Mismatches

Score 19; DB 3; Length 176; Pred. No. 2.5;

100.0%; 78.9%; F

Query Match Best Local Similarity 78.99 Matches 15; Conservative

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CCCCTGAATGCGGCTAATC 19

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The invention relates to an oligomucleotide (I) consisting of: (a) the target binding sequence of an oligomucleotide chosen from any one of the target binding sequence of ABBS6771; and (b) a sequence required for 10 sequence amplification or detection reaction. Also described: (1) a kit (KI) comprising (I), and one or more container that contains (I); and (2) detecting (MI) an enterovirus target sequence, involving: (a) amplifying the target sequence using first amplification primer having a sequence consisting essentially of target binding sequence of any one of ABBS6764 to ABBS6771 and optionally a sequence required for selected amplification reaction; and (b) detecting the amplified target sequence. (I), (MI) and (KI) are useful for detecting enterovirus target sequence. (I) specifically and selectively recognizes the enterovirus genome. (I) sensitively and rapidly detects fewer than 500 copies of enteroviral senome and allows detection of broad range of enterovirus serotypes. The present sequence represents a viral 5 untranslated polymucleotide sequence given in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                          Novel oligonucleotide comprising sequences for binding and amplifying or detecting target, useful for detecting enterovirus nucleic acids.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 19; DB 14; Length 198; 100.0%; Pred. No. 2.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human echovirus 9 5' untranslated polynucleotide sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 198 BP; 42 A; 53 C; 51 G; 52 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Prec. ....ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA detection; enteroviral detection; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Fig 1A-D; 34pp; English.
                                                                                                                                                                                                                                                                                        reang S, Price JA, Hellyer TJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 CCCCTGAATGCGGCTAATC 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CCCCTGAATGCGGCTAATC 25
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                                                                                           16-JAN-2004; 2004US-00760048.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16-JAN-2004; 2004US-00760048.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity 100.
nes 19; Conservative
                                                                                                                                                                                       (TSAN/) TSANG S.
(PRIC/) PRICE J A.
(HELL/) HELLYBR T J.
                                                                                                                                                                                                                                                                                                                                     WPI; 2005-512251/52.
GENBANK; U11707.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (TSAN/) TSANG S.
US2005158710-A1
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                                               21-JUL-2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AEB56860;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to an oligonucleotide (I) consisting of: (a) the target binding sequence of an oligonucleotide chosen from any one of the 10 sequence of ABB56762 to ABB56771; and (b) a sequence required for selected amplification or detection. Also described: (I) a kit (KI) comprising (I), and one or more container that contains (I); and (2) detecting (MI) an enterovirus target sequence, involving: (a) amplifying the target sequence using first amplification primer having a sequence consisting essentially of target binding sequence of any one of ABB56764 to ABB56771 and optionally a sequence required for selected amplification reaction; and (b) detecting the amplified target sequence. (I), (MI) and (KI) are useful for detecting the amplified target sequences. (I) specifically and selectively recognizes the enterovirus genome. (I) specifically and rapidly detects fewer than 500 copies of enteroviral genome and allows detection of broad range of enterovirus serotypes. The present sequence represents a viral 5, untranslated polynucleotide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel oligonucleotide comprising sequences for binding and amplifying or detecting target, useful for detecting enterovirus nucleic acids.
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                                                                     Human echovirus 12 5' untranslated polynucleotide sequence.
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                                                                                                                  DNA detection; enteroviral detection; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA detection; enteroviral detection; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Fig 1A-D; 34pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hellyer TJ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 CCCCTGAATGCGGCTAATC 19
                                                                                                                                                                                                                                                                                                               16-JAN-2004; 2004US-00760048
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                      (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 100.
Best Local Similarity 100.
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                        (TSAN/) TSANG S.
(PRIC/) PRICE J A.
(HELL/) HELLYER T J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tsang S, Price JA,
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GENBANK; U11706.
                                                                                                                                                                 Human echovirus 12
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                   22-SEP-2005
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RESULT 14

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detecting target, useful for detecting enterovirus nucleic acids.
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(PRIC/) PRICE J A. (HELL/) HELLYER T J.
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                                                                                                                                                                                                                                                                                                                                                                                                                            19;
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                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to an oligonucleotide (1) consisting of: (a) the target binding sequence of an oligonucleotide chosen from any one of the consisting dequence of ABBS6712 to ABBS6712 and (b) a sequence required for selected amplification or detection reaction. Also described: (1) a kit (K1) comprising (1), and one or more container that contains (1); and (2) detecting (M1) an enterovirus target sequence, involving: (a) amplifying the target sequence using first amplification primer having a sequence consisting essentially of target binding sequence of any one of ABBS674 to ABBS671 and optionally a sequence required for selected amplification reaction; and (b) detecting the amplified target sequence. (1), (M1) and (K1) are useful for detecting the amplified target sequence. (1) specifically and selectively recognizes the enterovirus genome. (1) specifically and rapidly detects fewer than 500 copies of enteroviral genome and allows detection of broad range of enterovirus serotypes. The present sequence represents a viral 5' untranslated polynucleotide
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                                                                                                                                   Novel oligonucleotide comprising sequences for binding and amplifying or detecting target, useful for detecting enterovirus nucleic acids.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sequence given in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 19; DB 14; Length 198;
Pred. No. 2.5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 198 BP; 39 A; 49 C; 52 G; 58 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA detection; enteroviral detection; ds.
                                                                                                                                                                                  Disclosure; Fig 1A-D; 34pp; English.
                                                   Hellyer TJ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 CCCCTGAATGCGGCTAATC 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CCCCTGAATGCGGCTAATC 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.
Matches 19; Conservative
 PRICE J A.
HELLYER T J.
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(PRIC/) PRICE J A.
(HELL/) HELLYBR T J.
                                                   Price JA,
                                                                                    WPI; 2005-512251/52
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2005-512251/52.
GENBANK; U11708.
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                                                                                                    GENBANK; U11710
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                                                   Tsang S,
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(PRIC/)
(HELL/)
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The invention relates to an oligonucleotide (1) consisting of: (a) the target binding sequence of an oligonucleotide chosen from any one of the 10 sequence of ABBS6771; and (b) a sequence required for selected amplification or detection reaction. Also described: (1) a kit (K1) comprising (1), and one or more container that contains (1); and (2) detecting (M1) an enterovirus target sequence, involving: (a) amplifying the target sequence using first amplification primer having a sequence consisting essentially of target binding sequence of any one of ABBS676 to ABBS6771 and optionally a sequence required for selected amplification reaction; and (b) detecting the amplified target sequence. (1) (M1) and (M1) are useful for detecting enterovirus target sequences. (1) specifically and selectively recognizes the enterovirus genome. (1) specifically and rapidly detects fewer than 500 copies of enteroviral genome and allows detection of broad range of enterovirus serotypes. The present sequence represents a viral 5 untranslated polymucleotide sequence given in the exemplification of the present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 198 BP; 43 A; 48 C; 50 G; 57 T; 0 U; 0 Other;
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Disclosure; Fig 1A-D; 34pp; English.
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            the target sequence using first amplification primer having a sequence consisting essentially of target binding sequence of any one of AEB56764 to ABB6771 and optionally a sequence required for selected amplification reaction; and (b) detecting the amplified target sequence. (I), (MI) and (KI) are useful for detecting enterovirus target sequence. (I) sensitively and selectively recognizes the enterovirus genome. (I) sensitively and rapidly detects fewer than 500 copies of enteroviral genome and allows detection of broad range of enterovirus serotypes. The present sequence represents a viral 5' untranslated polynucleotide.
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(a) amplifying
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel oligonucleotide comprising sequences for binding and amplifying or detecting target, useful for detecting enterovirus nucleic acids.
                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                            sequence given in the exemplification of the present invention
                                                                                                                                                                                                                                                                         100.0%; Score 19; DB 14; Length 237; 100.0%; Pred. No. 2.6;
  an enterovirus target sequence, involving:
                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                  Sequence 237 BP; 46 A; 54 C; 66 G; 71 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA detection; enteroviral detection; ds.
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                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100.0
....hes 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
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(PRIC/) PRICE J A.
(HELL/) HELLYER T J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tsang S, Price JA,
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The invention relates to an oligomucleotide (I) consisting of: (a) the target binding sequence of an oligomucleotide chosen from any one of the carget binding sequence of ABB56771; and (b) a sequence required for selected amplification or detection reaction. Also described: (I) a kit (KI) comprising (I), and one or more container that contains (I); and (2) detecting (MI) an enterovirus target sequence, involving: (a) amplifying the target sequence using first amplification primer having a sequence consisting essentially of target binding sequence of any one of ABB56764 to ABB56771 and optionally a sequence required for selected amplification reaction; and (b) detecting the amplified target sequence. (I), (MI) and (KI) are useful for detecting enterovirus target sequence. (I) specifically and selectively recognizes the enterovirus genome. (I) sensitively and rapidly detects fewer than 500 copies of enteroviral senome and allows detection of broad range of enterovirus serotypes. The present sequence represents a viral 5' untranslated polymucleotide sequence given in the exemplification of the present invention.
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present sequence represents a viral 5' untranslated polynucleotide sequence given in the exemplification of the present invention.
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                                                                                          Score 19; DB 14; Length 237; Pred. No. 2.6;
                                                                                                                                                                                                                                                                                                                                                                                                           Human poliovirus 3 5' untranslated polynucleotide sequence.
                                                                                                                              0; Indels
                                                       Seguence 237 BP; 48 A; 52 C; 66 G; 71 T; 0 U; 0 Other;
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                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA detection; enteroviral detection; ds.
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                                                                                                                                                                   1 CCCCTGAATGCGGCTAATC 19
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                                                                                                                                                                                                                                                                                                  AEB56879 standard; DNA; 237 BP.
                                                                                          100.0%;
                                                                                                                                                                                        CCCCTGAATGCGGCTAATC
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                                                                                                                              Matches 19; Conservative
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(PRIC/) PRICE J A.
(HELL/) HELLYER T J.
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                                                                                                             Local Similarity
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Matches
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AEB56879
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AEB56875;

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target binding sequence of an oligonucleotide chosen from any one of the 10 sequence of ABB56762 to ABB56771; and (b) a sequence required for selected amplification or detection reaction. Also described: (l) a kit (K1) comprising (l), and one or more container that contains (l); and (2) detecting (M1) an enterovirus target sequence, involving: (a) amplifying the target sequence using first amplification primer having a sequence consisting essentially of target binding sequence of any one of ABB56764
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           invention relates to an oligonucleotide (I) consisting of: (a) the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 specifically and selectively recognizes the enterovirus genome. (I) sensitively and rapidly detects fewer than 500 copies of enteroviral genome and allows detection of broad range of enterovirus serotypes.
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                                                                                                     Human poliovirus 1 5' untranslated polynucleotide sequence
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                                                                                                                                                     DNA detection; enteroviral detection; ds
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hellyer TJ;
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                                                     22-SEP-2005 (first entry)
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                                                                                                                                                                                                   Human poliovirus 1.
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les 19; Conserv
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       AEB56876;
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                                                                                                                                                                                                                                                                                                                   Human poliovirus 1 5' untranslated polynucleotide sequence.
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100.0%; Pred. No. 2.6;
Live 0; Mismatches
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                           47 CCCTGAATGCGGCTAATC 65
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1 CCCCTGAATGCGGCTAATC 19
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                                                                                                                                                                    AEB56875 standard; DNA; 237 BP.
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Best Local Similarity 100.
Matches 19; Conservative
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(PRIC/) PRICE J A.
(HELL/) HELLYER T J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2005-512251/52
                                                                                                                                                                                                                                                                                                                                                                                                                 Human poliovirus 1
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Isang S,

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Human poliovirus 1.

AEB56876 standard; DNA; 237 BP.

RESULT 21 AEB56876 ID AEB5 XX

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The invention relates to an oligonucleotide (1) consisting of: (a) the target binding sequence of an oligonucleotide chosen from any one of the 10 sequence of ABBS6771; and (b) a sequence required for selected amplification or detection reaction. Also described: (1) a kit (K1) comprising (1), and one or more container that contains (1); and (2) detecting (M1) an enterovirus target sequence, involving: (a) amplifying the target sequence using first amplification primer having a sequence consisting essentially of target binding sequence of any one of ABBS6764 to ABBS6771 and optionally a sequence required for selected amplification reaction; and (b) detecting the amplified target sequence. (1) (M1) and (K1) are useful for detecting enterovirus target sequence. (1) specifically and rapidly detects fewer than 500 copies of enteroviral senone and allows detection of broad range of enterovirus serotypes. The present sequence represents a viral 5' untranslated polymucleotide sequence given in the exemplification of the present invention.
                                                                                                                                                                                                     Novel oligonucleotide comprising sequences for binding and amplifying or detecting target, useful for detecting enterovirus nucleic acids.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 19; DB 14; Length 237; Pred. No. 2.6;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 237 BP; 48 A; 54 C; 65 G; 70 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                       Disclosure; Fig 1A-D; 34pp; English.
                                                                                           Hellyer TJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Price JA, Hellyer TJ;
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TSANG S.
PRICE J A.
HELLYER T J.
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(PRIC/) PRICE J A.
(HELL/) HELLYER T J.
                                                                                           Price JA,
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GENBANK; AF083069.
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Best Local Similarity
Matches 19; Conserv
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                       (PRIC/)
(HELL/)
  (TSAN/)
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                                                                                                                                                                                                                                                                                                                                                                                                               Novel oligonucleotide comprising sequences for binding and amplifying or detecting target, useful for detecting enterovirus nucleic acids.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human echovirus 9 5' untranslated polynucleotide sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Fig 1A-D; 34pp; English.
                                                                                                                                                                                                                                                                                                 Hellyer TJ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AEB56861 standard; DNA; 237 BP
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Matches 19; Conservative 0
                                                                                                                                                           16-JAN-2004; 2004US-00760048
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                                                                                                                                                                                                                                                                                                                                                                                                           Novel oligonucleotide
                                                                                                                                                                                                     (TSAN/) TSANG S.
(PRIC/) PRICE J A.
(HELL/) HELLYER T J.
                                                                                                                                                                                                                                                                                                 Isang S, Price JA,
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                                                                    21-JUL-2005
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RESULT 23

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                                                                                              The invention relates to an oligonucleotide (I) consisting of: (a) the target binding sequence of an oligonucleotide chosen from any one of the 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for selected amplification or detection. Also described: (I) a kit (KI) comprising (I), and one or more container that contains (I); and (2) detecting (MI) an enterovirus target sequence, involving: (a) amplifying the target sequence using fitst amplification primer having a sequence consisting essentially of target binding sequence of any one of AEB56764 to AEB56771 and optionally a sequence required for selected amplification reaction; and (b) detecting the amplified target sequence. (I), (MI) and (MI) are useful for detecting enterovirus target sequences. (I), (MI) and (MI) are useful for detecting enterovirus target sequences.
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Novel oligonucleotide comprising sequences for binding and amplifying or detecting target, useful for detecting enterovirus nucleic acids.
                                                                                                                                                                                                                                                                                                                                                                     E broad range of enterovirus serotypes. The viral 5' untranslated polynucleotide
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                                                                                                                                                                                                                                                                                                                           specifically and selectively recognizes the enterovirus genome. (I) sensitively and rapidly detects fewer than 500 copies of enteroviral genome and allows detection of broad range of enterovirus serotypes.
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                                                                                                                                                                                                                                                                                                                                                                                                           sequence given in the exemplification of the present invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Score 19; DB 14; Length 237; Pred. No. 2.6; 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 237 BP; 49 A; 59 C; 63 G; 66 T; 0 U; 0 Other;
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                                                               Disclosure, Fig 1A-D; 34pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 CCCCTGAATGCGGCTAATC 19
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                                                                                                                                                                                                                                                                                                                                                                                        present sequence represents a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 19; Conservative 0
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(PRIC/) PRICE J A.
(HELL/) HELLYER T J.
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GENBANK; D00820.
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                                                                       to AEB56771 and optionally a sequence required for selected amplification reaction; and (b) detecting the amplified target sequence. (I), (MI) and (KI) are useful for detecting enterovirus target sequences. (I)
               detecting (M1) an enterovirus target sequence, involving: (a) amplifying the target sequence using first amplification primer having a sequence consisting essentially of target binding sequence of any one of ABB56764
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel oligonucleotide comprising sequences for binding and amplifying or detecting target, useful for detecting enterovirus nucleic acids.
 comprising (I), and one or more container that contains (I); and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to an oligonucleotide (I) consisting of: (a) the
                                                                                                                             specifically and selectively recognizes the enterovirus genome. (I) sensitively and rapidly detects fewer than 500 copies of enteroviral genome and allows detection of broad range of enterovirus serotypes, present sequence represents a viral 5' untranslated polynucleotide
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                                                                                                                                                                                                             sequence given in the exemplification of the present invention
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                                                                                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                                                                                       Score 19; DB 14; Length
Pred. No. 2.6;
                                                                                                                                                                                                                                                 Sequence 237 BP; 54 A; 52 C; 60 G; 71 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA detection; enteroviral detection; ds
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Best Local Similarity 100.0
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(PRIC/) PRICE J A.
(HELL/) HELLYER T J.
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AEB56850
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     target binding sequence of an oligomucleotide chosen from any one of the target binding sequence of an oligomucleotide chosen from any one of the 10 sequence of ABB5672 to ABB6771; and (b) a sequence required for selected amplification or detection reaction. Also described: (1) a kit (KI) comprising (II), and one or more container that contains (I); and (2) detecting (MI) an enterovirus target sequence, involving: (a) amplifying the target sequence using first amplification primer having a sequence consisting essentially of target binding sequence of any one of ABB5674 to ABB56771 and optionally a sequence required for selected amplification reaction, and (b) detecting the amplified target sequence. (1), (MI) and (KI) are useful for detecting enterovirus target sequences. (1) specifically and selectively recognizes the enterovirus genome. (1) sensitively and rapidly detects fewer than 500 copies of enteroviral sensitively and allows detection of broad range of enterovirus serotypes. The present sequence represents a viral 5° untranslated polymucleotide sequence given in the exemplification of the present invention.
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genome and allows detection of broad range of enterovirus serotypes. The
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                                                                                                                 Gaps
             present sequence represents a viral 5' untranslated polynucleotide sequence given in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                  Human coxsackievirus B3 5' untranslated polynucleotide sequence.
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100.0%; Score 19; DB 14; Length 238;
Best Local Similarity 100.0%; Pred. No. 2.6;
Matches 19; Conservative 0; Mismatches 0; Indels (
                                                                                 100.0%; Score 19; DB 14; Length 237; 100.0%; Pred. No. 2.6; cive 0; Mismatches 0; Indels (
                                                       Sequence 237 BP; 54 A; 56 C; 64 G; 63 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                DNA detection; enteroviral detection; ds.
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                                                                                                                                            1 CCCCTGAATGCGGCTAATC 19
                                                                                                                                                                    47 CCCCTGAATGCGGCTAATC 65
                                                                                                                                                                                                                                               AEB56840 standard; DNA; 238 BP
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                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                  Local Similarity 100.
Les 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                             Human coxsackievirus B3
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(PRIC/) PRICE J A.
(HELL/) HELLYER T J.
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GENBANK; AH008164.
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                                                                                     Query Match
                                                                                                                 Matches
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The invention relates to an oligonucleotide (1) consisting of: (a) the target binding sequence of an oligonucleotide chosen from any one of the 10 sequence of ABB56762 to ABB56771; and (b) a sequence required for selected amplification or detection reaction. Also described: (1) a kit (K1) comprising (1), and one or more container that contains (1); and (2) detecting (M1) an enterovirus target sequence, involving: (a) amplifying the target sequence using first amplification primer having a sequence consisting essentially of target binding sequence of any one of ABB56764 to ABB5671 and optionally a sequence required for selected amplification reaction; and (b) detecting the amplified target sequence. (1), (M1) and (K1) are useful for detecting enterovirus target sequence. (1), specifically and selectively recognizes the enterovirus genome. (1) specifically and selectively recognizes the enterovirus genome. (1) sensitively and rapidly detects fewer than 500 copies of enteroviral genome and allows detection of broad range of enterovirus serotypes. The present sequence represents a viral 5, untranslated polymorized the
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                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA detection; enteroviral detection; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    reang S, Price JA, Hellyer TJ;
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ccccrcaarccccraarc 65
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                                                                                                                                                                 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AEB56878 standard; DNA; 238 BP
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                                                                                                                                                                 AEBS6850 standard; DNA; 238
                                                                                                                                                                                                                                                                                                 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human coxsackievirus B6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (TSAN/) TSANG S.
(PRIC/) PRICE J A.
(HELL/) HELLYER T J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2005-512251/52
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENBANK; AF039205
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                                                                                                                                                                                                                                                                                                    22-SEP-2005
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                                                                                                                                                                                                                                   AEB56850;
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                                                                                                       RESULT 28
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Gaps

AEB56878

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target binding sequence of an oligonucleotide chosen from any one of the los sequence of ABB56752 to ABB56771; and (b) a sequence required for selected amplification or detection reaction. Also described: (1) a kit (K1) comprising (1), and one or more container that contains (1); and (2) detecting (M1) an enterovirus target sequence, involving: (a) amplifying the target sequence using first amplification primer having a sequence consisting essentially of target binding sequence of any one of ABB56764 to ABB56771 and optionally a sequence required for selected amplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            reaction; and (b) detecting the amplified target sequence. (I), (M1) and (M1) are useful for detecting enterovirus target sequences. (I) specifically and selectively recognizes the enterovirus genome. (I) sensitively and rapidly detects fewer than 500 copies of enteroviral genome and allows detection of broad range of enterovirus serotypes. The present sequence represents a viral 5' untranslated polymocleotide sequence given in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel oligonucleotide comprising sequences for binding and amplifying or detecting target, useful for detecting enterovirus nucleic acids.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to an oligonucleotide (I) consisting of: (a) the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human coxsackievirus B3 5' untranslated polynucleotide sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 19; DB 14; Length 238; 100.0%; Pred. No. 2.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 238 BP; 53 A; 57 C; 61 G; 67 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA detection; enteroviral detection; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Fig 1A-D; 34pp; English
                                                                                                                                                                                                                                                                                                                                                          Hellyer TJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            47 cccricaariccecriaaric 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AEB56839 standard; DNA; 238 BP.
                                                                                                                                                    16-JAN-2004; 2004US-00760048
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  Human coxsackievirus B5.
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                                                                                                                                                                                                                                                                                                                                                        Tsang S, Price JA,
                                                                                                                                                                                                                                                (TSAN/) TSANG S..
(PRIC/) PRICE J A.
(HELL/) HELLYER T J.
                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2005-512251/52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US2005158710-A1.
                                               US2005158710-A1.
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                                                                                                 21-JUL-2005.
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Matches
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AEB56839
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to an oligonucleotide (I) consisting of: (a) the target binding sequence of an oligonucleotide chosen from any one of the 10 sequence of ABBS6721; and (b) a sequence required for selected amplification or detection reaction. Also described: (1) akit (K1) comprising (I), and one or more container that contains (I); and (2) detecting (M1) an enterovirus target sequence, involving: (a) amplifying the target sequence using first amplification primer having a sequence consisting essentially of target binding sequence of any one of ABBS6764 to ABBS6771 and optionally a sequence required for selected amplification reaction; and (b) detecting the amplified target sequence. (I), (M1) and (K1) are useful for detecting enterovirus target sequence. (I), (M1) and specifically and selectively recognizes the enterovirus genome. (I)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             specifically and selectively recognizes the enterovirus genome. (I) sensitively and rapidly detects fewer than 500 copies of enteroviral genome and allows detection of broad range of enterovirus serotypes. The present sequence represents a viral; untranslated polymucleotide sequence given in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel oligonucleotide comprising sequences for binding and amplifying or detecting target, useful for detecting enterovirus nucleic acids.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                       Human poliovirus 2 5' untranslated polynucleotide sequence.
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100.0%; Pred. No. ...
                                                                                                                                                                    DNA detection; enteroviral detection; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure, Fig 1A-D; 34pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Price JA, Hellyer TJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     47 ccccrcaarccccraarc 65
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                                                                  22-SEP-2005 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (TSAN/) TSANG S.
(PRIC/) PRICE J A.
(HELL/) HELLYER T J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2005-512251/52
                                                                                                                                                                                                                   Human poliovirus 2.
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GENBANK; X00595
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Tsang S,

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Mismatches

Query Match

Matches

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Matches
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                                                                                                                                                                 The invention relates to an oligonucleotide (1) consisting of: (a) the target binding sequence of an oligonucleotide chosen from any one of the target binding sequence of ABB56771; and (b) a sequence required for selected amplification or detection reaction. Also described: (1) a kit (K1) comprising (1), and one or more container that contains (1); and (2) detecting (M1) an enterovirus target sequence, involving: (a) amplifying the target sequence using first amplification primer having a sequence consisting essentially of target binding sequence of any one of ABB56764 to ABB56771 and optionally a sequence required for selected amplification reaction; and (b) detecting the amplified target sequence. (1), (M1) and (K1) are useful for detecting enterovirus target sequences. (1), (M1) and specifically and selectively recognizes the enterovirus genome. (1) specifically and selection of broad range of enterovirus penome and allows detects fewer than 500 copies of enteroviral present sequence represents a viral 5' untranslated polymucleotide sequence contains the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                              Novel oligonucleotide comprising sequences for binding and amplifying or detecting target, useful for detecting enterovirus nucleic acids.
                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                 Sequence 238 BP; 52 A; 54 C; 63 G; 69 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. 2.6;
                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA detection; enteroviral detection; ds.
                                                                                                                                                Disclosure; Fig 1A-D; 34pp; English.
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                                                       Hellyer TJ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                     1 CCCCTGAATGCGGCTAATC 19
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                                                                                                                                                                                                                                                                                                                                                                                                   100.08;
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Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human coxsackievirus B4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (TSAN/) TSANG S.
(PRIC/) PRICE J A.
(HELL/) HELLYER T J.
        (TSAN/) TSANG S.
(PRIC/) PRICE J A.
(HELL/) HELLYER T J.
                                                      Isang S, Price JA,
                                                                            WPI; 2005-512251/52.
GENBANK; AF169670.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tsang S, Price JA,
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GENBANK; D00149.
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The invention relates to an oligomucleotide (I) consisting of: (a) the target binding sequence of an oligomucleotide chosen from any one of the carget binding sequence of ABBS6771; and (b) a sequence required for selected amplification or detection reaction. Also described: (l) a kit (KI) comprising (I), and one or more container that contains (I); and (2) detecting (MI) an enterovirus target sequence, involving: (a) amplifying the target sequence using first amplification primer having a sequence consisting essentially of target binding sequence of any one of ABBS676 to ABBS6771 and optionally a sequence required for selected amplification reaction; and (b) detecting the amplified target sequence. (I), (MI) and (XI) are useful for detecting the amplified target sequence. (I), sensitively and selectively recognizes the enterovirus genome. (I) sensitively and rapidly detects fewer than 500 copies of enteroviral sensitively and selection of broad range of enterovirus serotypes. The present sequence represents a viral 5' untranslated polymucleotide sequence given in the exemplification of the present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to an oligonucleotide (I) consisting of: (a) the target binding sequence of an oligonucleotide chosen from any one of the 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for
Novel oligonucleotide comprising sequences for binding and amplifying or detecting target, useful for detecting enterovirus nucleic acids.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human coxsackievirus B4 5' untranslated polynucleotide sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 238 BP; 50 A; 55 C; 65 G; 68 T; 0 U; 0 Other;
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                                                                                                                                 Disclosure, Fig 1A-D; 34pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (TSAN/) TSANG S.
(PRIC/) PRICE J A.
(HELL/) HELLYER I J.
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selected amplification or detection reaction. Also described: (1) a kit (K1) comprising (1), and one or more container that contains (1); and (2) detecting (M1) an enterovirus target sequence, involving: (a) amplifying the target sequence using first amplification primer having a sequence of suppositions as sequence of any one of ABBS674 to ABBS6771 and optionally a sequence required for selected amplification reaction; and (b) detecting the amplified target sequence. (1), (M1) and (M2) are useful for detecting enterovirus target sequence. (1) specifically and selectively recognizes the enterovirus genome. (1) specifically and rapidly detects fewer than 500 copies of enteroviral genome and allows detection of broad range of enterovirus serotypes. The sequence represents a viral 5' untranslated polynucleotide sequence given in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to an oligonucleotide (I) consisting of: (a) the target binding sequence of an oligonucleotide chosen from any one of the lo sequence of ABBS6772 to ABBS6771; and (b) a sequence required for selected amplification or detection reaction. Also described: (1) a kit (K1) comprising (I), and one or more container that contains (I); and (2) detecting (M1) an enterovirus target sequence, involving: (a) amplifying the target sequence using first amplification primer having a sequence consisting essentially of target binding sequence of any one of ABBS6764 to ABBS6771 and optionally a sequence required for selected amplification reaction; and (b) detecting the amplified target sequence: (I), (M1) and specifically and selectively recognizes the enterovirus genome. (I)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel oligonucleotide comprising sequences for binding and amplifying or detecting target, useful for detecting enterovirus nucleic acids.
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                                                                                                                                                                                                                                                                                                                            Score 19; DB 14; Length 238; Pred. No. 2.6;
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Best Local Similarity 100.0%; Pred. No. ...
Matches 19; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AEB56838 standard; DNA; 238 BP
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(PRIC/) PRICE J A.
(HELL/) HELLYER T J.
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GENBANK; AF169665.
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The invention relates to an oligonucleotide (1) consisting of: (a) the target binding sequence of an oligonucleotide chosen from any one of the 10 sequence of ABS5672 to ABS577; and (b) a sequence required for selected amplification or detection reaction. Also described: (1) a kit (K1) comprising (1), and one or more container that contains (1); and (2) detecting (M1) an enterovirus target sequence, involving: (a) amplifying the target sequence using first amplification primer having a sequence consisting essentially of target binding sequence of any one of ABS5674 to ABS56771 and optionally a sequence required for selected amplification reaction; and (b) detecting the amplified target sequence. (1), (M1) and (K1) are useful for detecting enterovirus target sequences. (1) specifically and selectively recognizes the enterovirus genome. (1) specifically and rapidly detects fewer than 500 copies of enteroviral genome and allows detection of broad range of enterovirus serotypes. The present sequence represents a viral 5' untranslated polynucleotide
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                 genome and allows detection of broad range of enterovirus serotypes. The present sequence represents a viral 5' untranslated polynucleotide sequence given in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel oligonucleotide comprising sequences for binding and amplifying or detecting target, useful for detecting enterovirus nucleic acids.
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 sensitively and rapidly detects fewer than 500 copies of enteroviral
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                                                                                                                               100.0%; Score 19; DB 14; Length 238; 100.0%; Pred. No. 2.6; ive 0; Mismatches 0; Indels (
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                                                                                           Sequence 238 BP; 50 A; 56 C; 65 G; 67 T; 0 U; 0 Other;
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                                                                                                                                                                                                            1 CCCCTGAATGCGGCTAATC 19
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                                                                                                                                                                       Conservative
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(PRIC/) PRICE J A.
(HELL/) HELLYER T J.
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                                                                                                                                                   Local Similarity
ses 19; Conserv
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                                                                                                                                                                                                                                                                                                          RESULT 35
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target binding sequence of an original control of the sequence of ABB5672 to ABB5671; and (b) a sequence required for 10 sequence of ABB5672 to ABB56771; and (b) a sequence required for selected amplification or detection reaction. Also described: (1) a kit (K1) comprising (1), and one or more container that contains (1); and (2) detecting (M1) an enterovirus target sequence, involving: (a) amplifying the target sequence using first amplification primer having a sequence consisting essentially of target binding sequence of any one of ABB56774 to ABB56771 and optionally a sequence required for selected amplification reaction; and (b) detecting the amplified target sequence. (1), (M1) and (K1) are useful for detecting enterovirus target sequence. (1) and specifically and selectively recognizes the enterovirus genome. (1) sensitively and rapidly detects fewer than 500 copies of enteroviral genome and allows detection of broad range of enterovirus servicypes. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel oligonucleotide comprising sequences for binding and amplifying or detecting target, useful for detecting enterovirus nucleic acids.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  present sequence represents a viral 5' untranslated polynucleotide sequence given in the exemplification of the present invention.
                                                                                                                                  Human coxsackievirus B1 5' untranslated polynucleotide sequence.
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                                                                                                                                                                               DNA detection; enteroviral detection; ds
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  AEB56835 standard; DNA; 238 BP.
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                                                                                                                                                                                                                            Human coxsackievirus Bl.
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(PRIC/) PRICE J A.
(HELL/) HELLYER T J.
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sequence given in the exemplification of the present invention
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  Indels
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Mismatches
                                                                                                                                                                                                                                                                                                                                                                                     DNA detection; enteroviral detection; ds
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hellyer TJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                47 CCCCTGAATGCGGCTAATC 65
                                          1 CCCCTGAATGCGGCTAATC 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 CCCCTGAATGCGGCTAATC 19
                                                                         47 CCCCTGAATGCGGCTAATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16-JAN-2004; 2004US-00760048
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16-JAN-2004; 2004US-00760048.
                                                                                                                                                                                                      AEB56832 standard; DNA; 238
                                                                                                                                                                                                                                                                                            (first entry)
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Best Local Similarity 100..
Pest Local Similarity 100..
19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                  Human coxsackievirus A21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (TSAN/) TSANG S.
(PRIC/) PRICE J A.
(HELL/) HELLYER T J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tsang S, Price JA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2005-512251/52.
GENBANK; D00538.
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                                                                                                                                                                                                                                                   AEB56832;
                                                                                                                                                     RESULT 36
AEB56832
Matches
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Gaps

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0; Indels

Mismatches

DNA detection; enteroviral detection; ds.

RESULT 37 AEB56835

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target binding sequence of an oligonucleotide chosen from any one of the 10 sequence of ABB5672 to ABB5671; and (b) a sequence required for selected amplification or detection reaction. Also described: (1) and one or more contains that contains (1); and (2) detecting (M1) an enterovirus target sequence, involving: (a) amplifying the target sequence using first amplification primer having a sequence consisting essentially of target binding sequence of any one of ABB5674 to ABB56771 and optionally a sequence required for selected amplification reaction; and (b) detecting the amplification transpersed to sequence. (1) (M1) and (M2) are useful for detecting enterovirus target sequence. (1) (M1) and selectively recognizes the enterovirus genome. (1) sensitivally and selectively fewer than 500 copies of enteroviral genome and allows detection of broad range of enterovirus serotypes. The present sequence represents a viral 5' untranslated polynucleotide.
                                                                                                                                                                                                                                                      Novel oligonucleotide comprising sequences for binding and amplifying or detecting target, useful for detecting enterovirus nucleic acids.
                                                                                                                                                                                                                                                                                                                                                                          The invention relates to an oligonucleotide (I) consisting of: (a) the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequence given in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 19; DB 14; Length 238; 100.0%; Pred. No. 2.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human poliovirus 1 5' untranslated polynucleotide sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 238 BP; 52 A; 59 C; 64 G; 63 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA detection; enteroviral detection; ds.
                                                                                                                                                                                                                                                                                                                            Disclosure; Fig 1A-D; 34pp; English
                                                                                                                                       Tsang S, Price JA, Hellyer TJ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 CCCCTGAATGCGGCTAATC 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AEB56874 standard; DNA; 238 BP.
16-JAN-2004; 2004US-00760048.
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Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (TSAN/) TSANG S.
(PRIC/) PRICE J A.
(HELL/) HELLYER T J.
                                         (TSAN/) TSANG S.
(PRIC/) PRICE J A.
(HELL/) HELLYER T J.
                                                                                                                                                                                     WPI; 2005-512251/52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2005-512251/52
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                                                                                                                                                                                                             GENBANK; AF114384
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 40
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셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to an oligonucleotide (1) consisting of: (a) the target binding sequence of an oligonucleotide chosen from any one of the 10 sequence of ABBS6772 to ABBS6771; and (b) a sequence required for selected amplification or detection reaction. Also described: (1) a kit (K1) comprising (1), and one or more container that contains (1); and (2) detecting (M1) an enterovirus target sequence, involving: (a) amplifying the target sequence using first amplification primer having a sequence consisting essentially of target binding sequence of any one of ABBS6764 to ABBS6771 and optionally a sequence required for selected amplification reaction; and (b) detecting the amplified target sequence. (1), (M1) and (X1) are useful for detecting enterovirus target sequence. (1) specifically and selectively recognizes the enterovirus genome. (1) specifically and rapidly detects fewer than 500 copies of enteroviral genome and allows detection of broad range of enterovirus serotypes. The present sequence given in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel oligonucleotide comprising sequences for binding and amplifying or detecting target, useful for detecting enterovirus nucleic acids.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 238 BP; 52 A; 59 C; 64 G; 63 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 19; DB 1 100.0%; Pred. No. 2.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 100.0%; Pred. No. 2.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA detection; enteroviral detection; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Fig 1A-D; 34pp; English.
                                                                                                                                                                                                                                                                                                                                               Tsang S, Price JA, Hellyer TJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 CCCCTGAATGCGGCTAATC 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        47 ccccrcaarccccraarc 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AEB56852 standard; DNA; 238 BP.
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                     Human coxsackievirus B6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human coxsackievirus B6
                                                                                                                                                                                                                                                 (TSAN/) TSANG S.
(PRIC/) PRICE J A.
(HELL/) HELLYER T J.
                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2005-512251/52.
GENBANK; AF105342.
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**AEB**56852

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Gaps

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Indels

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The invention relates to an oligonucleotide (1) consisting of: (a) the target binding sequence of an oligonucleotide chosen from any one of the consequence of ABB5671; and (b) a sequence required for selected amplification or detection reaction. Also described: (1) a kit (K1) comprising (1), and one or more container that contains (1); and (2) detecting (M1) an enterovirus target sequence, involving: (a) amplifying the target sequence using first amplification primer having a sequence consisting essentially of target binding sequence of any one of ABB5674 to ABB56771 and optionally a sequence required for selected amplification reaction; and (b) detecting the amplified target sequence. (1), (M1) and (K1) are useful for detecting enterovirus target sequence. (1), (M1) and specifically and rapidly detects fewer than 500 copies of enteroviral genome and allows detection of broad range of enterovirus serotypes. The present sequence represents a viral 5' untranslated polymucleotide sequence given in the exemplification of the present invention.
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                                    Novel oligonucleotide comprising sequences for binding and amplifying or detecting target, useful for detecting enterovirus nucleic acids.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel oligonucleotide comprising sequences for binding and amplifying or detecting target, useful for detecting enterovirus nucleic acids.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 19; DB 14; Length 238; 100.0%; Pred. No. 2.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Consensus viral 5' untranslated polynucleotide sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 238 BP; 57 A; 54 C; 62 G; 65 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA detection; enteroviral detection; ds.
                                                                                           Disclosure; Fig 1A-D; 34pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                47 CCCCTGAATGCGGCTAATC 65
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CCCCTGAATGCGGCTAATC 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AEB56829 standard; DNA; 238 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19; Conservative
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(PRIC/) PRICE J A.
(HELL/) HELLYER T J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AEB56829;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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selected amplification or detection reaction. Also described: (1) a kit (K1) comprising (1), and one or more container that contains (1); and (2) detecting (M1) an enterovirus target sequence, involving: (a) amplifying the target sequence using first amplification primer having a sequence consisting essentially of target binding sequence of any one of ABB56764 to ABB56771 and optionally a sequence required for selected amplification reaction; and (b) detecting the amplified target sequence. (1), (M1) and (K1) are useful for detecting enterovirus target sequences. (1) specifically and selectively recognizes the enterovirus genome. (1) sensitively and rapidly detects fewer than 500 copies of enteroviral genome and allows detection of broad range of enterovirus serotypes. The present sequence represents a consensus viral 5' untranslated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to an oligonucleotide (I) consisting of: (a) the target binding sequence of an oligonucleotide chosen from any one of the 10 sequence of ABB56762 to ABB5671; and (b) a sequence required for selected amplification or detection reaction. Also described: (1) akit (K1) comprising (I), and one or more container that contains (I); and (2) detecting (M1) an enterovirus target sequence, involving: (a) amplifying the target sequence using first amplification primer having a sequence consisting essentially of target binding sequence of any one of ABB56764 to ABB56771 and optionally a sequence required for selected amplification reaction; and (b) detecting the amplified target sequence. (1), (M1) and (K1) are useful for detecting enterovirus target sequences. (1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel oligonucleotide comprising sequences for binding and amplifying or detecting target, useful for detecting enterovirus nucleic acids.
                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                          100.0%; Score 19; DB 14; Length 238; 100.0%; Pred. No. 2.6;
                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                        Sequence 238 BP; 51 A; 55 C; 65 G; 67 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                 ;
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                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA detection; enteroviral detection; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                        1 CCCCTGAATGCGGCTAATC 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                             ccccrgaargcggcraarc 65
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                                                                                                                                                                                                                                                                                                                                                               100.08;
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nes 19; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (TSAN/) TSANG S.
(PRIC/) PRICE J A.
(HELL/) HELLYER T J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2005-512251/52
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                                                                                                                                                                                                                                                                   invention.
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                                                                                                                                                                                                                                                                                                                                              Query Match
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Matches
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Pred. No. 2.6;

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The invention relates to an oligonucleotide (I) consisting of: (a) the target binding sequence of an oligonucleotide chosen from any one of the 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for selected amplification or detection reaction. Also described: (I) a kit (KI) comprising (I), and one or more container that contains (I); and (2) detecting (MI) an enterovirus target sequence, involving: (a) amplifying the target sequence using first amplification primer having a sequence consisting essentially of target binding sequence of any one of AEB56764 to AEB56771 and Optionally a sequence required for selected amplification reaction; and (b) detecting the amplified target sequence. (I) (KI) are useful for detecting enterovirus target sequences. (I) (MI) and
specifically and selectively recognizes the enterovirus genome. (I) ensistively and rapidly detects fewer than 500 copies of enteroviral genome and allows detection of broad range of enterovirus serotypes. The present sequence represents a viral 5' untranslated polynucleotide sequence given in the exemplification of the present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel oligonucleotide comprising sequences for binding and amplifying or detecting target, useful for detecting enterovirus nucleic acids.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       specifically and selectively recognizes the enterovirus genome. (I) sensitively and rapidly detects fewer than 500 copies of enteroviral genome and allows detection of broad range of enterovirus serotypes. Present sequence represents a viral 5' untranslated polynucleotide sequence given in the exemplification of the present invention.
                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human coxsackievirus B3 5' untranslated polynucleotide sequence.
                                                                                                                                                                                                      ö
                                                                                                                                                           Score 19; DB 14; Length 238; Pred. No. 2.6;
                                                                                                                                                                                                    Indels
                                                                                                                    Sequence 238 BP; 53 A; 58 C; 64 G; 63 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 238 BP; 54 A; 57 C; 62 G; 65 T; 0 U; 0 Other;
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                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA detection; enteroviral detection; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Fig 1A-D; 34pp; English.
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                                                                                                                                                                                                                                      1 CCCCTGAATGCGGCTAATC 19
                                                                                                                                                                                                                                                                             47 ccccrdaarcccccraarc 65
                                                                                                                                                                                                                                                                                                                                                                             AEB56845 standard; DNA; 238 BP
                                                                                                                                                           100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                             Best Local Similarity 100.
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human coxsackievirus B3.
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(PRIC/) PRICE J A.
(HELL/) HELLYER T J.
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                                                                                                                                                             Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel oligonucleotide comprising sequences for binding and amplifying or detecting target, useful for detecting enterovirus nucleic acids.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                consisting of: (a) the
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slated polynucleotide
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                                                                                                                                                                                                                                                                      Human echovirus 30 5' untranslated polynucleotide sequence.
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                               IndelB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             represents a viral 5' untranslated
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                               Mismatches
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                                                                                                                                                                                                                                                                                                      DNA detection; enteroviral detection; ds.
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100.08; PEN
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                                                            1 CCCCTGAATGCGGCTAATC
                                                                                            cccrcaarccccraarc
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                            19; Conservative
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Matches 19; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (TSAN/) TSANG S.
(PRIC/) PRICE J A.
(HELL/) HELLYER T J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2005-512251/52.
               Best Local Similarity
Matches 19; Conserv
                                                                                                                                                                                                                                                                                                                                      Human echovirus 30
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                                                                                                                                          RESULT 44
AEB56870
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100.0%; Score 19; DB 14; Length 238;

Query Match

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                            Novel oligonucleotide comprising sequences for binding and amplifying or detecting target, useful for detecting enterovirus nucleic acids.
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                                                                            Human coxsackievirus A9 5' untranslated polynucleotide sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. 2.6;
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                                                                                                   DNA detection; enteroviral detection; ds.
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           AEB56830 standard; DNA; 238
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                                                       (first entry)
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                                                                                                                         Human coxsackievirus A9
                                                                                                                                                                                                                                        (TSAN/) TSANG S.
(PRIC/) PRICE J A.
(HELL/) HELLYER T J.
                                                                                                                                                                                                                                                                                     Tsang S, Price JA,
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                                                       22-SEP-2005
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ID AEBS
XX AC AEBS
AC AEBS
DT 22-S
XX XX
AEB56830
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The invention relates to an oligonucleotide (I) consisting of: (a) the target binding sequence of an oligonucleotide chosen from any one of the 10 sequence of ABBS6712 to ABBS671; and (b) a sequence required for selected amplification or detection reaction. Also described: (I) a kit (KI) comprising (I), and one or more container that contains (I); and (2) detecting (MI) an enterovirus target sequence, involving: (a) amplifying the target sequence using first amplification primer having a sequence consisting essentially of target binding sequence of any one of ABBS6764 to ABBS6771 and optionally a sequence required for selected amplification reaction; and (b) detecting the amplified target sequence. (I), (MI) and (KI) are useful for detecting enterovirus target sequences. (I) specifically and selectively recognizes the enterovirus genome. (I) sensitively and rapidly detects fewer than 500 copies of enteroviral genome and allows detection of broad range of enterovirus serotypes. The present sequence represents a viral 5 untranslated polymucleotide specifically and the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel oligonucleotide comprising sequences for binding and amplifying or detecting target, useful for detecting enterovirus nucleic acids.
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dB.
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DNA detection; enteroviral detection;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tsang S, Price JA, Hellyer TJ;
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                                                                Human coxsackievirus A24
                                                                                                                                                                                                                                                                                                                                                                                   (TSAN/) TSANG S.
(PRIC/) PRICE J A.
(HELL/) HELLYER T J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2005-512251/52
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16-JAN-2004; 2004US-00760048.

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The invention relates to an oligomucleotide (I) consisting of: (a) the target binding sequence of an oligomucleotide chosen from any one of the consequence of ABBS6722 to ABBS6731; and (b) a sequence required for selected amplification or detection reaction. Also described: (1) a kit (K1) comprising (I), and one or more container that contains (I); and (2) of detecting (M1) an enterovirus target sequence, involving: (a) amplifying the target sequence using first amplification primer having a sequence consisting essentially of target binding sequence of any one of ABBS6784 consisting essentially of target binding sequence of any one of ABBS6784 consisting and optionally a sequence required for selected amplification reaction, and (b) detecting the amplified target sequence. (I) (M1) and (X1) are useful for detecting enterovirus target sequences. (I) (X1) are useful for detecting enterovirus target sequences. (I) (X2) are useful and selectively recognizes the enterovirus genome. (I) capacitively and selection of broad range of enterovirus serotypes. The present sequence represents a viral 5, untranslated polynucleotide
                                                                    Novel oligonucleotide comprising sequences for binding and amplifying or detecting target, useful for detecting enterovirus nucleic acids.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human coxsackievirus B3 5' untranslated polynucleotide sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sequence given in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 19; DB 14; Length 238;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 238 BP; 47 A; 53 C; 66 G; 72 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. 2.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
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                                                                                                                                            Disclosure; Fig 1A-D; 34pp; English
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(PRIC/) PRICE J A.
(HBLL/) HELLYER I J.
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2005-512251/52
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 100.0%; Score 19; DE
Best Local Similarity 100.0%; Pred. No. 2.6
Matches 19; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                               Disclosure; Fig 1A-D; 34pp; English.
                                                                                                                                                              Hellyer TJ;
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                    16-JAN-2004; 2004US-00760048
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                                                             (TSAN/) TSANG S.
(PRIC/) PRICE J A.
(HELL/) HELLYER T J.
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(PRIC/) PRICE J A.
(HELL/) HELLYER T J.
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                                                                                                                                                              Tsang S,
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Best Loca Matches

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RESULT 48 AEB56859

XIXBBBXBXBXBXBXBXBXBXGXX

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Gaps

(KI) are useful for detecting enterovirus target sequences. (I) specifically and selectively recognizes the enterovirus genome. (I) sensitively and rapidly detects fewer than 500 copies of enteroviral genome and allows detection of broad range of enterovirus serotypes. The present sequence represents a viral 5' untranslated polynucleotide

sequence given in the exemplification of the present

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target binding sequence of an oligonucleotide chosen from any one of the losequence of ABB56762 to ABB56771; and (b) a sequence required for selected amplification or detection reaction. Also described: (l) a kit (KI) comprising (I), and one or more container that contains (I); and (2) detecting (MI) an enterovirus target sequence, involving: (a) amplifying the target sequence using first amplification primer having a sequence or onsisting essentially of target binding sequence of any one of ABB5674 to ABB56771 and optionally a sequence required for selected amplification reaction, and (b) detecting the amplified target sequence. (I), (MI) and (KI) are useful for detecting enterovirus target sequences. (I) specifically and selectively recognizes the enterovirus genome. (I) sensitively and rapidly detects fewer than 500 copies of enteroviral sensitively and rapidly detects fewer than 500 copies of enteroviral present sequence represents a viral 5' untranslated polymucleotide present sequence given in the exemplification of the present invention.
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                                                                                                                                                                                                                                                                                                                                   Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                                                             Local Similarity
nes 19; Conserva
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(PRIC/) PRICE J A.
(HELL/) HELLYER T J.
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The invention relates to an oligonucleotide (I) consisting of: (a) the target binding sequence of an oligonucleotide chosen from any one of the 10 sequence of AEB56762 to AEB5671; and (b) a sequence required for selected amplification or detection reaction. Also described: (1) a kit (K1) comprising (I), and one or more container that contains (I); and (2) detecting (M1) an enterovirus target sequence, involving: (a) amplifying the target sequence using first amplification primer having a sequence consisting essentially of target binding sequence of any one of AEB56764 to AEB56771 and optionally a sequence required for selected amplification reaction, and (b) detecting the amplified target sequence. (I), (M1) and

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target binding sequence of an oligonucleotide chosen from any one of the 10 sequence of AEB5672 to AEB5671; and (b) a sequence required for sequence of AEB5672 to AEB5671; and (b) a sequence required for selected amplification or detection reaction. Also described: (1) a kit (KI) comprising (I), and one or more container that contains (I); and (2) detecting (MI) an enterovirus target sequence, involving: (a) amplifying the target sequence using first amplification primer having a sequence of the target sequence using first amplification primer having a sequence of any one of AEB5671 and optionally a sequence required for selected amplification reaction; and (b) detecting the amplified target sequence. (I), (MI) and (KI) are useful for detecting enterovirus target sequence. (I) specifically and rapidly detects fewer than 500 copies of enteroviral sensitively and rapidly detects fewer than 500 copies of enteroviral present sequence represents a viral 5' untranslated polymucleotide sequence represents a viral 5' untranslated polymucleotide sequence represents a viral 5' untranslated polymucleotide
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                                                                                                                                                           100.0%; Score 19; DB 14; Length 238; 100.0%; Pred. No. 2.6;
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                                                                                                                                                                                               0; Indels
                                                                                                                          Sequence 238 BP; 51 A; 55 C; 64 G; 68 T; 0 U; 0 Other;
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                                                                                                                                                                                               0; Mismatches
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                                                                                                                                                                                                                                                      CCCCTGAATGCGGCTAATC 65
                                                                                                                                                                                                                                                                                                                                                           AEB56867 standard; DNA; 238 BP.
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                                                                                                                                                                              Best_Local Similarity 100.0
Matches 19; Conservative
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(PRIC/) PRICE J A.
(HELL/) HELLYER T J.
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Novel oligonucleotide comprising sequences for binding and amplifying or detecting target, useful for detecting enterovirus nucleic acids.
                                                                                                                  Human echovirus 12 5' untranslated polynucleotide sequence
                                                                                                                                            DNA detection; enteroviral detection; ds.
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                                AEB56866 standard; DNA; 238 BP.
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                                                                                    22-SEP-2005 (first entry)
                                                                                                                                                                                                                                                                                                                (TSAN/) TSANG S.
(PRIC/) PRICE J A.
(HELL/) HELLYER I J.
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                                                                                                                                                                        Human echovirus 12
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                                                          AEB56866;
                 AEB56866
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  Score 19; DB 14; Length 238; Pred. No. 2.6;
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                              Indels
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                              Mismatches
                                                                                                                                                                                                                                                                    DNA detection; enteroviral detection; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Fig 1A-D; 34pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hellyer TJ;
                             ;
                                                         1 CCCCTGAATGCGGCTAATC 19
                                                                                 47 ccccrcaarccccraarc 65
                                                                                                                                                      AEB56844 standard; DNA; 238 BP
ch
1 Similarity 100.0%;
19; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                  16-JAN-2004; 2004US-00760048.
                                                                                                                                                                                                                                                                                                                                                                                                              16-JAN-2004; 2004US-00760048.
                                                                                                                                                                                                            22-SEP-2005 (first entry)
                                                                                                                                                                                                                                                                                                 Human coxsackievirus B3.
                                                                                                                                                                                                                                                                                                                                                                                                                                        (TSAN/) TSANG S.
(PRIC/) PRICE J A.
(HELL/) HELLYER T J.
Query Match
Best Local Similarity
Matches 19; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Price JA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2005-512251/52
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nes 19; Conserv
                                                                                                                                                                                                                                                                                                                             US2005158710-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENBANK; M88483
                                                                                                                                                                                                                                                                                                                                                         21-JUL-2005.
                                                                                                                                                                                  AEB56844;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tsang S,
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                                                   The invention relates to an oligonucleotide (I) consisting of: (a) the target binding sequence of an oligonucleotide chosen from any one of the 10 sequence of AEB56762 to AEB5671; and (b) a sequence required for selected amplification or detection. Also described: (I) a kit (KI) comprising (I), and one or more container that contains (I); and (2) detecting (MI) an enterovirus target sequence, involving: (a) amplifying the target sequence using first amplification primer having a sequence consisting essentially of target binding sequence of any one of AEB56764 to AEB56771 and optionally a sequence required for selected amplification reaction; and (b) detecting the amplified target sequence. (I), (MI) and specifically and selectively recognizes the enterovirus genome. (I) sensitively and rapidly detects fewer than 500 copies of enteroviral genome and allows detection of broad range of enterovirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 and allows detection of broad range of enterovirus serotypes. sequence represents a viral 5' untranslated polynucleotide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sequence given in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 19; DB 14; Length 238; Pred. No. 2.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human poliovirus 3 5' untranslated polynucleotide sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 238 BP; 50 A; 55 C; 64 G; 69 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
Disclosure, Fig 1A-D; 34pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 CCCCTGAATGCGGCTAATC 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ccccrdaargcggcraarc 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AEB56882 standard; DNA; 238 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Local 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22-SEP-2005 (first entry)
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0; Indels

Mismatches

1 CCCCTGAATGCGGCTAATC 19

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Conservative

Best Loc Matches

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The invention describes a polymerase chain reaction (PCR) and primers for detecting nucleic acids from the diabetogenic coxsackie B virus-4 (CBV-4) strain VD221, (Particularly VB1, VP2, VP3, VP4, P24, P24, P28, P26, P37, P38, P36, P30 and P3D nucleic acids). The methods and primers are used for the detection of CBV-4 strain VD2921 which is associated with diabetes (diabetogenic enterovirus). Early detection of the diabetes e.g. detection of diabetogenic enterovirus RNA in peripheral mononuclear cells, can improve prognosis by allowing treatment e.g. with antiviral drugs, to prevent further loss of beta cells and severe long term consequences of diabetes including blindness, renal failure and leg amputations. This sequence repersents a diabetogenic coxsackie B virus 4 (CBV-4) strain VD2921 associated polynucleotide
                                                                                                                                                                                                                                                                                                Polymerase chain reaction and primers for detecting nucleic acids from
the diabetogenic coxsackie B virus-4 strain VD2921.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Coxeackie virus strain VD2921; diabetogenic coxeackie B virus-4; strain VD2921; VP1; VP2; VP4; P2A; P2B; P2C; P3A; P3B; P3C; diabetes; diabetogenic enterovirus; beta cell loss; blindness; renal failure; leg amputation; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Coxsackie B virus 4 (CBV-4) strain VD2921 associated DNA #6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 19; DB 8; Length 497; 100.0%; Pred. No. 2.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 497 BP; 119 A; 134 C; 129 G; 115 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 72; 79pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     365 CCCCTGAATGCGGCTAATC 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 CCCCTGAATGCGGCTAATC 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABX12451 standard; DNA; 502 BP.
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                                                                                                                                                            (INNO-) INNOVENTUS PROJECT AB
                                                               19-JUN-2002; 2002WO-IB003278.
                                                                                                              20-JUN-2001; 2001SE-00002198.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19-JUN-2002; 2002WO-IB003278.
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                                                                                                                                                                                                           Frisk GE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Frisk GE,
                                                                                                                                                                                                                                                    WPI; 2003-278229/27.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Coxsackievirus,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27-DEC-2002
                   27-DEC-2002
                                                                                                                                                                                                      Tuvemo HT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tuvemo HT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABX12451;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to an oligonucleotide (I) consisting of: (a) the target binding sequence of an oligonucleotide chosen from any one of the 10 sequence of ABS6771; and (b) a sequence required for selected amplification or detection reaction. Also described: (I) a kit (KI) comprising (I), and one or more container that contains (I); and (2) detecting (MI) an enterovirus target sequence, involving: (a) amplifying the target sequence using first amplification primer having a sequence consisting essentially of target binding sequence of any one of ABB6764 to ABB56771 and optionally a sequence required for selected amplification reaction; and (b) detecting enterovirus target sequence. (I), (MI) and (XI) are useful for detecting enterovirus target sequences. (I) specifically and selectively recognizes the enterovirus genome. (I) specifically and selectively recognizes the enterovirus genome. (I) sensitively and rapidly detects fewer than 500 copies of enteroviral consent sequence represents a viral S, untranslated polynucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel oligonucleotide comprising sequences for binding and amplifying or detecting target, useful for detecting enterovirus nucleic acids.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Coxeackie virus strain VD2921; diabetogenic coxsackie B virus-4; CBV-4; strain VD2921; VD1; VP2; VP3; VP4; P2A; P2B; P2C; P3A; P3B; P3C; P3D; diabetes; diabetogenic entervirus; beta cell loss; blindness; renal failure; leg amputation; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 19; DB 14; Length 238; 100.0%; Pred. No. 2.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Coxsackie B virus 4 (CBV-4) strain VD2921 associated DNA #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 238 BP; 57 A; 54 C; 62 G; 65 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                   DNA detection; enteroviral detection; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Fig 1A-D; 34pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                Hellyer TJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 CCCCTGAATGCGGCTAATC 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 47 ccccrcaarccccraarc 65
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                                                                                                                                                                                                        16-JAN-2004; 2004US-00760048.
                                                                                                                                                                                                                                                    16-JAN-2004; 2004US-00760048.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABX12446 standard; DNA; 497
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Best Local Similarity
Matches 19; Conservat
                                                                                                                                                                                                                                                                                                (TSAN/) TSANG S.
(PRIC/) PRICE J A..
(HELL/) HELLYER T J.
                                                                                                                                                                                                                                                                                                                                                                                                Tsang S, Price JA,
                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2005-512251/52
                                                               Human poliovirus 3.
                                                                                                              US2005158710-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENBANK; X04468
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                                                                                                                                                          21-JUL-2005.
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RESULT 55 ABX12446

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0; Indels

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05-AUG-1998;
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                                                    The invention describes a polymerase chain reaction (PCR) and primers for detecting nucleic acids from the diabetogenic coxsackie B virus-4 (CBV-4) strain VD2921, (particularly VP1, VP2, VP3, VP4, P2A, P2B, P2C, P3A, P3B, P3C and P3D nucleic acids). The methods and primers are used for the detection of CBV-4 strain VD2921 which is associated with diabetes (diabetogenic enterovirus). Early detection of the diabetes e.g. certain volume of cBV-4 strain VD2921 which is peripheral monouclear detection of diabetogenic enterovirus RNA in peripheral monouclear cells, can improve prognosis by allowing treatment e.g. with antiviral consequences of diabetes including blindness, renal failure and leg amputations. This sequence represents a diabetogenic coxsackie B virus 4
Polymerase chain reaction and primers for detecting nucleic acids from the diabetogenic coxsackie B virus-4 strain VD2921.
                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Internal ribosomal entry site; IRES; picornavirus; tumour; cancer; glioblastoma multiforme; meduiloblastoma; mammary carcinoma; prostate carcinoma; colorectal carcinoma; hepatocellular carcinoma; bronchial carcinoma; cytostatic; therapy; ss.
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                                                                                                                                                                                                                                    100.0%; Score 19; DB 8; Length 502; 100.0%; Pred. No. 2.8; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                            Sequence 502 BP; 120 A; 132 C; 128 G; 122 T; 0 U; 0 Other;
                                                                                                                                                                                      (CBV-4) strain VD2921 associated polynucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Poliovirus IRES domain II-VI region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            *tag= c
note= "domain III"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                346. .454
/*tag= g
/note= "domain V"
                               Disclosure; Page 73; 79pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    *tag= a
note= "domain II"
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note= "domain IV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              note= "domain VI"
                                                                                                                                                                                                                                                                                                 368 CCCCTGAATGCGGCTAATC 386
                                                                                                                                                                                                                                                                                    1 CCCCTGAATGCGGCTAATC 19
                                                                                                                                                                                                                                                                                                                                                                   AAZ58487 standard; RNA; 514 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     70. .83 /
/*tag= b
84. .120
                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
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Best Local Similarity 100.0
Matches 19; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                  (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human poliovirus 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200008166-A1
                                                                                                                                                                                                                                                                                                                                                                                                                 15-SEP-2003
23-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Key
stem_loop
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                                                                                                                                                                                                                                                                                                                                             RESULT 57
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17-FEB-2000.

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site (TRES) of wild-type poliovirus type 1 Mahoney. The invention provides non-pathogenic, oncolytic, recombinant polioviruses (1) in which the IRES of the wild-type poliovirus is exchanged with the IRES of another picornavirus, such as human rhinovirus type 2, and optionally the P1, P3 or 3' untranslated region is exchanged with that of Sabin poliovirus. (1) may contain a composite IRES encompassing IRES domains from both wild-type poliovirus and from another virus. (1) are useful for treating malignant tumors such as glioblastoma multiforme, and epidermoid carcinomas (claimed). (Updated on 15-SEP-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Monitoring microbiological quality of water, useful particularly for controlling water purification, uses oligonucleotide probes to detect at
                                                                                                                                                                                                            domains II-VI of the internal ribosomal entry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                               Chimeric recombinant poliovirus useful for treating malignant tumors comprises internal ribosomal entry site derived from picornaviruses.
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 19; DB 3; Length 514;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 514 BP; 122 A; 134 C; 132 G; 0 T; 126 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lacroix B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Probe; microorganism detection; microbiological quality;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Vachon C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. 2.8;
4; Mismatches
(UYNY ) UNIV NEW YORK STATE RES FOUND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Micro-organism detection probe #54.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mabilat C,
                                                                                                                                                                    Disclosure, Fig 2; 99pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     349 CCCCUGAAUGCGGCUAAUC 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 CCCCTGAATGCGGCTAATC 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABL53112 standard; DNA; 520 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 06-JUL-2001; 2001WO-FR002191.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         78.98;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 78.9
tes 15; Conservative
                                                                                                                                                                                                              This sequence represents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              water purification; ss.
                                       Wimmer E;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Guillot E,
Laffaire P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (revised)
                                                                         WPI; 2000-205717/18.
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                                     Gromeier M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           07-AUG-2003
25-JUN-2002
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Armand M,
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RESULT 60
ABL53113
                                                                                                                                        Matches
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                                            The present invention relates to a method for monitoring microbiological quality of an aqueous environmental medium that potentially contains many different microorganisms. A reference set of at least three microorganisms is chosen that, separately or collectively, represent microbiological quality. The test medium is treated, then any microorganisms, or their fragments, in the treated medium is contacted with a set of at least three probes for specific identification and multiple determination of selected microorganisms. This determination represents the level of microbiological quality. The method is useful for identifying and quantifying microorganisms in water and provides results that are used to control water purification/production processes. The present sequence is a probe which was used to illustrate the invention. (Updated on 07-AUG-2003 to correct OS field.)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention relates to a method for monitoring microbiological quality of an aqueous environmental medium that potentially contains many different microorganisms. A reference set of at least three microorganisms is chosen that, separately or collectively, represent microbiogical quality. The test medium is treated, then any microbiogical quality. The test medium is treated, then any microcorganisms, or their fragments, in the treated medium is contacted with a set of at least three probes for specific identification and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Monitoring microbiological quality of water, useful particularly for controlling water purification, uses oligonucleotide probes to detect at least three representative microbes.
                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                           100.0%; Score 19; DB 6; Length 520;
                                                                                                                                                                                                                                  Sequence 520 BP; 113 A; 141 C; 131 G; 135 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lacroix B,
                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Probe; microorganism detection; microbiological quality; water purification; 88.
                                                                                                                                                                                                                                                                      Pred. No. 2.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Vachon C,
                                                                                                                                                                                                                                                                                  0; Mismatches
least three representative microbes.
                      Claim 24; Page 75-76; 85pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Micro-organism detection probe #53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mabilat C,
                                                                                                                                                                                                                                                                                                                               386 CCCCTGAATGCGGCTAATC 404
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                                                                                                                                                                                                                                                                                                           1 CCCCTGAATGCGGCTAATC 19
                                                                                                                                                                                                                                                                      100.0%;
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                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.
Matches 19; Conservative
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Laffaire P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      (revised)
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25-JUN-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Poliovirus.
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Armand M,
                                                                                                                                                                                                                                                                                                                                                                                                                             ABL53111;
                                                                                                                                                                                                                                                                                                                                                                         RESULT 59
                                                                                                                                                                                                                                                                                                                                                                                      ABL53111
#X%X000000000000000X%
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multiple determination of selected microorganisms. This determination represents the level of microbiological quality. The method is useful for identifying and quantifying microorganisms in water and provides results that are used to control water purification/production processes. The present sequence is a probe which was used to illustrate the invention. (Updated on 07-AUG-2003 to correct OS field.)
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                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                        100.0%; Score 19; DB 6; Length 521; 100.0%; Pred. No. 2.8;
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                                                                                                                                                                                                                                       Sequence 521 BP; 113 A; 140 C; 138 G; 130 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Probe; microorganism detection; microbiological quality;
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Pred. No. 2.8;
                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Micro-organism detection probe #55.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CCCCTGAATGCGGCTAATC 405
                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CCCCTGAATGCGGCTAATC 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ВР.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%;
100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             06-JUL-2000; 2000FR-00008839.
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nes 19; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Guillot E,
Laffaire P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (revised)
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Best Local Similarity
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25-JUN-2002
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Armand M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABL53113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             387
                                                                                                                                                                                                                                                                                                            Query Match
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Matches

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The invention describes a polymerase chain reaction (PCR) and primers for detecting nucleic acids from the diabetogenic coxsackie B virus-4 (CBV-4) strain VD221, (particularly VP1, VP2, VP3, VP4, P2A, P2B, P2C, P3A, P3B, P3C and P3D nucleic acids). The methods and primers are used for the detection of CBV-4 strain VD291 which is associated with diabetes (diabetogenic enterovirus). Early detection of the diabetes e.g. detection of diabetogenic enteroviral RNA in peripheral mononuclear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cells, can improve prognosis by allowing treatment e.g. with antiviral drugs, to prevent further loss of beta cells and severe long term consequences of diabetes including blindness, renal failure and leg amputations. This sequence represents a diabetogenic coxsackie B virus 4 (CBV-4) strain VD2921 associated polynucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Polymerase chain reaction and primers for detecting nucleic acids from the diabetogenic coxsackie B virus-4 strain VD2921.
                                                                                      Coxsackie virus strain VD2921; diabetogenic coxsackie B virus-4; strain VD2921; VP1; VP2; VP4; P2A; P2B; P2C; P3A; P3B; P3C; diabetes; diabetogenic enterovirus; beta cell loss; blindness; renal failure; leg amputation; ds.
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                                              Coxsackie B virus 4 (CBV-4) strain VD2921 associated DNA #8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 19; DB 8; Length 551;
Pred. No. 2.9;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       364 CCCCTGAATGCGGCTAATC 382
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100.0%;
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                                                                                                                                                                                                                                                                                                                         19-JUN-2002; 2002WO-IB003278.
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      (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Frisk GE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2003-278229/27.
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Best Local Similarity
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                                                                                                                                                                                                Coxsackievirus.
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      10-MAY-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention describes a polymerase chain reaction (PCR) and primers for detecting nucleic acids from the diabetogenic coxsackie B virus-4 (CBV-4) strain VD291, (particularly VP1, VP2, VP3, VP4, P28, P28, P22, P32, P33, P38, P36, P30 and P30 nucleic acids). The methods and primers are used for the detection of CBV-4 strain VD2921 which is associated with diabetes (diabetogenic enterovirus). Early detection of the diabetes e.g. detection of diabetogenic enteroviral mononuclear cells, can improve prognosis by allowing treatment e.g. with antiviral drugs, to prevent further loss of beta cells and severe long term
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      consequences of diabetes including blindness, renal failure and leg amputations. This sequence represents a diabetogenic coxsackie B virus 4 (CBV-4) strain VD2921 associated polynucleotide
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      Gaps
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                                                                                                                                                                                                                                                                                                                                                             Coxsackie virus strain VD2921; diabetogenic coxsackie B virus-4; strain VD2921; VP2; VP3; VP4; P2A; P2B; P2C; P3A; P3B; P3C; diabetes; diabetogenic enterovirus; beta cell loss; blindness; renal failure; leg amputation; ds.
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                                                                                                                                                                                                                                                                                                                     Coxsackie B virus 4 (CBV-4) strain VD2921 associated DNA #3.
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    Indels
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    Mismatches
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                                                                                   391 cccrigaariccecriaaric 409
                                            1 CCCCTGAATGCGGCTAATC 19
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ID ABX12453 standard; DNA; 551
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AC ABX12453;
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  Conservative
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Best Local Similarity 100.
Matches 19; Conservative
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RESULT 62

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                                                                                                                               Polymerase chain reaction and primers for detecting nucleic acids from the diabetogenic coxsackie B virus-4 strain VD2921.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Coxsackie virus strain VD2921; diabetogenic coxsackie B virus-4;
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                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 19; DB 8; Length 552; 100.0%; Pred. No. 2.9;
                                                                                                                                                                                                                                                                                                                                   Sequence 552 BP; 131 A; 143 C; 140 G; 138 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                             (CBV-4) strain VD2921 associated polynucleotide
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                   19-JUN-2002; 2002WO-IB003278.
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                                          20-JUN-2001; 2001SE-00002198.
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                                                                                     Tuvemo HT, Frisk GE,
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                                                                                                         WPI; 2003-278229/27.
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tes 19; Conserv
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27-DEC-2002
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                                                                                                                                      The invention describes a polymerase chain reaction (PCR) and primers for detecting nucleic acids from the diabetogenic cossackie B virus-4 (CBV-4) strain VD2921, (particularly VP1, VP2, VP3, VP4, P2A, P2B, P2C, P3A, P3B, P3C and P3D nucleic acids). The methods and primers are used for the diabetogenic enterovirus). Barly detection of the diabetes e.g. detection of GBV-4 strain VD2921 which is associated with diabetes e.g. detection of diabetogenic enteroviral RNA in peripheral monounclear cells, can improve prognosis by allowing treatment e.g. with antiviral drugs, to prevent further loss of beta cells and severe long term consequences of diabetes including blindness, renal failure and leg amputations. This sequence repersents a diabetogenic coxeackie B virus 4 (CBV-4) strain VD2921 associated polynucleotide
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P3D;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 19; DB 8; Length 554; Pred. No. 2.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 554 BP; 130 A; 149 C; 142 G; 133 T; 0 U; 0 Other;
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the diabetogenic coxsackie B virus-4 strain VD2921.
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                                                                        Disclosure; Page 75; 79pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             362 CCCCTGAATGCGGCTAATC 380
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Best Local Similarity
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ABX12456 standard; DNA; 559 BP.

RESULT 67

ABX12456

10-MAY-2003

ABX12456;

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consequences of diabetes including blindness, renal failure and leg
amputations. This sequence represents a diabetogenic coxsackie B virus
(CBV-4) strain VD2921 associated polynucleotide
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                                                                                                                                                   Gaps
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                                                                                                             Score 19; DB 8; Length 556;
Pred. No. 2.9;
                                                                           Sequence 556 BP; 125 A; 153 C; 143 G; 135 T; 0 U; 0 Other;
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100.0%; Pred. No. 2...
0; Mismatches
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19; Conservative 0
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Best Local Similarity
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                                                                                                                                  Coxeackie virus strain VD2921; diabetogenic coxeackie B virus-4; strain VD2921; VP1; VP2; VP3; VP4; P2A; P2B; P2C; P3A; P3B; P3C; diabetes; diabetogenic enterovirus; beta cell loss; blindness; renal fallure; leg amputation; ds.
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                                                                                                    Coxsackie B virus 4 (CBV-4) strain VD2921 associated DNA #11.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Frisk GE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2003-278229/27.
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tes 19; Conserv
                                                                                                                                                                                                                                                                 WO2002103060-A2
                                                                                                                                                                                                                               Coxsackievirus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Tuvemo HT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABX12447;
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365 ccccreariccecraarc 383

1 CCCCTGAATGCGGCTAATC 19

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Best Local Similarity 100. Matches 19; Conservative

Query Match

Score 19; DB 8; Length 556; Pred. No. 2.9;

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The invention describes a polymerase chain reaction (PCR) and primers for
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                                                                                                                                  Polymerase chain reaction and primers for detecting nucleic acids from the diabetogenic coxsackie B virus-4 strain VD2921.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Coxsackie virus strain VD2921; diabetogenic coxsackie B virus-4; strain VD2921; VP1; VP2; VP3; VP4; P2A; P2B; P2C; P3A; P3B; P3C; diabetes; diabetogenic enterovirus; beta cell loss; blindness;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Coxsackie B virus 4 (CBV-4) strain VD2921 associated DNA #10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 19; DB 8; Length 562; 100.0%; Pred. No. 2.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 562 BP; 134 A; 148 C; 140 G; 140 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 74; 79pp; English.
                                                                                                                                                                                            Disclosure; Page 74; 79pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             renal failure; leg amputation; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.08; F1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CCCCTGAATGCGGCTAATC 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 CCCCTGAATGCGGCTAATC 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABX12455 standard; DNA; 567 BP.
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                 (INNO-) INNOVENTUS PROJECT AB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20-JUN-2001; 2001SE-00002198.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                         Frisk GE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Frisk GE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2003-278229/27
                                                                                               WPI; 2003-278229/27
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tes 19; Conserv
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                                                       Tuvemo HT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABX12455;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABX12455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention describes a polymerase chain reaction (PCR) and primers for detecting nucleic acids from the diabetogenic coxeackie B virus-4 (CBV-4) strain VD2921, (particularly VP1, VP2, VP3, VP4, P24, P24, P28, P26, P33, P3B, P3C and P3D nucleic acids). The methods and primers are used for the detection of CBV-4 strain VD2921 which is associated with diabetes edetection of GBV-8 strain VD2921 which is passociated with diabetes edgenic enterovirus). Barly detection of the diabetes e.g. detection of diabetogenic enteroviral RNA in peripheral mononuclear cells, can improve prognosis by allowing treatment e.g. with antiviral drugs, to prevent further loss of beta cells and severe long term consequences of diabetes including blindness, renal failure and leg amputations. This sequence repersents a diabetogenic coxeackie B virus 4 (CBV-4) strain VD2921 associated polynucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CBV-4;
P3D;
                                                                                                                                                                                                                                                                                                                                                                                    Polymerase chain reaction and primers for detecting nucleic acids from the diabetogenic coxsackie B virus-4 strain VD2921.
strain VD2921; VP1; VP2; VP3; VP4; P2A; P2B; P2C; P3A; P3B; P3C; P3D; diabetes; diabetogenic enterovirus; beta cell loss; blindness; renal failure; leg amputation; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Coxeackie virus strain VD2921; diabetogenic coxeackie B virus-4; estrain VD2921; VP1; VP2; VP4; P2A; P2B; P2C; P3A; P3B; P3C; diabetes; diabetogenic enterovirus; beta cell loss; blindness; renal failure; leg amputation; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Coxsackie B virus 4 (CBV-4) strain VD2921 associated DNA #9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 19; DB 8; Length 560; 100.0%; Pred. No. 2.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 560 BP; 135 A; 143 C; 144 G; 138 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 72; 79pp; English.
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                                                                                                                                                                                                                                                                   (INNO-) INNOVENTUS PROJECT AB
                                                                                                                                                                                        19-JUN-2002; 2002WO-IB003278.
                                                                                                                                                                                                                               20-JUN-2001; 2001SE-00002198.
                                                                                                                                                                                                                                                                                                           Yin H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19-JUN-2002; 2002WO-IB003278.
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Best Local Similarity 100.
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                           Tuvemo HT, Frisk GE,
                                                                                                                                                                                                                                                                                                                                                WPI; 2003-278229/27.
                                                                                                                WO2002103060-A2
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                                                                           Coxsackievirus
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RESULT 69

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detecting nucleic acids from the diabetogenic coxsackie B virus-4 (CBV-4 strain VD2921, (particularly VP1, VP2, VP3, VP4, P2A, P2B, P2C, P3A, P3E P3C and P3D nucleic acids). The methods and primers are used for the detection of CBV-4 strain VD2921 which is associated with diabetes (diabetogenic enterovirus). Early detection of the diabetes e.g. detection of diabetogenic enteroviral RNA in peripheral mononuclear cells, can improve prognosis by allowing treatment e.g. with antiviral consequences of diabetes including blindness, renal failure and leg amputations. This sequence represents a diabetogenic coxsackie B virus (CBV-4) strain VD2921 associated polynucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Heterodimer platelet-derived-growth factor (PDGF) prodn. - using a polycistronic vector system in mammalian host cells for equimolar prodn
                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mielke H;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Poliovirus type 1 5'-UTR with C to G substn. at position 610.
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                                                                                                                                                                                                           Score 19; DB 8; Length 567; Pred. No. 2.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Platelet-Derived Growth Factor; heterodimer; PDGF-AB; recombinant protein production; PDGF-A chain; PDGF-B chain; bicistronic vector system; 88.
                                                                                                                                                                              Sequence 567 BP; 140 A; 147 C; 141 G; 139 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                       Mismatches
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H;
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(GBFB ) GBF GES BIOTECH FORSCHUNG GMBH.
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                                                                                                                                                                                            100.0%; Scur
100.0%; Pre
0; '
                                                                                                                                                                                                                                                                                    366 CCCCTGAATGCGGCTAATC 384
                                                                                                                                                                                                                                                                     1 CCCCTGAATGCGGCTAATC 19
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lrth M, Hauser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human poliovirus 1 Mahoney
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(first entry)
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/*tag≈ P
610
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                                                                                                                                                                                                          Query Match
Best Local Similarity 100.
Matches 19; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1994-101191/12
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of A- and B-chains.
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Dirks W, W
                                                                                                                                                                                                                                                                                                                                                                                                     AAQ58715;
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5'UTR
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-B and PDGF-A chains. The preferred IRES sequence for inclusion in the bicistronic construct is the 5'-UTR from Poliovirus type 1 Mahoney strain of sequence AAG58715. (Updated on 25-MAR-2003 to correct PN field.) (Updated on 27-AUG-2003 to correct OS field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Heterodimeric proteins can be recombinantly produced using a multicistronic (esp. bicistronic) expression unit in which a sequence responsible for internal translation start (designated "IRES") is located between cistrons coding for the different subunits. The preferred IRES sequence is the 5'-UTR from Poliovirus type 1 Mahoney strain of sequence AAQS8726. (Updated on 25-MAR-2003 to correct PN field.) (Updated on 27-
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                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              producing equimolar amts.
                                                                                                                                                                                                                                                                                                                                                                                                                      88.
                                                                                                                                                                                                                                                                                                                                                                                                     Multicistronic expression unit; recombinant protein production; internal translation start; initiation; 5'-untranslated region;
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/note= "wild-type C has been substituted by
                                                                                                  2; Length 628;
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Pred. No. 2.9;
                                                                     Sequence 628 BP; 143 A; 165 C; 162 G; 158 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 628 BP; 143 A; 165 C; 162 G; 158 T; 0 U; 0 Other;
                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Achterberg V;
                                                                                               100.0%; Score 19; DB 2
100.0%; Pred. No. 2:9;
ive 0; Mismatches
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Mielke H;
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(GBFB ) GBF GES BIOTECH FORSCHUNG GMBH
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                                                                                                                                                                                   451 CCCCTGAATGCGGCTAATC 469
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                                                                                                                                                       1 CCCCTGAATGCGGCTAATC 19
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Doerschner A, Meyer-Ingold W,
                                                                                                                                                                                                                                                          ВР
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                                                                                                                              Conservative
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(revised)
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                                                                                               Query Match
Best Local Similarity
Matches 19; Conserv
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29-SEP-1994
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5'UTR
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Echo virus (ECV12) 5' non-translated region (NTR) sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention relates to a new bicistronic retroviral vector. These are used for (over) expression of proteins, suppressing expression of fnon-) viral RNA and/or proteins by the antisense technique, e.g. to suppress a dominant-negative phenotype, also infectious viral particles that contain the vectors, in gene therapy, particularly for control of guest versus host disease, especially where haematopoietic cells are transduced with the vector or where T cells are transduced, for adoptive immunotherapy, but also for treating severe combined immune deficiency syndrome and for expression cloning of genes. The present sequence is a vector sequence fragment shown in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                        Bicistronic retroviral vector, useful in gene therapy, particularly of graft versus host disease, contains components of both murine embryonic stem cell and myeloproliferative sarcoma viruses.
                                                                                                                                                                                   immunosuppressive; gene therapy; vector; bicistronic retroviral vector; severe combined immune deficiency syndrome; protein expression;
 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                              Novel bicistronic retroviral vector related poliovirus IRES sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 639 BP; 146 A; 171 C; 164 G; 158 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
 Indels
                                                                                                                                                                                                                                                                                                                                                               Strathmann G;
 ..
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                              Gindullis F, Hannemann J,
                                                                                                                                                                                                                                                                                                                                        (CELL-) CELLTECH GMBH BIOTECHNOLOGIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 70; 91pp; German.
                                          451 CCCCTGAATGCGGCTAATC 469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    455 CCCCTGAATGCGGCTAATC 473
                     1 CCCCTGAATGCGGCTAATC 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 CCCCTGAATGCGGCTAATC 19
                                                                                               ADP74707 standard; DNA; 639 BP
                                                                                                                                                                                                                                                                                              09-DEC-2002; 2002EP-00027555.
                                                                                                                                                                                                                                                                                                                    09-DEC-2002; 2002EP-00027555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAC85153 standard; RNA; 646
                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 100.
Matches 19; Conservative
19; Conservative
                                                                                                                                                                                                          antisense; ds; gene.
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                                                                                                                                                                                                                                                   EP1428886-A1
                                                                                                                                                                                                                                                                                                                                                              Heberlein C,
                                                                                                                                                                                                                             Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  08-MAY-2001
                                                                                                                                         26-AUG-2004
                                                                                                                                                                                                                                                                         16-JUN-2004.
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                                                                                                                     ADP74707;
Matches
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                                                                           RESULT 73
                                                                                    ADP74707
ID ADP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Recombinant enterovirus genome for use as vector or vaccine, modified by replacing a part or all of its 5'non-translated region by 5'NTR of enterovirus genome that encodes virus modified in tropism or virulence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
Gene therapy; enterovirus; vaccine; diagnostic; RT-PCR; primer;
Coxsackievirus B3; CVB3; NTR; non-translated region; echo virus; ds.
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Pred. No. 2.9;
4; Mismatches 0; Indels
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                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                       '*tag= c
'note= "Domain III"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        *tag= g
'note= "Domain VII"
                                                                                                                                                                                                                                           /*tag= b
/note= "Domain II"
183. .232
                                                                                                                                                                                                                                                                                                                                                                                              /*tag= d
/note= "Domain IV"
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/note= "Domain VI"
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                                                                                                                                                   2. .87
/*tag= a
/note= "Domain I"
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note= "Domain V"
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454 CCCCUGAAUGCGGCUAAUC 472
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Best Local Similarity 78.9%;
Matches 15; Conservative
                                                                                                                                                                                                                    .180
                                                                                                                                                                                                                                                                                                                                                                     .443
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                                                                                                                                                                                                                                                                                                                                                                          240.
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                                                                         Scho virus
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                                                                                                                                                stem_loop
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AAC85173

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The invention provides an enterovirus genome (1) for use as a vector or vaccine, modified to produce a virus (V1) having a restricted or altered species or tissue tropism, compared to an equivalent unmodified virus, or modified to produce an attenuated virus (V2), by replacing a part or all of the 5'non-translated region (5'NTR) of (1) with a 5'NTR of an enterovirus genome that encodes V1 or V2. (1) is useful as vaccine or vector in targeting genes of interest to specific cells or tissues. (1) is also useful for diagnostic purposes, e.g. to identify virulent, versus nonvirulent strains of an enterovirus. The present sequence represents
                                                                                                                                                                                                                                                                     Recombinant enterovirus genome for use as vector or vaccine, modified by replacing a part or all of its 5'non-translated region by 5'NTR of enterovirus genome that encodes virus modified in tropism or virulence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (non-translated region) of a non-cardiovirulent enterovirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 19; DB 4; Length 660; Pred. No. 2.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 660 BP; 157 A; 170 C; 166 G; 167 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Coxsackie virus B5 polynucleotide sequence SEQ ID NO:67.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA detection; enteroviral detection; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Coxsackievirus B3 (CVB3)/CO strain
                                                                                                                                                                                    Dunn JJ;
                                                                                                                                                                                                                                                                                                                                                     Example 2; Page 25; 49pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        373 CCCCTGAATGCGGCTAATC 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tsang S, Price JA, Hellyer TJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 CCCCTGAATGCGGCTAATC 19
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                                                          08-JUL-2000; 2000WO-US018681
                                                                                                    99US-0143104P
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1es 19; Conservative
                                                                                                                                                                                    Bradrick SS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human goxsackievirus B5
                                                                                                                                           (UYNE-) UNIV NEBRASKA
                                                                                                                                                                                                                             WPI; 2001-138310/14.
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(PRIC/) PRICE J A.
(HELL/) HELLYER T J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2005-512251/52.
GENBANK; AF169665.
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                                                                                                 09-JUL-1999;
                   18-JAN-2001
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                                                                                                                                                                                    Romero JR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the 5' NTR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 77
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention provides an enterovirus genome (I) for use as a vector or vaccine, modified to produce a virus (VI) having a restricted or altered species or tissue tropism, compared to an equivalent unmodified virus, or modified to produce an attenuated virus (V2), by replacing a part or all of the 5'non-translated region (5'NTR) of (I) with a 5'NTR of an enterovirus genome that encodes VI or V2. (I) is useful as vaccine or vector in targeting genes of interest to specific cells or tissues. (I) is also useful for diagnostic purposes, e.g. to identify virulent, versus nonvirulent strains of an enterovirus. The present sequence represents the 5'NTR (non-translated region) of the cardiovirulent enterovirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Recombinant enterovirus genome for use as vector or vaccine, modified by replacing a part or all of its 5'non-translated region by 5'NTR of enterovirus genome that encodes virus modified in tropism or virulence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                    Coxsackievirus B3 (CVB3)/AS 5' non-translated region (NTR) sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Coxsackievirus B3 (CVB3)/CO 5' non-translated region (NTR) sequence.
                                                                                                                                                                                Gene therapy; enterovirus; vaccine; diagnostic; RT-PCR; primer; Coxeackievirus B3; CVB3; NTR; non-translated region; ds.
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Coxsackievirus B3; CVB3; NTR; non-translated region; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dunn JJ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 CCCCTGAATGCGGCTAATC 19
             AAC85173 standard; DNA; 654 BP
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                                                                                               (first entry)
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                                                                                                                                                                                                                                             Coxsackievirus
                                                                                                                                                                                                                                                                                      WO200104136-A1
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Best Loca Matches

RESULT 7

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Gaps

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Indels

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The invention relates to an oligonucleotide (I) consisting of: (a) the target binding sequence of an oligonucleotide chosen from any one of the to sequence of ARBS672 to ARBS671; and (b) a sequence required for selected amplification or detection. Also described: (1) a kit (KI) comprising (I), and one or more container that contains (I); and (2) detecting (MI) an enterovirus target sequence, involving: (a) amplifying the target sequence using first amplification primer having a sequence consisting essentially of target binding sequence of any one of ARBS6764 to ARBS6771 and optionally a sequence required for selected amplification reaction; and (b) detecting the amplified target sequence. (I), (MI) and (KI) are useful for detecting enterovirus target sequence. (I) specifically and selectively recognizes the enterovirus genome. (I) specifically and rapidaly detects fewer than 500 copies of enterovirus serotypes. The present sequence represents a coxsackie virus B5 polynucleotide sequence, which is given in the exemplification of the present invention. Note: the present sequence is designated as SSQ ID NO:67 in the Sequence Listing. Use the drawings.
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   amplifying or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Enteroviral genus related disease; Prima7-related disease; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated or recombinant virus, useful for detecting a molecule capable of specifically binding the virus in a sample, and as a vaccine or medicament for treating or preventing Prima7-related disease.
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Novel oligonucleotide comprising sequences for binding and amplisdetecting target, useful for detecting enterovirus nucleic acids.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 19; DB 14; Length 660;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 660 BP; 157 A; 170 C; 166 G; 167 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. 2.9;
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                                                      Disclosure; SEQ ID NO 67; 34pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           373 CCCCTGAATGCGGCTAATC 391
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADU77356 standard; DNA; 682 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Prima7 virus 5' UTR region DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Van Den Broek PJM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-MAY-2003; 2003EP-00076529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21-MAY-2003; 2003EP-00076529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (PRIM-) PRIMAGEN HOLDING BV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 100.
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2004-823915/82.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Prima7 virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EP1479761-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10-FEB-2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24-NOV-2004.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Maas HCGI,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADU77356;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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The present invention provides a new isolated or recombinant virus called Prima7 (which belong to enteroviral species) comprising a nucleic acid

Example; SEQ ID NO 39; 51pp; English

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sequence or its functional part, derivative or analogue of the said virus. The invention is useful for detecting and/or identifying a Prima7 enterovirus in a sample and for diagnosing an enteroviral genus related disease. The vaccine or medicament prepared from the Prima7 virus is useful for preventing and/or treating a Prima7-related disease. The invention is also useful in gene therapy. The present sequence is Prima7 virus 5' UTR region DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             vector; neurological disease; ds; gene therapy; internal ribosome entry site; cystic fibrosis; cns-gen.; respiratory-gen.; factor VIII deficiency; hemostatic; genetic disorder; factor IX deficiency; Duchenne dystrophy; muscular-gen.; Becker's disease; cancer; cytostatic; neoplasm; acquired immune deficiency syndrome; anti-hiv; infectious disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Enterovirus 71 5' untranslated region internal ribosome entry site DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New nucleic acid vector for the expression of at least two cistrons comprising a nucleotide sequence comprising an internal ribosome entry site (IRES) e.g. enterovirus 71 (EV71), useful for treating a patient having e.g. AIDS.
                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                 ö
                                                                                                                                                                                            100.0%; Score 19; DB 13; Length 682; 100.0%; Pred. No. 2.9;
                                                                                                                                                          Sequence 682 BP; 176 A; 157 C; 159 G; 190 T; 0 U; 0 Other;
                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human enterovirus 71; strain TW/2086/98.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 2; SEQ ID NO 1; 23pp; English.
                                                                                                                                                                                                                                                                                                            390 CCCCTGAATGCGGCTAATC 408
                                                                                                                                                                                                                                                                     1 CCCCTGAATGCGGCTAATC 19
                                                                                                                                                                                                                                                                                                                                                                                                      BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 08-JUL-2003; 2003US-00614283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    09-JUL-2002; 2002US-0394269P
                                                                                                                                                                                                                                                                                                                                                                                                      AEA00424 standard; DNA; 709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lee J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2005-371616/38.
                                                                                                                                                                                                              Local Similarity
les 19; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US2005112095-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WU T.
LEE J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     antimicrobial.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HSU T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wu T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26-MAY-2005.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28-JUL-2005
                                                                                                                                                                                                                                                                                                                                                                                                                                         AEA00424;
                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (HSUT/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (LEEJ/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (WUTT/
                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                  RESULT 79
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Location/Qualifiers

(first entry)

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10. .34 /\*tag= a /note= "stemloop B

\*tag= d note= "Domain I"

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\*tag= b note= "stemloop

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/\*tag= c /note= "stemloop D 105. .181 \*tag= e note= "Domain II" note= "Domain III"

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tag=

\*tag= g note= "Domain IV"

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Coxsackievirus B3 (CVB3) 5' non-translated region (NTR) sequence.
                                                                                                                                                                                                                                                          Gene therapy; enterovirus; vaccine; diagnostic; RT-PCR; primer;
Coxsackievirus B3; CVB3; NTR; non-translated region; ds.
     AAC85152
ID AAC85152 standard; RNA; 745 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200104136-A1
                                                                                                                                                                                                                                                                                                                                              Coxsackievirus
                                                                                                                                              08-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18-JAN-2001
                                                                                       AAC85152;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention provides a system for making SARS-coronavirus virus -like particles (SARS-COV-VIPS) comprising one or more recombinant vectors that expresses the SARS-COV E (small membrane)-protein, SARS-COV M (membrane)-protein and SARS-COV E (spike)-protein. The invention is useful for inducing cellular and/or humoral immune response. The invention is also useful to reduce the symptoms of SARS-COV infections and in vaccine preparations. The present sequence is Poliovirus type I strain mahoney internal ribosomal entry site (IRES) coha, This coha sequence is used in the preparation of plasmid for the expression of SARS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New system comprising one or more recombinant vectors that expresses the SARS-COV E-protein, SARS-COV M-protein, and SARS-COV S-protein, useful for making SARS-coronavirus virus-like particles.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SARS-coronavirus virus-like particle; SARS-COV-VLP; cellular immune response; humoral immune response; vaccine; immunogenicity; cytotoxic T-lymphocyte; internal ribosomal entry site;
                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Poliovirus type 1 strain mahoney internal ribosomal entry site cDNA
                                                                                                                                                                        ;
0
                                                                                                              DB 14; Length 709;
3;
                                                       Sequence 709 BP; 165 A; 185 C; 172 G; 187 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 743 BP; 175 A; 185 C; 181 G; 202 T; 0 U; 0 Other;
                                                                                                                                                                     Indels
                                                                                                                                                                     ö
                                                                                                           / Match
Local Similarity 100.0%; Score 19; DB
Local Similarity 100.0%; Pred. No. 3;
Ne 19; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 2; SEQ ID NO 21; 111pp; English
untranslated region (UTR) IRES DNA
                                                                                                                                                                                                                                                                     420 CCCCTGAATGCGGCTAATC 438
                                                                                                                                                                                                                                                                                                                                                                                                                         ADW37919 standard; cDNA; 743 BP.
                                                                                                                                                                                                                       1 CCCCTGAATGCGGCTAATC 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               04-MAY-2004; 2004US-00839729.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      06-MAY-2003; 2003US-0468703P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'B and S proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2005-065191/07.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human poliovirus 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (HERO/) HEROLD J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US2005002953-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24-MAR-2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        06-JAN-2005.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Herold J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADW37919;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IRES; 88.
                                                                                                                 Query Match
                                                                                                                                           Best Loca
Matches
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The invention provides an enterovirus genome (1) for use as a vector or vaccine, modified to produce a virus (V1) having a restricted or altered species or tissue tropism, compared to an equivalent unmodified virus, or modified to produce an attenuated virus (V2), by replacing a part or all of the 5'non-translated region (5'NTR) of (1) with a 5'NTR of an enterovirus genome that encodes V1 or V2. (1) is useful as vaccine or vector in targeting genes of interest to specific cells or tissues. (1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Recombinant enterovirus genome for use as vector or vaccine, modified by replacing a part or all of its 5'non-translated region by 5'NTR of enterovirus genome that encodes virus modified in tropism or virulence.
                                                                                                                                                                                                                                                                                   Dunn JJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure, Fig 1, 49pp, English.
08-JUL-2000; 2000WO-US018681.
                                                                                                                                                                                                                                                                              Romero JR, Bradrick SS,
                                                                                                                                                                                  (UYNE-) UNIV NEBRASKA
                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-138310/14.
                                                                                           09-JUL-1999;
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Gaps

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100.0%; Score 19; DB 14; Length 743; 100.0%; Pred. No. 3; ive 0; Mismatches 0; Indels (

448 CCCCTGAATGCGGCTAATC 466

1 CCCCTGAATGCGGCTAATC 19 llarity 100.0%; F Conservative 0;

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Local Similarity es 19; Conserv

Best Loca Matches

Query Match

\*tag= j note= "Domain VII"

\*tag= i note= "Domain VI"

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\*tag= h note= "Domain V"

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is also useful for diagnostic purposes, e.g. to identify virulent, versus nonvirulent strains of an enterovirus. The present sequence represents the enterovirus Coxsackievirus B3 (CVB3) 5' NTR (non-translated region)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Creating nucleic acid sequence for carrying out translation by internal ribosome entry site element and expressing nucleotide sequence of interest in eukaryotic cell, by creating a nucleic acid having adeninerich block.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gleba Y;
                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Poliovirus internal ribosome entry site-containing mRNA 5' UTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ivanov P,
                                                                                                                                                                               DB 4; Length 745;
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                                                                                                                             Sequence 745 BP; 184 A; 192 C; 181 G; 1 T; 187 U; 0 Other;
                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Internal ribosome entry site; IRES; translation; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Skulachev M, Ivanov P,
                                                                                                                                                                            t; Score 19; DB
: Pred. No. 3;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
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                                                                                                                                                                                                                                                                                                         455 CCCCUGAAUGCGGCUAAUC 473
                                                                                                                                                                                                                                                                                  1 CCCCTGAATGCGGCTAATC 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACC48197 standard; cDNA; 745 BP.
                                                                                                                                                                         Query Match
Best Local Similarity 78.9%;
Matches 15; Conservative 4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Dorokhov Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tailor-made activity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11-AUG-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Poliovirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACC48197;
                                                                                 seguence
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5'UTR
                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 82
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IID ACC4

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ACC4

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ACC4

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ACC4

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ACC4

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ACC5

BIJL-A

BIJL-A
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The invention relates to a novel method for detecting and/or quantifying Human metapneumovirus (hMPV) in a sample comprising providing at least cone probe or primer specific for a nucleic acid sequence of hMPV, contacting the one probe and/or primer with the sample to allow annealing of the probe and/or primer with the sample to allow annealing and/or quantifying the nucleic acid sequence using the annealed probe and/or primer. The method of the invention may be useful for detecting and/or quantifying Human metapneumovirus (hMPV) in a sample. The current sequence is that of the Human coxsackievirus BI complete genomic DNA of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Detecting and/or quantifying human, metapneumovirus (hMPV) in a sample comprises contacting the at least one probe and/or primer with the sample to allow annealing of the probe and/or primer with the nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 810 BP; 243 A; 180 C; 190 G; 197 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                Human coxsackievirus B1 complete genomic DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 32; SEQ ID NO 137; 158pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADU47469 standard; cDNA; 1560 BP
                                          454 CCCCTGAATGCGGCTAATC 472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Enterovirus type 71 (EV71) cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22
19
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                                                                                                                                                                   BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CCCCTGAATGCGGCTAATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19-DEC-2003; 2003WO-CA001994.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19-DEC-2002; 2002CA-02411264 24-JAN-2003; 2003CA-02418004
                                                                                                                                                                   ADP82873 standard; DNA; 810
                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27-JAN-2005 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                B
                                                                                                                                                                                                                                                                                                                                                                                                                Human coxsackievirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2004-500307/47.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
nes 19; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (UYLA-) UNIV LAVAL
                                                                                                                                                                                                                                                                                                                                                             hMPV detection; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO2004057021-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the invention
                                                                                                                                                                                                                                                                   23-SEP-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          08-JUL-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Boivin G;
                                                                                                                                                                                                                   ADP82873;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADU47469;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seguence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                 RESULT 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 84
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Gaps

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0; Indels

100.0%; Score 19; DB 8; 100.0%; Pred. No. 3; iive 0; Mismatches 0;

Best\_Local Similarity 100. Matches 19; Conservative

Query Match

Length 745;

Gaps

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Indels

Enterovirus

primer\_bind

Kev

primer\_bind

misc\_binding

primer\_bind

primer\_bind

misc\_binding

misc\_binding

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The invention relates to the production of platelet-derived growth factor (PDGF) comprising a transgenic mammal whose somatic and germ cells comprise a nucleic acid sequence (I) encoding PDGF, operably linked to a promoter directing expression into mammalian gland epithelial cells, and obtaining the milk from the transgenic mammal where at least 30% of the PDGF in the milk is as a dimer. Also described is a method of producing a transgenic mammal capable of expressing an active PDGF molecule in milk.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Platelet-derived growth factor expression cassette insert used in pBC701.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Production of platelet derived growth factor (PDGF) comprises expression in the milk of a non-human transgenic animal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pharmaceutical compositions can be obtained from this milk and can be used to stimulate or enhance the wound healing process, in particular diabetic foot ulcers, decubitus ulcers and venous stasis ulcers.

Transgenic POGF (II) can also be used in the treatment of periodontal regeneration, stimulation of bone formation, ophthalmic diseases or healing of prosthetic vascular grafts. (II) can also be used for non-medical applications, e.g., as a supplement for cell culture media or as a component of diagnostic kits. The present sequence represents the platelet-derived growth factor expression cassette insert used in pBC701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Platelet-derived growth factor; PDGF; transgenic; milk; gene; wound healing; diabetic foot ulcer; decubitus ulcer; ophthalmic disease; venous stasis ulcer; periodontal regeneration; bone formation; prosthetic vascular graft; pBC701; ds
at least one synthetic nucleotide sequence fixed on a solid substrate detecting hybridisation. The present sequence is the enterovirus type (EV71) cDNA.
                                                                                                                         100.0%; Score 19; DB 13; Length 1560; 100.0%; Pred. No. 3.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 19; DB 6; Length 2076; 100.0%; Pred. No. 3.4;
                                                                                        Sequence 1560 BP; 421 A; 401 C; 346 G; 392 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2076 BP; 441 A; 612 C; 607 G; 416 T; 0 U; 0 Other;
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                                                                                                                                   100.0%; Prec. ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Echelard Y, Meade H, Bichner W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (GENZ ) GENZYME TRANSGENICS CORP.
                                                                                                                                                                                                                             456 CCCCTGAATGCGGCTAATC 474
                                                                                                                                                                                                    1 CCCCTGAATGCGGCTAATC 19
                                                                                                                                                                                                                                                                                                                                   ABK14791 standard; DNA; 2076 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 1; Fig 1; 59pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19-JUN-2001; 2001WO-US041044.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19-JUN-2000; 2000US-0212406P.
                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                           Local Similarity 100.
Les 19; Conservative
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                              08-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                        ABK14791;
                                                                                                                         Query Match
                                                                                                                                               Best Loc
Matches
                                                                                                                                                                                                                                                                                            RESULT 85
                                                                                                                                                                                                                                                                                                                 ABK14791
             SKSSS
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                                                                                                                                                                                                                                     셤
                                                                                                                                                                                                                                                                                                                                     The invention provides a method and a kit for detecting and differentiating an enterovirus type 71 (BV71) in a sample. The method involves contacting nucleic acids in the sample with a pair of primers to form an amplification product, contacting the amplification product with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New kit comprising a pair of oligonucleotide primers for nucleic acid amplification, useful in detecting and differentiating an enterovirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /*tag= 1
/bound_moiety= "71-2/16-2 probe"
1454. 1481
/*tag= m
/bound_moiety= "71-3 probe"
1485. 1504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              *tag= k
bound_moiety= "16-1 probe"
.390. .1419
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                                                                                                                                                                                                                                                                                                                                               *tag= e
bound moiety= "pl probe"
14. .546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 *tag= g
bound moiety= "p3 probe"
83. .602
                                                                                                                                                                                                                                                                                                                                                                                                          *tag= f
bound_moiety= "p2 probe"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Wang
         Detection; enterovirus type, 71; EV71; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; SEQ ID NO 16; 14pp; English.
                                                                                                                   /*tag= a
/note= "f1 primer"
167. .187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /*tag= i
/note= "rl primer"
1179. .1198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /*tag= j
/note= "f7 primer"
1344. .1373
                                                                                    location/Qualifiers
                                                                                                                                                                                            note= "f2 primer"
                                                                                                                                                                                                                                     *tag= c
note= "f3 primer"
23. .439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       *tag= h
note= "r2 primer"
27. 645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Wang Y,
                                                                                                                                                                                                                                                                                                            note= "f5 primer"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "r3 primer"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-NOV-2000; 2000US-00724678.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28-NOV-2000; 2000US-00724678
                                                                                                                                                                                                                                                                                                                             .474
                                                                                                                                                                                                                 48. .266
                                                                                                                                                                                                                                                                                                                                                                                                                                                 47. .574
                                                                                                                                                                                *tag=
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misc\_binding

primer\_bind

primer\_bind

primer\_bind

misc\_binding

misc\_binding

primer\_bind

US6818397-B1

Matches

ઠ 셤 AAH20890;

RESULT 86

AAH20890

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Viral vector that expresses single-chain interleukin-12 and costimulator, useful for treatment of tumors, viral infections, e.g. human immunodeficiency virus, and prion diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention relates to a viral vector that includes a nucleic acid encoding a single-chain interleukin-12 (IL-12) and a co-stimulatory protein. Viral vectors and virus particles derived from them are useful for treatment of tumours, infectious diseases (e.g. HIV, hepatitis A, B or C, cytomegalovirus or human papilloma virus), or prion diseases. The present sequence is a triciatronic expression cassette used in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         immunosuppressive; gene therapy; vector; bicistronic retroviral vector; severe combined immune deficiency syndrome; protein expression;
                                                                                                                                        Tricistronic expression cassette containing murine coding sequences.
                                                                                                                                                                         cytostatic; virucide; anti-HIV; hepatotropic; neuroprotective; immunostimulant; expression cassette; viral vector; interleukin-12; co-stimulatory protein; cancer; infection; ds; gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 5252 BP; 1347 A; 1386 C; 1300 G; 1219 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 19; DB 12; Length 5252; Pred. No. 3.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel bicistronic retroviral vector related vector #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (UYHA-) UNIV HAMBURG-EPPENDORF KLINIKUM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Fig 18; 129pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2739 ccccrdaarcccccraarc 2757
  ADO07652
ID AD007652 standard; DNA; 5252 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADP74699 standard; DNA; 7185 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                       10-OCT-2003; 2003WO-EP011252
                                                                                                                                                                                                                                                                                                                                                                                                                                                              11-OCT-2002; 2002DE-01048141
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                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Schnieders F;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                            Mus sp.
Synthetic.
Unidentified.
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Unidentified
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                                                                                                 15-JUL-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Waehler R',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADP74699;
                                                           AD007652;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This invention describes a novel nucleic acid (I) comprising elements that encode a signal peptide (SP) that provides transfer of expressed polypeptide into the endoplasmic reticulum, a fragment (FI) of HIV gp41 protein, containing a segment from a hepted repeat region, a transmembrane anchor (MSD) of a type I membrane protein and a flexible linker (hinge) linking FI and MSD, therefore the formula of (I) is SP-FI-hinge-MSD. The products of the invention have antiviral activity and act as HIV replication inhibitors. Vectors containing (I), also T lymphocytes or hematopoietic stem cells transfected in vitro with (I), are used in gene therapy of HIV infection. (Updated on 11-SEP-2003 to standardise OS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New nucleic acid encoding membrane-anchored gp41 fusion protein, useful for gene therapy of human immunodeficiency virus (HIV) infection, prevents entry of virus into cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
    Gaps
                                                                                                                                                                                                                                                                                                                                                           Transmembrane anchor; gene therapy; endoplasmic reticulum; gp41; antiviral; HIV replication inhibitor; T lymphocyte; viral infection;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 4148;
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  Indels
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Mismatches
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 19;
                                                                                                                                                                                                                                                                                                                      Vector containing HIV gp41 DNA SEQ ID 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
1438. .1773
/*tag= a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 11; Page 28-30; 39pp; German
                                                                      1203 CCCTGAATGCGGCTAATC 1221
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                                       1 CCCCTGAATGCGGCTAATC 19
                                                                                                                                                                             AAH20890 standard; DNA; 4148 BP
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Best Local Similarity 100.0%; P. Matches 19; Conservative 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Human immunodeficiency virus 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2000WO-EP011733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99DE-01057838
                                                                                                                                                                                                                                                                                                                                                                                                    hematopoietic stem cell; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (PETT-) PETTE INST HEINRICH
                                                                                                                                                                                                                                                            (revised)
(first entry)
19; Conservative
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24-AUG-2001
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Gaps

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Indels

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RESULT 87

"HSV-TK splice variant"

ره. .2615 /\*tag= د اکتر

95. .1487 \*tag= a standard

S'UTR

SOS

626. .3250

misc\_RNA

tag=

name=

298. .4098

SOS

LIR

ø standard

taga

product=

ocation/Qualifiers

Key LTR

antisense; ds; gene

Synthetic. Unidentified

standard\_name= "3'-LTR"

EP1428886-A1 16-JUN-2004

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bicistronic retroviral vector, useful in gene therapy, particularly of graft versus host disease, contains components of both murine embryonic stem cell and myeloproliferative sarcoma viruses.
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Best Local Similarity 100.0%; Pred. No. 4;
Matches 19; Conservative 0; Mismatches
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Location/Qualifiers
424. .994
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product= "HSV-TK"
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standard name=
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"neo"
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'*tag= e
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standard
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                                                   The present invention relates to a new bicistronic retroviral vector. These are used for (over) expression of proteins, suppressing expression of (non-) viral RNA and/or proteins by the antisense technique, e.g. to suppress a dominant-negative phenotype, also infectious viral particles that contain the vectors, in gene therapy, particularly for control of guest versus host disease, especially where haematopoietic cells are transduced with the vector or where T cells are transduced, for adoptive immunotherapy, but also for treatling severe combined immune deficiency syndrome and for expression cloning of genes. The present sequence is a vector sequence shown in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                  Sequence 7185 BP; 1581 A; 2013 C; 1942 G; 1649 T; 0 U; 0 Other;
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Disclosure; Page 63-65; 91pp; German.
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les 19; Conserv
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ID ADP7
XX
AC ADP7
XX
DT 26-P
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immunosuppressive; gene therapy; vector; bicistronic retroviral vector; severe combined immune deficiency syndrome; protein expression;

Novel bicistronic retroviral vector related vector #3.

(first entry)

26-AUG-2004

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ADP74701;

3074 CCCCTGAATGCGGCTAATC 3092

1 CCCCTGAATGCGGCTAATC 19

ð 셤 ADP74701 standard; DNA; 7185 BP.

RESULT 89

ADP74701

B

particularly of murine embryonic

Strathmann G;

Gindullis F, Hannemann J,

WPI; 2004-452367/43.

Heberlein C,

CELL-) CELLTECH GMBH BIOTECHNOLOGIE

09-DEC-2002; 2002EP-00027555. 09-DEC-2002; 2002EP-00027555. Bicistronic retroviral vector, useful in gene therapy, graft versus host disease, contains components of both stem cell and myeloproliferative sarcoma viruses.

immunosuppressive; gene therapy; vector; bicistronic retroviral vector; severe combined immune deficiency syndrome; protein expression;

antisense; ds; gene.

Synthetic. Unidentified.

Location/Qualifiers

. 994

Çey Lirk

\*tag=

name≔

.1537 /\*tag= a /standard )

5'UTR

\*tag= \*tag=

/product= "HSV-TK splice variant"
2676. .3300

.2665

538.

SOS

'standard name= "IRES"

\*tag=

misc\_RNA

3348. .4148

CDS

'product= "neo'

4395. .4981

STR.

/standard\_name= "3'-LTR'

EP1428886-A1

16-JUN-2004

Novel bicistronic retroviral vector related vector #7.

(first entry)

26-AUG-2004

ADP74715;

ADP74715 standard; DNA; 7235 BP.

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The present invention relates to a new bicistronic retroviral vector. These are used for (over)expression of proteins, suppressing expression of (non-) viral RNA and/or proteins by the antisense technique, e.g. to suppress a dominant-negative phenotype, also infectious viral particles that contain the vectors, in gene therapy, particularly for control of guest versus host disease, especially where haematopoietic cells are transduced with the vector or where T cells are transduced with the vector or where T cells are transduced, for adoptive immunotherapy, but also for treating severe combined immune deficiency syndrome and for expression cloning of genes. The present sequence is a vector sequence shown in the exemplification of the invention.
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                                             immunosuppressive; gene therapy; vector; bicistronic retroviral vector; severe combined immune deficiency syndrome; protein expression;
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Novel bicistronic retroviral vector related vector #6.
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/standard
995. 1537
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/standard_name= "3'-LTR"
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3348. .4148
/*tag= e
/product= "neo"
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1538. .;
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                                                                                                            antisense; ds; gene.
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Unidentified
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bicistronic retroviral vector, useful in gene therapy, particularly of graft versus host disease, contains components of both murine embryonic stem cell and myeloproliferative sarcoma viruses.
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Strathmann G;

Heberlein C, Gindullis F, Hannemann J,

WPI; 2004-452367/43.

(CELL-) CELLTECH GMBH BIOTECHNOLOGIE

09-DEC-2002; 2002EP-00027555. 09-DEC-2002; 2002EP-00027555.

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Gaps

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Indels

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; Pred. No. 4; 0; Mismatches

100.08;

Ouery Match Best Local Similarity 100. Matches 19; Conservative

3124 CCCTGAATGCGGCTAATC 3142

RESULT 91 ADP74715

1 CCCCTGAATGCGGCTAATC 19

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100.0%; Score 19; DB 12; Length 7235;

Gaps

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Indels

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Mismatches

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Query Match
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immunosuppressive; gene therapy; vector; bicistronic retroviral vector; severe combined immune deficiency syndrome; protein expression; antisense; ds; gene.
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'standard_name= "3'-LTR"
               Pred. No.
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                                                                                3124 CCCCTGAATGCGGCTAATC 3142
100.0%; Pre-
                                                          1 CCCCTGAATGCGGCTAATC 19
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Matches 19; Conserv
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Unidentified.
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                                                                                                                                                                                                                immunosuppressive; gene therapy; vector; bicistronic retroviral vector; severe combined immune deficiency syndrome; protein expression; antisense; ds; gene.
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95. .1537
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        3124 CCCCTGAATGCGGCTAATC 3142
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538.
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                                                                                                                                                                                                                                                                                   Synthetic.
Unidentified
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misc\_RNA

SOS

LIR

5'UTR

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These are used for (over) expression of proceins, suppressing expression of (non-) viral RNA and/or proteins by the antisense technique, e.g. to suppress a dominant-negative phenotype, also infectious viral particles that contain the vectors, in gene therapy, particularly for control of guest versus host disease, especially where haematopoietic cells are transduced with the vector or where T cells are transduced, for adoptive immunotherapy, but also for tracting severe combined immune deficiency syndrome and for expression cloning of genes. The present sequence is a
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Strathmann G;
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WPI; 1991-165150/23
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                                                                                                                                                                            Coxeackie virus strain VD2921; diabetogenic coxeackie B virus-4; CBV-4; strain VD2921; VD1, VP3; VP3; VP4; P2A; P2B; P2C; P3A; P3B; P3C; P3D; diabetes; diabetogenic entervirus; beta cell loss; blindness; renal failure; leg amputation; ds.
                                              Gaps
               Sequence 7235 BP; 1593 A; 2025 C; 1950 G; 1667 T; 0 U; 0 Other;
                                             ö
vector sequence shown in the exemplification of the invention.
                                                                                                                                                               Diabetogenic coxsackie B virus 4 (CBV-4) strain VD2921 genome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1034. .5029
/*tag= 1
/note= "Specifically claimed in claim 44"
                                                                                                                                                                                                                                          . .87
*tag= a
note= "Specifically claimed in claim 16"
                                                                                                                                                                                                                                                                        *tag= b
note= "Specifically claimed in claim 19"
13. .742
                                                                                                                                                                                                                                                                                                *tag= c
note= "Specifically claimed in claim 22"
                                                                                                                                                                                                                                                                                                                      *tag= d
note= "Specifically claimed in claim 25"
43. .7303
                                                                                                                                                                                                                                                                                                                                                                    *tag= e
note= "Specifically claimed in claim 26"
                                                                                                                                                                                                                                                                                                                                                                                           *tag= g
note= "Specifically claimed in claim 29"
                                                                                                                                                                                                                                                                                                                                                                                                                *tag= h
note= "Specifically claimed in claim 32"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    note= "Specifically claimed in claim 38"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      *tag= k
note= "Specifically claimed in claim 41"
                                                                                                                                                                                                                                                                                                                                                                                                                                               note = "Specifically claimed in claim 35'
                                            0; Indels
                              100.0%; Score 19; DB 12; Length ilarity 100.0%; Pred. No. 4; Conservative 0; Mismatches 0; Indele
                                                                                                                                                                                                                                                                                                                                                    "Polyprotein"
                                                                                                                                                                                                                                   Location/Qualifiers
                                                                    3124 CCCCTGAATGCGGCTAATC 3142
                                                            1 CCCCTGAATGCGGCTAATC 19
                                                                                                                ABX12440 standard; DNA; 7392 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19-JUN-2002; 2002WO-IB003278
                                                                                                                                                                                                                                                                                                                                                                                                                                                     7. .3737
                                                                                                                                                                                                                                                                                                                                                                                                                                 442. .3296
                                                                                                                                                                                                                                                                                                                                                                                                         .2441
                                                                                                                                                                                                                                                                                                                                                                                  .1726
                                                                                                                                                                                                                                                                                                                                              *tag= f
'product=
                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                            43. .952
                                                                                                                                                                                                                                                                 8. .512
                                                                                                                                                                                                                                                                                                                                                                                                                                          *tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                               *tag=
                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO2002103060-A2
                                                                                                                                                                                                                    Coxsackievirus
                                                                                                                                                                                                                                                                                                                                                                                                                              misc_feature
                                                                                                                                                                                                                                        misc_feature
                                                                                                                                                                                                                                                                misc_feature
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                                                                                                                                               10-MAY-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27-DEC-2002.
                                                                                                                                 ABX12440;
                                                                                                  RESULT 94
                                                                                                         SXS
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Enteroviruses, monoclonal antibodies, myocarditis, myositis, meningitis, encephalitis, pancreatitis, post viral fatigue syndrome; ss.
                                                                                                                                                  Polymerase chain reaction and primers for detecting nucleic acids from the diabetogenic coxsackie B virus-4 strain VD2921.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 7392 BP; 2095 A; 1724 C; 1809 G; 1764 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 19; DB 8; Length 7392; 100.0%; Pred. No. 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product= "enteroviral polypeptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (PLAC ) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RNA encoding enteroviral polypeptide.
                                                                                                                                                                                                     Example 5; Page 64-66; 79pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
742. .7299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          455 CCCCTGAATGCGGCTAATC 473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAQ11816 standard; RNA; 7399 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 CCCCTGAATGCGGCTAATC 19
                                 (INNO-) INNOVENTUS PROJECT AB
                                                                 Yin H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          89DE-03939200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          89DE-03939200
20-JUN-2001; 2001SE-00002198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity 100.
Les 19; Conservative
                                                                 Prisk GE,
                                                                                                WPI; 2003-278229/27.
P-PSDB; ABG75961.
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05-AUG-1991
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                                                                 HT,
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Gaps

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Length 7399; Indels

100.0%; Score 19; DB 10; 100.0%; Pred. No. 4; ive 0; Mismatches 0;

Conservative

踞.

(first entry)

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arrhythmia, reperfusion injury, atherosclerosis, to promote angiogenesis, etc. The vesicles are highly stable and can be produced in large quantities, making them ideal for gene therapy
                                                                                                                                                                                                                                                                       Swine vesicular disease virus (SVDV) N3 mutant strain gene sequence.
                                                        Sequence 7399 BP; 2128 A; 1724 C; 1807 G; 1740 T; 0 U; 0 Other;
    enhance expression of proteins for treatment of heart failure,
                                                                                                                                                                                                                                                                                             Swine vesicular disease virus; SVDV; swine vesicular disease; Taiwan Yu-Li strain; foot and mouth disease; coxsackie virus; differentiation; vaccine; prevent; ss.
                                                                                                                                                                                                     AAZ98719 standard; cDNA; 7400
                                                                                                                                                                                                                                                                                                                                         Swine vesicular disease virus
                                                                                     Local Similarity
es 19; Conserv
                                                                                                                                                                                                                                                                                                                                                                          misc_feature
                                                                                                                                                                                                                                                 20-JUN-2000
                                                                                                                                                                                                                           AAZ98719;
                                                                              Query Match
                                                                                                     Matches
                                                                                                                                                                                 RESULT 97
                                                                                                                                                                                             AAZ98719
   8888888
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                                                                                                                                                                                                      ö
                                                                                     This RNA encodes an enteroviral polypeptide which is used to raise poly-
or monoclonal antibodies (Abs). These are useful in assays for detecting enterovirus specific antigens, as an indication of enteroviral disease.
All 70 serotypes of the enteroviral family can be detected. Diseases such
                                                                                                                                   myocarditis, myositis, menin- gitis, encephalitis and pancreatitis can diagnosed using the Abs. (Updated on 25-MAR-2003 to correct PA field.)
                         - for
                                                                                                                                                                                                                                                                                                                                                                                                        hepatitis B virus; cardiovascular disease; heart; antiarrhythmic; antiarteriosclerotic;
                                                                                                                                                                                                                 Gaps
                      New enteroviral polypeptide for raising group specific antibodies detecting any type of enterovirus in blood or serum, also new DNA encoding it.
                                                                                                                                                                                                                 ö
                                                                                                                                                                 Sequence 7399 BP; 2128 A; 1724 C; 1807 G; 0 T; 1740 U; 0 Other;
                                                                                                                                                                                         2; Length 7399;
                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                                                   Coxsackievirus capsid protein VP1 nucleic acid.
                                                                                                                                                                                         DB
                                                                                                                                                                                                               4; Mismatches
                                                                                                                                                                                                    4;
                                                                                                                                                                                         Score 19;
Pred. No. 4
                                                                  Claim 7; Page 17-21; 26pp; German.
                                                                                                                                                                                                                                                 454 CCCCUGAAUGCGGCUAAUC 472
                                                                                                                                                                                                                                    1 CCCCTGAATGCGGCTAATC 19
                                                                                                                                                                                                                                                                                                                 ABV76134 standard; DNA; 7399 BP
                                                                                                                                                                                       100.0%;
                                                                                                                                                                                                   78.9%;
                                                                                                                                                                                      Query Match
Best Local Similarity 78.99
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                               capsid protein; gene;
                                                                                                                                                                                                                                                                                                                                                                                                        Gene therapy; vector;
                                                                                                                                                                                                                                                                                                                                                                                                                     cardiant; vasotropic;
P-PSDB; AAR12141.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200287594-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Coxsackievirus
                                                                                                                                                                                                                                                                                                                                                             07-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               07-NOV-2002
                                                                                                                                                                                                                                                                                                                                        ABV76134;
                                                                                                                                                                                                                                                                                            RESULT 96
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ઠે 셤 Location/Qualifiers

2693. .2710.

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(SDVD) gene sequence from the SUDV strain N3. SVDV is the causative agent of swine vesicular disease, which is very similar to foot and mouth of swine vesicular disease, which is very similar to foot and mouth sequence. The invention relates to the wild-type Tawan Yu-Li strain cDNA sequence, and the gene sequences of the mutant SVDV strains N3. H31 and SP7. The mutant SVDV nucleotide sequence can be used in a vaccine for the prophylaxis of swine vesicular disease. The invention also includes a method for differentiating the mutant SVDV nucleotide sequences from the wild type strain of SVDV, coxsackie virus and foot-and-mouth disease wild type strain of SVDV, coxsackie virus and foot-and-mouth disease is not present in the specification, but has been derived from the wild-type Taiwan Xu-Li strain SVDV gene sequence (see AA298117) shown on pages 34-38 of the specification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mutant strains of swine vesicular disease virus (SVDV) used in vaccines to prevent swine vesicular disease.
/*tag= a
/notes= Nucleotides in this position replace the wild-
type nucleotide sequence of strain Taiwan Yu-Li (see
AAZ98717)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sequence represents the full length Swine vesicular disease virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 7400 BP; 2084 A; 1786 C; 1862 G; 1668 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Jeng K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (BIOT-) DEV CENT BIOTECHNOLOGY
                                                                                                                                                                                                                                                                                                                                                                                   98EP-00306486.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 4; Page; 66pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hwong CL, Lo C, Yang Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2000-258616/23.
                                                                                                                                                                                                                                                                                                                                                                                   14-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14-AUG-1998;
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                                                                                                                                                                                                                EP982403-A1
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Novel non-viral vector comprises vesicular membrane with hepatitis B envelope protein with cardiac targeting sequence, and nucleotide sequence for gene therapy useful for treating, e.g., heart failure, arrhythmia and atherosclerosis.

30-APR-2002; 2002WO-US013644.

30-APR-2001; 2001US-0287423P

CALIFORNIA Hoshijima M;

(REGC ) UNIV

Chien KR,

WPI; 2003-111844/10.

nucleic acid. The invention provides a non-viral vesicie vector for the delivery of nucleic acid to various cardiac cell types. The vesicle vector contains the hepartitis B virus envelope protein in which at least part of the liver targetting sequence is deleted and replaced with a specific cardiac cell targetting sequence. For example, the coxsackie virus B3, Vpl sequence can be used to target the vector to cardiomyocytes. The vesicle vector can be delivered intravenously or intra-arterially rather than by more invasive methods such as direct cardiac injection. It can be used to deliver gene products to replace or

present sequence is that of a coxsackie virus B3 capsid protein VP1

Disclosure; Page 27-31; 53pp; English.

/\*tag= a /note= "Nucleotides in this position replace the wild-type nucleotide sequence of strain Taiwan Yu-Li AA298717"

Location/Qualifiers 2705. .2710

Chang EL;

Jeng K,

CENT BIOTECHNOLOGY.

98EP-00306486. 98EP-00306486.

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Mutant strains of swine vesicular disease virus (SVDV) used in vaccines
                           Swine vesicular disease virus (SVDV) H21 mutant strain gene sequence.
                                                   Swine vesicular disease virus; SVDV; swine vesicular disease; Taiwan Yu-Li strain; foot and mouth disease; coxsackie virus; differentiation; vaccine; prevent; ss.
                                                                                                                                                                                                                                                                                                                                                                                                              to prevent swine vesicular disease.
                                                                                                       Swine vesicular disease virus
                                                                                                                                                                                                                                                                                                                                             Hwong CL, Lo C, Yang Y,
20-JUN-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                      WPI; 2000-258616/23.
                                                                                                                                                                                                                                                                 14-AUG-1998;
                                                                                                                                                                                                                                                                                           14-AUG-1998;
                                                                                                                                           misc_feature
                                                                                                                                                                                                             EP982403-A1.
                                                                                                                                                                                                                                       01-MAR-2000.
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Matches
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  8XCCCCCCCCCCX8X41X8X1X8X54X6X6X141111X8XXXX8X6X6X
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                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This sequence represents the full length Swine vesicular disease virus (SVDV) gene sequence from the SVDV strain Taiwan Yu-Li. SVDV is the causative agent of swine vesicular disease, which is very similar to foot and mouth disease. The invention relates to the wild-type Taiwan Yu-Li strain cDNA sequence, and the gene sequences of the mutant SVDV strains N3, H21 and SP7. The mutant SVDV nucleotide sequence can be used in a vaccine for the prophylaxis of swine vesicular disease. The invention also includes a method for differentiating the mutant SVDV nucleotide sequences from the wild type strain of SVDV, coxsacktevirus and foot-and-mouth disease virus through the use of polymerase chain reaction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mutant strains of swine vesicular disease virus (SVDV) used in vaccines
                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 7400 BP; 2082 A; 1786 C; 1862 G; 1670 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                        ö
                                                                                                                                                                                                                                                              Swine vesicular disease virus, SVDV; swine vesicular disease, Taiwan Yu-Li strain; foot and mouth disease; coxsackie virus; differentiation; vaccine; prevent; ss.
             100.0%; Score 19; DB 3; Length 7400; 100.0%; Pred. No. 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 19; DB 3; Length 7400; 100.0%; Pred. No. 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
                                       Indels
                                                                                                                                                                                                                                    Swine vesicular disease virus (SVDV) gene sequence.
                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chang EL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              prevent swine vesicular disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Yang Y, Jeng K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Page 34-38; 66pp; English
                                                                                                                                                          AAZ98717 standard; cDNA; 7400 BP.
                                                                                 454 CCCCTGAATGCGCTAATC 472
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                                       ;
0
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                                                                 1 CCCCTGAATGCGGCTAATC 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                  (BIOT-) DEV CENT BIOTECHNOLOGY
                                                                                                                                                                                                                                                                                                                    Swine vesicular disease virus
                                                                                                                                                                                                                                                                                                                                                                                                98EP-00306486.
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                                                                                                                                                                                                            (first entry)
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hes 19; Conservative
                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2000-258616/23.
            Query Match
Best Local Similarity
Matches 19; Conserv
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                                                                                                                                                                                  AAZ98717;
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                                                                                                                                 RESULT 98
                                                                                                                                             AAZ98717
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                                    This sequence represents the full length Swine vesicular disease virus (SDVD) gene sequence from the SVDV strain H21. SVDV is the causative agent of swine vesicular disease, which is very similar to foot and mouth disease. The invention relates to the wild-type Taiwan Yu-Li strain cDNA sequence, and the gene sequences of the mutant SVDV strains N3, H21 and SP7. The mutant SVDV nucleotide sequence can be used in a vaccine for the prophylaxis of swine vesicular disease. The invention also includes a method for differentiating the mutant SVDV nucleotide sequences from the wild type strain of SVDV, coxeackie virus and foot-and-mouth disease virus through the use of polymerase chain reaction. Note: This sequence is not present in the specification, but has been derived from the wild-type Taiwan Yu-Li strain SVDV gene sequence (see AAZ99717) shown on pages 34-38 of the specification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Swine vesicular disease virus; SVDV; vesicular disease; vaccine; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 7400 BP; 2082 A; 1785 C; 1863 G; 1670 T; 0 U; 0 Other;
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 19; DB 3; Length 7400; 100.0%; Pred. No. 4; tive 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Swine vesicular disease virus (SVDV) nucleotide sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAA29863 standard; cDNA; 7400 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CCCCTGAATGCGGCTAATC 472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 CCCCTGAATGCGGCTAATC 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Swine vesicular disease virus.
Claim 3; Page; 66pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity 100.
nes 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-AUG-2000
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AAZ98718 standard; cDNA; 7400 BP.

RESULT 99 AAZ98718

AAZ98718;

SQ Sequence 7400 BP; 2082 A; 1786 C; 1862 G; 1670 T; 0 U; 0 Other;

Query Match
Best Local Similarity 100.0%; Score 19; DB 3; Length 7400;
Best Local Similarity 100.0%; Pred. No. 4;

Matches 19; Conservative 0; Mismatches 0; Indels 0;

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Method and reagent for inhibiting HBV viral replication Patent: EP 128296-A 449 05-MRR-2003;
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Method for controlling the microbiological quality of an aqueous medium and kit therefor
Patent: WO 0202811-A 72 10-JAN-2002;
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Viruses; seRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
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Viruses, saskNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 19; DB 6; Length 30; 100.0%; Pred. No. 9.4;
                                                                                                                                                                          linear
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    30
forgatism="Human coxsackievirus A21"
fmol type="unassigned DNA"
/db_xref="taxon:12069"

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Human poliovirus 2"
/mol_type="unassigned DNA"
/db_xref="taxon:12083"
                                                                                                                                                                          DNA
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100.0%; Pred. No. 9.4; tive 0; Mismatches
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AX348202
                                                                                                                                                                   30 bp
Sequence 70 from Patent WO0202811.
AX348200
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
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                                                   1 CCCCTGAATGCGGCTAATC 19
                                                                                   ccccrcaarccccraarc 27
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Human poliovirus 2
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                   19; Conservative
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Matches 19; Conservative
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Best Local Similarity
Matches 19; Conserva
Best Local Similarity
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VERSION KEYWORDS SOURCE ORGANISM

AUTHORS TITLE

JOURNAL PUBMED

COMMENT

FEATURES

REFERENCE

DEFINITION

ACCESSION

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FULLSAL 100 bp RNA linear VRL 21-MAY-2003
Human poliovirus 1 RNA, 5'UTR, partial sequence, vaccine strains
Sabin 1, Cox, CHAT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FULIUSA 100 bp RNA linear VRL 21-MAY-2003
Human poliovirus 1 RNA, 5'UTR, partial sequence, wild-type isolate
p1/2171/USA/77.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    non-coding region of
f serotype 1, 2, 3 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="451 bp downstream of the 5' end of virion RNA."
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1 (Dases 1 to 100)

Minor, P.D. and Dunn, G.

The effect of sequences in the 5' non-coding region or replication of polioviruses in the human gut
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                                                                                                                                                                                                                                                                                                                  Virtues, SERNA positive-strand viruses, no DNA stage, Picornaviridae, Enterovirus.

1 (Dases 1 to 100)
Minor, P.D. and Dunn, G. The effect of sequences in the 5' non-coding region of polioviruses in the human gut
J. Gen. Virol. 69 (Pt 5), 1091-1096 (1988)
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/mol type="genomic RNA"
/isoTate="wild-type isolate P1/2171/USA/77"
/db_xref="taxon:12080"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Human poliovirus 1"
/mol_type="genomic RNA"
/strain="vaccine strains Sabin 1,
/db_xref="taxon:12080"
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5' non-coding region; poliovirus.
Human poliovirus 1
Human poliovirus 1
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Human poliovirus 1
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CCCCTGAATGCGGCTAATC 25
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  Human poliovirus 1 RNA, 5'UTR, partial sequence, wild-type isolate P1/8-3827/Brazil/81.
                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Human poliovirus 1"
/mol type="qenomic RNA"
/isolate="wild-type isolate P1/8-3827/Brazil/81"
/db xref="taxon:12080"
/noTe="451 bp downstream of the 5' end of virion RNA."
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1 (bases 1 to 100)
Minor, P.D. and Dunn, G.
Minor, P.D. and polnoviruses in the 5' non-coding region on the replication of polioviruses in the human gut
J. Gen. Virol. 69 (Pt 5), 1091-1096 (1988)
                                                                                                                                                                                                                                                        region on the
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                                                                                                                                            Viruses serNA positive-strand viruses, no DNA stage, Picornavirdae, Enterovirus.

1 (bases 1 to 100)

Minor P.D. and Dunn, G.

The effect of sequences in the 5' non-coding region or replication of polioviruses in the human gut J. Gen. Virol. 69 (Pt 5), 1091-1096 (1988)
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/isolate="wild-type isolate P1/15/HK/81"
/db_xref="taxon:12080"
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                                                                                             5' non-coding region; poliovirus.
Human poliovirus 1
Human poliovirus 1
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f. non-coding region; poliovirus
Human poliovirus 1
Human poliovirus 1
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ORGANISM

KEYWORDS SOURCE

AUTHORS TITLE

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5'UTR ORIGIN

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FEATURES

5'UTR ORIGIN

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19; Conservative
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Human poliovirus 3 RNA, 5'UTR, partial sequence, wild-type isolate
P3/3054/Brazil/81.
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Human poliovirus 2 RNA, 5'UTR, partial sequence, vaccine strain
Sabin 2.
/note="451 bp downstream of the 5' end of virion RNA." <1. .>100
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I (Dases 1 to 100)

Minor, P.D. and Dunnio.

The effect of sequences in the 5' non-coding region on the replication of polioviruses in the human gut

J. Gen. Virol. 69 (Pt 5), 1091-1096 (1988)
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1 (bases 1 to 100)
Minor, P.D. and Dunn, G.

The effect of sequences in the 5' non-coding region on replication of polioviruses in the human gut
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                                                                                Length 100
                                                                                                              Indels
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/note="451 bp downstream of the 5'
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                                                                                13;
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/strain="vaccine strain Sabin 2"
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                                                                             Query Match
100.0%; Score 19; DB 13
Best Local Similarity 100.0%; Pred. No. 9.5;
Matches 19; Conservative 0; Mismatches
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5' non-coding region; poliovirus.
Human poliovirus 2
Human poliovirus 2
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5' non-coding region; poliovirus.
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ORIGIN
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POL2SA2
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POL3FIN 100 bp RNA linear VRL 21-MAY-2003
Human poliovirus 3 RNA, 5'UTR, partial sequence, wild-type isolates
P3/Pin/60212/85, P3/Fin/25725/85.
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Location/Qualifiers
                                                        /organism="Human poliovirus 3"
/mol_type="genomic RNA"
/isolate="wild-type isolate P3/3054/Brazil/81"
/db_xref="taxon:12086"
/nofe==451 bp downstream of the 5' end of virion RNA."
<1. .>100
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Human poliovirus 3 RNA, 5'UTR, partial sequence, vaccine strain
USOL-D-BAC.
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wild-type isolates of serotype 1, 3 were determined in [1]. Location/Qualifiers
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/mol type="genomic RNA"
/isolate="wild-type isolates P3/Fin/60212/85,
P3/Fin/25725/85"
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5' non-coding region; poliovirus.
Human poliovirus 3
Human poliovirus 3
Viruses; seRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
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1 (bases 1 to 100)

1 Inch.P.D. and Dunn, G.

The effect of sequences in the 5' non-coding replication of polioviruses in the human gut 2836553
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Pred. No. 9.5;
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/note="451 bp downstream of the <1. .>100
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7 non-coding region; poliovirue.
Human poliovirus 3
Human poliovirus 3
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DQ029090.1 GI:66473298
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Human echovirus 11
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Unpublished (2005)
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Matches 19; Conserv
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                                                                                                   non-coding region of
f serotype 1, 2, 3 and
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Human poliovirus 3 RNA, 5'UTR, partial sequence, wild-type isolate
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                                                                                                                                                                               /organism="Human poliovirus 3"
/mol_type="ganomic RNA"
/strain="vaccine strain USOL-D-BAC"
/db xref="taxon:12086"
/noTe="451 bp downstream of the 5' end of virion RNA."
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/isolate="wild-type isolate P3/Yunan/2/84"
/db_xref="taxon:12086"
/note="451 bp downstream of the 5' end of virion RNA."
<1. .>100
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polioviruses which include vaccine strains of serotype 1, 2
wild-type isolates of serotype 1, 3 were determined in [1].
Location/Qualifiers
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I (Dases 1 to 100)

Minor, P.D. and Dunn, G.

The effect of sequences in the 5' non-coding region on the replication of polioviruses in the human gut
J. Gen. Virol. 69 (Pt 5), 1091-1096 (1988)
1 (bases 1 to 100)
Minor, P.D. and Dunn, G.
The effect of sequences in the 5' non-coding region on the replication of polioviruses in the human gut
J. Gen. Virol. 69 (Pt 5), 1091-1096 (1988)
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Human echovirus 11 strain MON-ES9 5' UTR.
DQ029090
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F. non-coding region; poliovirus
Human poliovirus 3
Human poliovirus 3
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Best Local Similarity 100..
"hes 19; Conservative
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Matches 19; Conserv
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AUTHORS
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POL3YUN
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phenotypes
Unpublished (2005)
2 (bases 1 to 109)
Gharbi,J., Elhiar,R., Ben M'Hadheb,M., Jaidane,H., Bouslama,L.,
N'Saiblas,S. and Aouni,M.
Direct Submission
Olivert Submission
Institute of Biotechnology, Avicenne Street, Monastir 5000, Tunisia
Location/Qualifiers
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Gharbi,J., Elhiar,R., Ben M'Hadheb,M., Jaidane,H., Bouslama,L.,
N'Sablia,S. and Aouni,M.
Submitet Submission .
Submitted (06-MAY-2005) Virology, Faculty of Pharmacy & Higher
Institute of Biotechnology, Avicenne Street, Monastir 5000, Tunisia
Location/Qualifiers
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1 (Dases 1 to 109)
Gharbi,J., Elhiar,R., Ben M'Hadheb,M., Jaidane,H., Bouslama,L., N'Sablias,S. and Abuni,M.
N'Sablias,S. and Abuni,M.
Nucleotide sequences of the IRES domains IV and V of natural isolates ECHO virus type 11 with different replicative capacities
Human echovirus 11
Human echovirus 11
Human echovirus 11
Viruses; saRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
1 (bases 1 to 109)
Gharbi,J., Elhiar,R., Ben M'Hadheb,M., Jaidane,H., Bouslama,L.,
N'Saibia,S. and Aouni,M.
N'Saibia,S. and Aouni,M.
Nucleotide sequences of the IRES domains IV and V of natural isolates ECHO virus type 11 with different replicative capacities
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/note="domain V of IRES (internal ribosome entry site)"
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Muman echovirus 11 strain MON-ES36 5' UTR.
DQ029091.1 GI:66473299
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/mtain="WON-ES36"
/db_xref="taxon:12078"
/country="Tunisia"
<1. .>109
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/strain="MON-ES9"
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/country="Tunisia"
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Best Local Simi
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Picornaviridae; Enterovirus.

1 (Dases 1 to 109)
Gharbi,J., Elhiar,R., Ben M'Hadheb,M., Jaidane,H., Bouslama,L.,
N'Salbia,S. and Aouni,M.
N'Salbia,S. and Aouni,M.
Nucleotide sequences of the IRES domains IV and V of natural isolates ECHO virus type 11 with different replicative capacities
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Nucleotide sequences of the IRES domains IV and V of natural isolates ECHO virus type 11 with different replicative capacities
/note="domain V of IRES (internal ribosome entry site)"
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/note="domain V of IRBS (internal ribosome entry site)"
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Direct Submission
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Human echovirus 11

Viruses; ssRMA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
1 (bases 1 to 109)
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Human echovirus 11 strain STE-11730 5' UTR.
DQ029094
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Human echovirus 11 strain STE-5793 5' UTR
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                                              ch 100.0%; Score 19; DB Similarity · 100.0%; Pred. No. 9.5 19; Conservative 0; Mismatches
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/strain="STE-5793"
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DQ029092.1 GI:66473300
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Unpublished (2005)
2 (bases 1 to 109)
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Unpublished (2005)
2 (Dases 1 to 109)
3 (Dases 1 to 109)
Gharbi, J., Elhiar, R., Ben M'Hadheb, M., Jaidane, H., Bouslama, L.,
N'Saibia, S. and Aouni, M.
Direct Submission
Submitted (06-MAY-2005) Virology, Faculty of Pharmacy & Higher
Institute of Biotechnology, Avicenne Street, Monastir 5000, Tunisia
Location/Qualifiers
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Unpublished (2005)
2 (bases 1 to 109)
Gharbi,J., Elhiar,R., Ben M'Hadheb,M., Jaidane,H., Bouslama,L.,
N'Saibia,S. and Aouni,M.
Direct Submission
Submitted (06-MAY-2005) Virology, Faculty of Pharmacy & Higher
Institute of Biotechnology, Avicenne Street, Monastir 5000, Tunisia
Location/Qualifiers
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Picornaviridae; Enterovirus.
1 (bases 1 to 109)
Gharbi,J., Elhiar,R., Ben M'Hadheb,M., Jaidane,H., Bouslama,L.,
N'Salbia,S. and Aouni,M.
N'Salbia,S. and Aouni,M.
Nucleotide sequences of the IRES domains IV and V of natural isolates ECHO virus type 11 with different replicative capacities
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/note="domain V of IRES (internal ribosome entry site)"
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/note="domain V of IRES (internal ribosome entry site)"
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Human echovirus 2 strain MON-ECV2 5' UTR.
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100.0%; Pred. No. 9.5;
vative 0; Mismatches 0;
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/strain="STE-11730"
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/strain="MON-ECV2"
/db_xref="taxon:35294"
/country="Tunisia"
                                                                                                                                                                                                                                                                                                                                             /db xref="taxon:12078"
/country="France"
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Human echovirus 2
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nr.38U624 120 bp ss-RNA linear VRL 05-JUN-2001
Human poliovirus 3 5' untranslated region, partial sequence.
AF380624
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Direct Submission
Submitted (14-WAY-2001) Medical Microbiology, University of Wales,
College of Medicine, Heath Park, Cardiff, Wales CF14 4XN, UK
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Viman poliovirus 1
Viman poliovirus 1
Viruses; saRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
I (bases 1 to 120)
Mengistu, A., Neale, M.L. and Fox, J.D.
Detection and Typing of Enteroviruses by Analysis of the 2C Gene
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Human poliovirus 1 5' untranslated region, partial sequence.
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Human poliovirus 3
Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
1 (bases 1 to 120)
                                                                         Length 120;
                                                                                                                 Indels
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/specific_host="Homo sapiens"
/db_xref="taxon:12080"
/note="wild type isolate from 1999"
<1. .>120
                                                                     100.0%; Score 19; DB 13;
ilarity 100.0%; Pred. No. 9.5;
Conservative 0; Mismatches 0;
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Mengistu, A., Neale, M.L. and Fox, J.D.
Direct Submission
/note="vaccine-derived"
<1. .>120
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2 (bases 1 to 120)
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (06-MAY-2005) Virology, Paculty of Pharmacy & Higher Institute of Biotechnology, Avicenne Street, Monastir 5000, Tunisia Location/Qualifiers
                                                         VRL 29-MAY-2005
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University of Wales,
University of Wales,
Submitted (14-MAY-2001) Medical Microbiology, University of Wales,
Submitted (14-MAY-2001) Medical Microbiology, University of Wales,
College of Medicine, Heath Park, Cardiff, Wales CF14 4XN, UK
Location/Qualifiers
---invoirus 1"
                                                                                                                                           Human echovirus 12

Viruses, saRNA positive-strand viruses, no DNA stage,

Picornaviridae, Enterovirus.

1 (bases 1 to 109)

Gharbi, J., Elhiar, R., Ben M'Hadheb, M., Jaidane, H., Bouslama, L.,

N'Saibia, S. and Aouni, M.

N'Saibia, S. and Aouni, M.

Nucleotide sequences of the IRES domains IV and V of natural isolates ECHO virus type 11 with different replicative capacities
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human poliovirus 1
Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
1 (bases 1 to 120)
Mengistu, A., Neale, M.L. and Fox, J.D.
Detection and Typing of Enteroviruses by Analysis of the 2C Gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="domain V of IRES (internal ribosome entry site)"
                                                                                                                                                                                                                                                                                                                      phenotypes
Unpublished (2005)
2 (bases 1 to 109)
6 harbi,J., Elliar,R., Ben M'Hadheb,M., Jaidane,H., Bouslama,L.,
Direct Submission
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Human poliovirus 1 5' untranslated region, partial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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                                             אוו RNA linear Human echovirus 12 strain Travis prototype 5' UTR.
DQ029096
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/specific host="Homo sapiens"
/db xref="taxon:12080"
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/strain="Travis prototype"
/db_xref="taxon:35293"
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Matches 19; Conservative
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Genomic mutations in oral poliovirus vaccine strains:Implications for the eradication of poliovirus Unublished
2 (Dases 1 to 128)
Pavlov, D.N.
Direct Submission
Submitted (12-701-2004) Pavlov D.N., Medical Virology, University of Pretoria, P.O.Box 2034, Pretoria, Gauteng, 0001, SOUTH AFRICA Location/Qualifiers
                                                                                                                                                                                                                                                                                                'isolation_source="stool specimen from immunodeficient
                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 19; DB 13; Length 128; ilarity 100.0%; Pred. No. 9.5; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                    /specific_host="Homo sapiens"
/db_xref="taxon:12080"
/country="South Africa:Gauteng"
<1. .>128
                                                                                                                                                                                                                            /organism="Human poliovirus 1"
/virion
                                                                                                                                                                                                                                                           /mol_type="genomic RNA"
/isolate="P20"
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Human coxsackievirus B2
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Best Local Similarity
Matches 19; Conserv
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                                        Pavlov, D.N.
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Human poliovirus 2 5' untranslated region, partial sequence.
AF380623
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Human poliovirus 1, partial 5'UTR, genomic RNA, isolate P20.
AJ783777
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Submitted (14-MAY-2001) Medical Microbiology, University of Wales, College of Medicine, Heath Park, Cardiff, Wales CF14 4XN, UK Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 (bases 1 to 122)
Mengistu.A., Neale, M.L. and Rox, J.D.
Direct Submission
Submitted (14-MAY-2001) Medical Microbiology, University of Wales,
College of Medicine, Heath Park, Cardiff, Wales CF14 4XN, UK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mengistu, A., Neale, M.L. and Fox, J.D. Detection and Typing of Enteroviruses by Analysis of the 2C Gene
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Human poliovirus 1
Viruses; ssRNA positive-strand viruses, no DNA stage;
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Picornaviridae; Enterovirus.
1 (bases 1 to 122)
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                                                                  /organism="Human poliovirus 3"
/virion
/mol type="genomic RNA"
/specific_host="Homo sapiens"
/db_xref="texon:12086"
/noTe="wild type isolate from 1999"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /mol_type="genomic RNA"
/specific host="Momo sapiens"
/db_xref="taxon:12083"
/note="wild type isolate from 1999"
<1. .>122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            organism="Human poliovirus 2"
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100.0%; Pred. No. 9.5
ive 0; Mismatches
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Human poliovirus 2
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                                   FEATURES
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Gaps

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VRL 02-JUL-2003
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Molecular identification and typing of enteroviruses isolated from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /isolate="IT99-5106"
/db xref="taxon:82639"
/lab host="LLC-MK2 cell culture"
/note="throat swab from child with aseptic meningitis,
dote="throat swab from child with aseptic meningitis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      æ
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Submitted (08-MAY-2001) Muscillo M., Environmental Hygiene,
Istituto Superiore di Sanita', Viale Regina Elena 299, Rome,
ньмэлгоуо 145 bp RNA linear VRL (
Human coxsackievirus B2 partial 5'UTR, strain /ra/Roma99
AJ312090
                                                                                                                                                                                                                                    Viruses; ssRNA positive-strand viruses, no DNA stage;
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J. Clin. Microbiol. 40 (12), 4554-4560 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        organism="Human coxsackievirus B2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /mol_type="genomic RNA"
/strain="/ra/Roma99"
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CCCCTGAATGCGGCTAATC
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AF314004
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AF316322
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                                                                                                                                                                                                                                                                                                                                      Molecular identification and typing of enteroviruses isolated from
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1 (Dases 1 to 147)
Singh,S., Chow,V.T.K., Phoon,M.C., Chan,K.P. and Poh,C.L.
Direct Detection of Enterovirus 71 (EV71) in Clinical Specimens from a Hand, Poot, and Mouth Disease Outbreak in Singapore by Reverse Transcription-PCR with Universal Enterovirus and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /mol_type="genomic RNA"
/strain="/ro/Roma98"
/isolate="IT98-5102"
/db xref="tavero cell culture"
/lab host="vero cell culture"
/note="throat swab from child with aseptic meningitis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
Submitted (08-MAY-2001) Muscillo M., Environmental Hygiene,
Istituto Superiore di Sanita', Viale Regina Blena 299, Rome,
                                                                                                                                         HEN312091 145 bp RNA linear VRL 0
Human coxsackievirus B2 partial 5'UTR, strain /ro/Roma98.
AJ312091
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                                                                                                                                                                                                                                                             Viruses; ssRNA positive-strand viruses, no DNA stage;
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Enterovirus 5506/SIN/001309 5' UTR, partial sequence.
                 Indels
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J. Clin. Microbiol. 40 (12), 4554-4560 (2002)
12454151
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/organism="Human coxsackievirus B2"
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J. Clin. Microbiol. 40 (8), 2823-2827 (2002)
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               Mismatches
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 100.0%; Pred. No.
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Enterovirus 5506/SIN/001309
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                                             1 CCCCTGAATGCGGCTAATC 19
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Human coxsackievirus B2
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                                                                                                                                                                                                  AJ312091.1 GI:16555709
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Similarity 100.
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19; Conserva
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VERSION
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               Matches
                                                                                                                      RESULT 27
HEN312091
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REFERENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human entercoirus 71
Viruses; ssRNA positive-strand viruses, no DNA stage;
Viruses; ssRNA positive-strand viruses, no DNA stage;
Viruses; ssRNA positive-strand viruses, no DNA stage;
1 (bases 1 to 147)
Singh, S., Chow, V.T.K., Phoon, M.C., Chan, K.P. and Poh, C.L.
Direct Detection of Entercoirus 71 (EV71) in Clinical Specimens
Direct Detection of Entercoirus 71 (EV71) in Clinical Specimens
Crom a Hand, Poot, and Mouth Disease Outbreak in Singapore by
Reverse Transcription PCR with Universal Enterovirus and
EV71-Specific Primers
J. Clin. Microbiol. 40 (8), 2823-2827 (2002)
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Singh,S., Chow,V.T.K. and Poh,C.L.
Direct Submitssion
Submitted (24-0CT-2000) Department of Microbiology, National
University of Singapore, 5, Science Drive 2, Singapore 117597,
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2 (bases 1 to 107)
Singh,S., Chow,V.T.K. and Poh,C.L.
Direct Submission
Submitted (18-007-2000) Microbiology, National University
Singapore, 5 Science Drive 2, Singapore 117597, Singapore
Location/Qualifiers
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/isolate="5855/sin/000009"
                                                                                                                                                                                                                     /mol_type="mRNA"
/strain="5506/SIN/001309"
/db_xref="taxon:150715"
<1...>147
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                                                                               Enterovirus 5589/SIN/001809
Enterovirus 5589/SIN/001809
Viruses, saRNA positive-strand viruses, no DNA stage,
Picornaviridae, Enterovirus.
1 (bases 1 to 153)
Singh,S., Chow,V.T.K., Phoon,M.C., Chan,K.P. and Poh,C.L.
Direct Detection of Enterovirus 71 (EV71) in Clinical Specimens from a Hand, Root, and Mouth Disease Outbreak in Singapore by
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Enterovirus 5627/SIN/002009
Enterovirus 5627/SIN/002009
Viruses; BSRMA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.

1 (bases 1 to 154)
Singh,S., Chow,V.T.K., Phoon,M.C., Chan,K.P. and Poh,C.L.
Direct Detection of Enterovirus 71 (EV71) in Clinical Specimens from a Hand, Poot, and Mouth Disease Outbreak in Singapore by Reverse Transcription-PCR with Universal Enterovirus and
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Singh.S., Chow, V.T.K. and Poh, C.L.
Direct Submission
Submitted (18-0CT-2000) Microbiology, National University of Singapore, 5 Science Drive 2, Singapore 117597, Singapore 3 (Dases 1 to 153)
Singh.S., Chow, V.T.K. and Poh, C.L.
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                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (23-FEB-2001) Microbiology, National University Singapore, 5 Science Drive 2, Singapore 117597, Singapore Sequence update by submitter
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Singh, S., Chow, V.T.K. and Poh, C.L.
Direct Submission
Submitted (18-027-2000) Microbiology, National University
Singapore, 5 Science Drive 2, Singapore 117597, Singapore
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AF314004 1inear V
Enterovirus 5589/SIN/001809 5' UTR, partial sequence.
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AF314003
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/mol_type="mRNA"
/strain="5589/SIN/001809"
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J. Clin. Microbiol. 40 (8), 2823-2827 (2002)
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100.0%; Pred. No. 9.5
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                                                    AF314004.2 GI:13111667
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Matches 19, Conservative
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1 (bases 1 to 154)
Singh,S., Chow,V.T.K., Phoon,M.C., Chan,K.P. and Poh,C.L.
Singh,S., Chow,V.T.K., Phoon,M.C., Chan,R.P. and Poh,C.L.
Singh,S., Chow,V.T.K., Phoon,M.C., Chan,R.P. and Poh,C.L.
Singh,S., Chow,V.T.K., Phoon,M.C., Chan,R.P. and Poh,C.L.
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Direct Submission
Submitted (23-FEB-2001) Microbiology, National University on
Singapore, 5 Science Drive 2, Singapore 117597, Singapore
Sequence update by submitter
On Feb 23, 2001 this sequence version replaced gi:12667226.
Location/Qualifiers
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Enterovirus 5656/SIN/002209 5' UTR, partial seguence.
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/mol_type="mRNA"
/strain="5627/SIN/002009"
/db_rref="taxon:150719"
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Singh, S., Chow, V.T.K. and Poh, C.L.
Direct Submission
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/strain="5656/SIN/002209"
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AY027865.1 GI:13591398
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AY027864.1 GI:13591397
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Singh,S., Chow,V.T.K. and Poh,C.L.

Direct Submission

Submitted (18-0CT-2000) Microbiology, National University of Singapore, 5 Science Drive 2, Singapore 117597, Singapore 3 (bases 1 to 154)

Singh,S., Chow,V.T.K. and Poh,C.L.

Direct Submission

Submitted (23-FEB-2001) Microbiology, National University of Singapore, 5 Science Drive 2, Singapore 117597, Singapore Sequence update by submitter

On Feb 23, 2001 this sequence version replaced gi:12667230.

Location/Qualifiers
                                                                                                               Enterovirus 5536/SIN/V01409
Viruses; ssRNA positive-strand viruses, no DNA stage;
Viruses; ssRNA positive-strand viruses, no DNA stage;
Viruses; ssRNA positive-strand viruses, no DNA stage;
Viruses; Enterovirus

1 (bases in to 154)
Singh,S., Chow,V.T.K., Phoon,M.C., Chan,K.P. and Poh,C.L.
Direct Detection of Enterovirus 71 (EV71) in Clinical Specimens
from a Hand, Foot, and Mouth Disease Outbreak in Singapore by
Reverse Transcription-PCR with Universal Enterovirus and
EV71.Specific Primers
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Enterovirus 5546/SIN/000009

Viruses; seRNA positive-strand viruses, no DNA stage;

Viruses: Louder Enterovirus:

1 (bases 1 to 154)

Singh,S., Chow,V.T.K., Phoon,M.C., Chan,K.P. and Poh,C.L.

Direct Detection of Enterovirus 71 (EV71) in Clinical Specimens from a Hand, Foot, and Mouth Disease Outbreak in Singapore by Reverse Transcription-PCR with Universal Enterovirus and
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Singh, S., Chow, V.T.K. and Poh, C.L.
Direct Submission
Submitted (18-027-2000) Microbiology, National University of
Singapore, 5 Science Drive 2, Singapore 117597, Singapore
Location/Qualifiers
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     AF314007 1536/SIN/001409 5' UTR, partial sequence.
AF314007
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/mol_type="mRNA"
/strain="5536/SIN/001409"
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J. Clin. Microbiol. 40 (8), 2823-2827 (2002)
12149336
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Enterovirus TS/SIN/001002
Enterovirus TS/SIN/001002
Enterovirus TS/SIN/001002
Enterovirus TS/SIN/001002
Picuraviridae; Enterovirus.

1 (bases 1 to 154)
Singh,S., Chow,V.T.K., Phoon,M.C., Chan,K.P. and Poh,C.L.
Direct Detection of Enterovirus 71 (EV71) in Clinical Specimens from a Hand, Poot, and Mouth Disease Outbreak in Singapore by Reverse Transcription-PCR with Universal Enterovirus and EV71-Specific Primers
J. Clin, Microbiol. 40 (8), 2823-2827 (2002)
                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Singh, S., Chow, V.T.K. and Poh, C.L. Direct Submission Submitted (12-FBB-2001) Microbiology, National University of Singapore, 5 Science Drive 2, Singapore 117597, Singapore
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Enterovirus TF/SIN/000704
Viruses; ssRNA positive-strand viruses, no DNA stage; Piconnaviridae; Enterovirus.
1 (bases I to 154)
Singh,S., Chow,V.T.K. and Poh,C.L.
                                                                                                                                                                        Length 154;
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organism="Enterovirus 5546/SIN/00009"
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/note="isolated from throat swab"
<1. .>154
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                         /mol_type="mRNA"
/strain="5546/SIN/000009"
/db_xref="taxon:150717"
<1._.>154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /mol_type="genomic RNA"
/strain="TS/SIN/001002"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        organism="Enterovirus"
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GI:14139958
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       AJ295181.1
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HEN312088
LOCUS
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                disease ...
Unpublished
2 (bases 1 to 154)
Singh, S., Chow, V.T.K. and Poh, C.L.
Direct Submission
Submitted (22-FEB-2001) Microbiology, National University of Singapore 5 Science Drive 2, Singapore 117597, Singapore Location/Qualifiers
154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Enterovirus 5571/SIN/001809
Enterovirus 5571/SIN/001809
Viruses; 85RNA positive-strand viruses, no DNA stage;
Viruses; Barerovirus.

1 (Dases 1 to 154)
Singhls., Chow, V.T.K. and Poh, C.L.
Enterovirus strains from an outbreak of Hand, Foot and Mouth disease in Singapore (2000)
Enterovirus strains from an outbreak of Hand, Foot and Mouth disease in Singapore (2000)
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Singh, S., Chow, V.T.K. and Poh, C.L.
Direct Submission
Submission
Submission
Singapore, 5 Science Drive 2, Singapore 117597, Singapore
Location/Qualifiers
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100.0%; Score 19; DB 13; Length 154;
Best Local Similarity 100.0%; Pred. No. 9.5;
Matches 19; Conservative 0; Mismatches 0; Indels
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100.0%; Score 19; DB 13; Length 154;
Best Local Similarity 100.0%; Pred. No. 9.5;
Matches 19; Conservative 0; Mismatches 0; Indels
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Enterovirus 5571/SIN/001809 5'UTR, partial sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Enterovirus 5571/SIN/001809"
/mol_type="genomic RNA"
/mol_type="genomic RNA"
/ptrain="5571/SIN/001809"
/db_xref="taxon:155430"
/noTe="isolated from stool sample"
                                                                                                                                                                                            /db xref="taxon:155429"
/note="isolated from tissue fluid"
<1. .>154
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AY027866.1 GI:13591399
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HCO295181/c
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ORIGIN
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AY027866
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Molecular identification and typing of enteroviruses isolated from
                                                                                                                                                                                                                       A phylogenetic analysis of the two echovirus 30 isolated in Rome (Italy) in 1997 from an outbreak of aseptic meningitis associated with swimming pools
                                                                                                                                       Muscillo, M., La Rosa, G., Marianelli, C., Capobianchi, M.R.,
Zaniratti, S., Cattani, P., Manzara, S., Fadda, G., Comparcola, D. and
                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
Submitted (03-NOV-2000) Muscillo M., Environmental Hygiene,
Istituto Superiore di Sanita', Viale Regina Elena 299, Rome, RM
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Human enterovirus 71 partial 5'UTR, strain /di/Roma98.
AJ312088
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100.0%; Score 19; DB 13; Length 171;
Best Local Similarity 100.0%; Pred. No. 9.5;
Matches 19; Conservative 0; Mismatches 0; Indels
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Human enterovirus 71
Viruses; BRRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
                                                        no DNA stage;
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    171
    172
    Organism="Human coxsackievirus B5"
/mol_type="genomic RNA"
/strain="P/Roma99"

    172
/organism="Human enterovirus 71"
/virion

                                                     Viruses; ssRNA positive-strand viruses,
Picornaviridae; Enterovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /isolate="ITA99-21"
/specific_host="Homo sapiens"
/db_xref="taxon:12074"
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/strain="/di/Roma98"
/isolate="IT98-5114"
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Human coxsackievirus B5
Human coxsackievirus B5
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                                                                                                                                                                                                                                                                                                          Unpublished 2 (bases 1 to 171) Muscillo, M.
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(bases 1 to 184)
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Human echovirus 30
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Best Local Similarity 100.
Matches 19; Conservative
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                                    AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A phylogenetic analysis of the two echovirus 30 isolated in Rome (Italy) in 1997 from an outbreak of aseptic meningitis associated with swimming pools
                                                                                                                                                                                                                                                                                                                                                                                                                                  Muscillo,M., La Rosa,G., Marianelli,C., Capobianchi,M.R.,
Zaniratti,S., Cattani,P., Manzara,S., Fadda,G., Comparcola,D. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
Submitted (03-NOV-2000) Muscillo M., Environmental Hygiene,
Istituto Superiore di Sanita', Viale Regina Elena 299, Rome, RM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /mol_type="genomic RNA"
/strain="Bastianni"
/isolate="ATCC VR-322"
/db_xref="taxon:145390"
/noTe="isolated from fecal specimen of 10-year-old boy with symptoms of headache, stiff neck, fever"
<1. .>177
/db_xref="taxon:39054"
/lab_host="vero cell cultures"
/note="throat swab from child with aseptic meningitis,
dentified by immunofluorescence assay"
<1. .>172
                                                                                                                                           Gaps
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partial sequence.
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Picornaviridae; Enterovirus.
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Human echovirus 13
Viruses; ssRNA positive-strand viruses, no DNA stage;
                                                                                                             Score 19; DB 13; Length 172;
Pred. No. 9.5;
                                                                                                                                           0; Indels
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Human echovirus 13 isolate BE00-82 5' U
AF521491.1 GI:31790833
                                                                                                       100.0%; Score 19; L2
100.0%; Pred. No. 9.5
tive 0; Mismatches
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                                                                                                                                                                                                                                                                             177 bp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   172 CCCCTGAATGCGGCTAATC 154
                                                                                                                                                                        1 CCCCTGAATGCGGCTAATC 19
                                                                                                                                                                                         6 CCCTGAATGCGGCTAATC 24
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                                                                                                                                                                                                                                                                                                                             AJ295207.1 GI:14140008
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2 (bases 1 to 177)
                                                                                                                                           19; Conservative
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Best Local Similarity
Matches 19; Conserv
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VERSION
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                                                                                                                                                                                                                                                    RESULT 40
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Thoelen, I., Lemey, P., van der Donck, I., Beuselinck, K., Lindberg, M.A. and Van Ranst, M. Direct Submission

Direct Submission

Submitted (12-701-2002) Laboratory of Clinical & Epidemiological Submitted (12-701-2002) Laboratory of Clinical & Epidemiological Virology, Department of Microbiology and Immunology, Rega Institute for Medical Research, University of Leuven, Minderbroedersstraat 10, Leuven BE-3000, Belgium

Location/Qualifiers
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Picornaviridae, Enterovirus.

1 (bases 1 to 184)
Thoelen,I., Lemey,P., Van Der Donck,I., Beuselinck,K.,
Lindberg,A.M. and Van Ranst,M.
Molecular typing and epidemiology of enteroviruses identified from an outbreak of aseptic meningitis in Belgium during the summer of
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/db_xref="taxon:41846"
<1._.>185
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/db_xref="taxon:47501"
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Meman echovirus 30 isolate BE00-14 5' UTR, partial sequence
AFS21433
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1 (bases 1 to 185)

Thoelen, I., Lemey, P., Van Der Donck, I., Beuselinck, K., Lindberg, A.M. and Van Ranst, M.
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    .184
    /organism="Human echovirus 13"

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Pred. No. 9.5;
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12767006
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/isolate="BE00-14"
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/isolate="BE00-82"
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Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological Virology, Department of Microbiology and Immunology, Rega Institute for Medical Research, University of Leuven, Minderbroedersstraat 10, Leuven BE-3000, Belgium Location/Qualifiers
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Submitted (12-UTM-2002) Laboratory of Clinical & Epidemiological
Virology, Department of Microbiology and Immunology, Rega Institute
for Medical Research, University of Leuven, Minderbroedersstraat
10, Leuven BE-3000, Belgium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae; Enterovirus.

1 (bases 1 to 185)
Thoelen,I., Lemey,P., Van Der Donck,I., Beuselinck,K.,
Lindberg,A.M. and Van Ranst,M.
Molecular typing and epidemiology of enteroviruses identified from an outbreak of aseptic meningitis in Belgium during the summer of
outbreak of aseptic meningitis in Belgium during the summer
                                                                                                                                                                                                                                                                                                                                                                 /isolation_source="patient 1 - zipcode Belgium 9840"
/db_xref="taxon:12074"
<1. .....85
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/db xref="taxon:41846"
<1. .>185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AF521436 1801at BE00-2 5' UTR, partial sequence.
AF521436
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                                                                                                      Donck, I., Beuselinck, K.
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/organism="Human coxsackievirus B5"
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Best Local Similarity 100.0%; Pred. No. 9.5;
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                                      J. Med. Virol. 70 (3), 420-429 (2003)
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/isolate="BE00-1"
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/isolate="BE00-2"
                                                                              2 (bases 1 to 185)
Thoelen, I., Lemey, P., van der 1
Lindberg, M.A. and Van Ranst, M.
Direct Submission
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Human echovirus 30
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AUTHORS
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JOURNAL
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                                                             PUBMED
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SOURCE
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                                                                                                                                                                                                                                                           AF521434 linear VRL 17-JUN-2003
Human coxeackievirus B5 isolate BE00-15 5' UTR, partial sequence. ,
AF521434
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Lindberg, A.M. and Van Ranst, M.
Molecular typing and epidemiology of enteroviruses identified from
an outbreak of aseptic meningitis in Belgium during the summer of
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Lindberg, A.M. and Van Ranst, M.
Molecular typing and epidemiology of enteroviruses identified from
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Human coxsackievirus BS isolate BE00-1 5' UTR, partial sequence.
AF521435
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/db_xrefe"taxon:12074"
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Direct Submission
                                        Length 185;
                                                                                                                                                                                                                                                                                                                                                                                                       Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
1 (bases 1 to 185)
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Picornaviridae; Enterovirus.
1 (bases 1 to 185)
                                                                            Indels
                                      Score 19; DB 13;
Pred. No. 9.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'organism="Human coxsackievirus
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                                                                          Mismatches
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/isolate="BE00-15"
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Human coxsackievirus B5
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Human coxsackievirus B5
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Best Local Similarity 100.
Matches 19; Conservative
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Matches 19; Conserv
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Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological
Virology, Department of Microbiology and Immunology, Rega Institute
for Medical Research, University of Leuven, Minderbroedersstraat
10, Leuven BE-3000, Belgium
Location/Qualifiers
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Viruses; ssRNA positive-strand viruses, no DNA stage;
Viruses; ssRNA positive-strand viruses, no DNA stage;
Viconavirudae; Enterovirus.

1 (bases 1 to 185)
Thoelen, I., Lemey, P., Van Der Donck, I., Beuselinck, K.,
Indobergh, A.M. and Van Ranst, M.
Molecular typing and epidemiology of enteroviruses identified from an outbreak of aseptic meningitis in Belgium during the summer of
                                                                                                                                                                                                         Human echovirus 6
Human echovirus 6
Viruses; sRNAM positive-strand viruses, no DNA stage;
Viruses; sRNAM positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.

1 (bases 1 to 185)
Thoelen, I., Lemey, P., Van Der Donck, I., Beuselinck, K.,
Lindberg, A.M. and Van Ranst, M.
Molecular typing and epidemiology of enteroviruses identified from
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/db_xref="taxon:12062"
<1. .>185
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Human echovirus 6 isolate BE00-3 5' UTR, partial sequence.
AF521437
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Human echovirus 6 isolate BE00-4 5' UTR, partial sequence.
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12767006
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/virion
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/isolate="BE00-3"
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               CCCCTGAATGCGGCTAATC 19
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AF521438.1 GI:31790780
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Direct Submission
Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological
Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological
Virology, Department of Microbiology and Immunology, Rega Institute
for Medical Research, University of Leuven, Minderbroedersstraat
10, Leuven BE-3000, Belgium
Location/Qualifiers
Thoelen, I., Lemey, P., van der Donck, I., Beuselinck, K., Lindberg, M.A. and Van Ranst, M. Direct Submission

Direct Submission
Submitted (12-70N-2002) Laboratory of Clinical & Epidemiological Virology, Department of Microbiology and Immunology, Rega Institute for Medical Research, University of Leuven, Minderbroedersstraat 10, Leuven BE-3000, Belgium
Location/Qualifiers
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Human echovirus 6

Viruses; seRNA positive-strand viruses, no DNA stage;

Viruses; seRNA positive-strand viruses, no DNA stage;

1 (bases 1 to 185)

Thoelen,I., Lemey,P., Van Der Donck,I., Beuselinck,K.,

Lindberg,A.M. and Van Ranst,M.

Molecular typing and epidemiology of enteroviruses identified from an outbreak of aseptic meningitis in Belgium during the summer of
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/db_xref="taxon:12062"
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/db_xref="taxon:12062"
<1. .>185
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Human echovirus 6 isolate BE00-5 5' UTR, partial sequence.
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Thoelen, I., Lemey, P., van der Donck, I., Beuselinck, K.,
Lindberg, M.A. and Van Ranst, M.
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ilarity 100.0%; Pred. No. 9.5;
Conservative 0; Mismatches 0:
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/isolate="BE00-4"
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/isolate="BE00-5"
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Thoelen, I., Lemey, P., van der Donck, I., Beuselinck, K., Lindbargy, M., and Van Ranst, M. Lindbargy, M. and Van Ranst, M. Direct Submission Bubmitted (12-JUN-2002) Laboratory of Clinical & Epidemiological Virology, Department of Microbiology and Immunology, Rega Institute for Medical Research, University of Leuven, Minderbroedersstraat 10, Leuven BB-3000, Belgium
Location/Qualifiers
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Picornaviridae; Enterovirus.
I (bases 1 to 185)
Thoelen, I., Lemey, P., Van Der Donck, I., Beuselinck, K.,
Lindberg, A.M. and Van Ranst, M.
Molecular typing and epidemiology of enteroviruses identified from an outbreak of aseptic meningitis in Belgium during the summer of
   University of Leuven, Minderbroedersstraat
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Human echovirus 6 isolate BE00-10 5' UTR, partial sequence.
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Human echovirus 6 isolate BE00-8 5' UTR, partial sequence.
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/db_xref="taxon:12062"
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                                                                             /organism="Human echovirus
                                                                                                                   /mol_type="genomic RNA"
/isolate="BE00-7"
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/isolate="BE00-8"
for Medical Research, Univers
10, Leuven BE-3000, Belgium
Location/Qualifiers
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AF521442
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                                                       VRL 17-JUN-2003
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Lindberg, A.M. and Van Ranst, M.
Molecular typing and epidemiology of enteroviruses identified from
an outbreak of aseptic meningitis in Belgium during the summer of
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Lindberg,A.M. and Van Ranst,M.
Molecular typing and epidemiology of enteroviruses identified from
an outbreak of aseptic meningitis in Belgium during the summer of
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/db_xref="taxon:41846"
<1. .>185
                                           ar>21440
Human echovirus 30 isolate BE00-6 5' UTR, partial sequence.
AFS21440
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Human echovirus 6 isolate BE00-7 5' UTR, partial sequence.
AF521441
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Thoslen, I., Lemey, P., van der Donck, I., Beuselinck, K.,
Lindberg, M.A. and Van Ranst, M.
Direct Submission
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Direct Submission
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Human echovirus 6
Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
                                                                                                                                                                                       Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
1 (bases 1 to 185)
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Pred. No. 9.5;
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/isolate="BE00-6"
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Human echovirus 30
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Best Local Similarity 100.
Matches 19; Conservative
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VRL 17-JUN-2003

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Direct Submission
Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological
Virology, Department of Microbiology and Immunology, Rega Institute
for Medical Research, University of Leuven, Minderbroedersstraat
10, Leuven BE-3000, Belgium
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Molecular typing and epidemiology of enteroviruses identified from an outbreak of aseptic meningitis in Belgium during the summer of
           /mol type="genomic RNA"
/isolate="BE00-11"
/isolation.source="patient 11 - zipcode Belgium 9400"
/db_xref="taxon:41846"
<11. .>185
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/isolate="BE00-12"
/isolation.source="patient 12 - zipcode Belgium 9402"
/db_xref="taxon:41846"
-11. ->185
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Human echovirus 16 isolate BE00-13 5' UTR, partial sequence.
AF521446
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Human echovirus 30 isolate BE00-12 5′ UTR, partial sequence.
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Thoelen,I., Lemey,P., van der Donck,I., Beuselinck,K.,
Lindberg,M.A. and Van Ranst,M.
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Human echovirus 30
Human echovirus 30
Viruses; seRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
1 (Dases 1 to 185)
Thoelen, I., Lemey, P., Van Der Donck, I., Beuselinck, K.,
Lindberg, A.M. and Van Ranst, M.
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                                                                                                                                                                     100.0%; Score 19; DB 13; Length 185; 100.0%; Pred. No. 9.5;
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                                                                                                                                                                                                                 0; Mismatches
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AF521445.1 GI:31790787
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Direct Submitsed (12-70N-2002) Laboratory of Clinical & Epidemiological Virology, Department of Microbiology and Immunology, Rega Institute for Medical Research, University of Leuven, Minderbroedersstraat 10, Leuven BE-3000, Belgium

Location/Qualifiers
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1 (bases 1 to 185)
Thoelen,I., Lemey,P., Van Der Donck,I., Beuselinck,K.,
Thoelen,I., Lamey,P., Van Der Donck,I., Beuselinck,K.,
Molecular typing and epidemiology of enteroviruses identified from an outbreak of aseptic meningitis in Belgium during the summer of
                                                                                                                                                                                                               Molecular typing and epidemiology of enteroviruses identified from an outbreak of aseptic meningitis in Belgium during the summer of
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Human echovirus 30 isolate BE00-11 5' UTR, partial sequence.
AF521444
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                                                                                                     Viruses; seRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
1 (bases 1 to 0.85)
Thoelen, I., Lemey, P., Van Der Donck, I., Beuselinck, K.,
Lindberg, A.M. and Van Ranst, M.
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Thoslen, I., Lemey, P., van der Donck, I., Beuselinck, K.,
Lindberg, M. A. and Van Ranst, M.
Lirect Submission
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    .185
/organism="Human echovirus
/virion

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/isolate="BE00-10"
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                      AF521443.1 GI:31790785
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VRL 17-JUN-2003

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Location/Qualifiers
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Best Local Similarity 100.0%; Pr
Matches 19; Conservative 0;
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Location/Qualifiers
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Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological
Virology, Department of Microbiology and Immunology, Rega Institute
For Medical Research, University of Leuven, Minderbroedersstraat
10, Leuven BE-3000, Belgium
Location/Qualifiers
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                                                 Thoelen, I., Lemey, P., Van Der Donck, I., Beuselinck, K., Lindberg, A.M. and Van Ranst, M. Molecular typing and epidemiology of enteroviruses identified from an outbreak of aseptic meningitis in Belgium during the summer of
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/db_xref="taxon:41846"
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Human echovirus 30 isolate BE00-30 5' UTR, partial sequence
AF521447
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Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
1 (bases 1 to 185)
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Human echovirus 30
Viruses, seRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
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/db_xref="taxon:47504"
<1._.>185
                                                                                                                                                                                                                                                                                                                                                       organism="Human echovirus 16"
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100.0%; Pred. No. >---

    Med. Virol. 70 (3), 420-429 (2003)

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/isolate="BE00-13"
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Best Local Similarity 100.
Matches 19; Conservative
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AF521447
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AF521448 17-JUN-2003
Human coxeackievirus BS isolate BE00-31 5' UTR, partial sequence.
AF521448
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Human coxsackievirus B5
Viruses; saRNA postiive-strand viruses, no DNA stage;
Viruses; saRNA postiive-strand viruses, no DNA stage;
Dicornaviridae; Enterovirus.
1 (bases 1 to 185)
Thoslen,T., Lemey,P., Van Der Donck,I., Beuselinck,K.,
Thoslen,T., Lemey,A.M. and Van Ranst,M.
Molecular typing and epidemiology of enteroviruses identified from an outbreak of aseptic meningitis in Belgium during the summer of
                                                        Gaps
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Human echovirus 30 isolate BE00-32 5' UTR, partial sequence.
AF521449
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Lindberg, M.A. and Van Ranst, M.
  Length 185;
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Score 19; DB 13;
Pred. No. 9.5;
); Mismatches 0;
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[ bases 1 to 185]

Thoelen, I., Lemey, P., Van Der Donck, I., Lindberg, A.M. and Van Ranst, M.
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/db_xref="taxon:12074"
<1._.>185
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/isolate="BE00-31"
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Thoelen, I., Lemey, P., van der Donck, I., Beuselinck, K.,
Lindberg, M.A. and Van Ranst, M.
Lindberg, M.A. and Van Ranst, M.
Direct Submission
Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological
Virology, Department of Microbiology and Immunology, Rega Institute
for Medical Research, University of Leuven, Minderbroedersstraat
10, Leuven BE-3000, Belgium
Location/Qualifiers
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Human echovirus 6

Viruses; saRNA positive-strand viruses, no DNA stage;

Viruses; saRNA positive-strand viruses, no DNA stage;

Dicornaviridae; Enterovirus.

1 (bases 1 to 185)

Thoelen,I., Lemey,P., Van Der Donck,I., Beuselinck,K.,

Lindberg,A.M. and Van Ranst,M.

Molecular typing and epidemiology of enteroviruses identified from an outbreak of aseptic meningitis in Belgium during the summer of
                                                                                                                                                                                                                                                                                                                  Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.

1 (bases 1 to 185)
Thoelen, I., Lemey, P., Van Der Donck, I., Beuselinck, K.,
Lindberg, A.M. and Van Ranst, M.
Molecular typing and epidemiology of enteroviruses identified from
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/isolate="BE00-34"
/isolation source="patient 34 - zipcode Belgium 1770"
/db_xref="taxon:41846"
-1. ->185
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  Gaps
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Human echovirus 30 isolate BE00-34 5' UTR, partial sequence.
AF521451
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Muman echovirus 6 isolate BE00-35 S' UTR, partial sequence.
AF521452
AF521452.1 GI:31790794
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                                       1 CCCCTGAATGCGGCTAATC 19
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                                                              CCCCTGAATGCGGCTAATC
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Human echovirus 30
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Best Local Similarity 100.
Matches 19; Conservative
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                                                                                                         Thoelen, L. Cares, P., van der Donck, I., Beuselinck, K., Lindberg, M.A. and Van Ranst, M. Direct Submission
Submitted (12-JUM-2002) Laboratory of Clinical & Epidemiological Virology, Department of Microbiology and Immunology, Rega Institute for Medical Research, University of Leuven, Minderbroedersstraat 10, Leuven BE-3000, Belgium
Location/Qualifiers
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Direct Submission

Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological Virology, Department of Microbiology and Immunology, Rega Institute for Medical Research, University of Leuven, Minderbroedersstraat
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locoraviridae; Enterovirus.
l (bases 1 to 185)
Thoelen,I., Lemey,P., Van Der Donck,I., Beuselinck,K.,
Lindberg,A.M. and Van Ranst,M.
Molecular typing and epidemiology of enteroviruses identified from an outbreak of aseptic meningitis in Belgium during the summer of
Molecular typing and epidemiology of enteroviruses identified from an outbreak of aseptic meningitis in Belgium during the summer of
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/db_xref="taxon:41846"
<1._.>185
                                                                                                                                                                                                                                                                                                                                                                        /isolation_source="patient 32 - zipcode Belgium 1703" /db_xref="taxon:41846" <1. .>185
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Human echovirus 30 isolate BE00-33 5' UTR, partial sequence.
AF521450
AF521450.1 GI:31790792
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12767006
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12767006
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/isolate="BE00-32"
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/isolate="BE00-33"
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Location/Qualifiers
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Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological Virology, Department of Microbiology and Immunology, Rega Institute for Medical Research, University of Leuven, Minderbroedersstraat 10, Leuven BE-3000, Belgium
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locoravirades, Enterovirus.
1 (bases 1 to 185)
Thoelen,I., Lemey,P., Van Der Donck,I., Beuselinck,K.,
Indeberg,A.M. and Van Ranst,M.
Molecular typing and epidemiology of enteroviruses identified from an outbreak of aseptic meningitis in Belgium during the summer of
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Picornaviridae; Enterovirus.

1 (bases 1 to 185)
1 (bases 1, L Lemey, P., Van Der Donck, I., Beuselinck, K.,
Lindberg, A.M. and Van Ranst, M.
Molecular typing and epidemiology of enteroviruses identified from an outbreak of aseptic meningitis in Belgium during the summer of
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Lindbergy, M. A. and Van Ranst, M.
Direct Submission
Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological
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/db_xref="taxon:12062"
<1. .>185
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Human echovirus 6 isolate BE00-41 5' UTR, partial sequence
AFS21456
                                                                                      AFS21455 linear VRL 17.
Human echovirus 6 isolate BE00-39 5' UTR, partial sequence
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                                                          Direct Submission
Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological
Virology, Department of Microbiology and Immunology, Rega Institute
for Medical Research, University of Leuven, Minderbroedersstraat
10, Leuven BB-3000, Belgium
Location/Qualifiers
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                                                                                                                                                                                                                              /mol_type="genomic RNA"
/isolate="BE00-35"
/isolation.source="patient 35 - zipcode Belgium 3270"
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<1. .>185
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Human echovirus 6 isolate BE00-36 5' UTR, partial sequence
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Thoelen,I., Lemey,P., van der Donck,I., Beuselinck,K.,
Lindberg,M.A. and Van Ranst,M.
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Picornaviridae; Enterovirus.
1 (bases 1 to 185)
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Pred. No. 9.5;
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/db_xref="taxon:12062"
<1._.>185
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/isolate="BE00-36"
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AF521453.1 GI:31790795
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Matches 19; Conservative
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Matches 19; Conservative
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Human echovirus 6
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        Thoelen, I.
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AF521453
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Matches

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RESULT 65

AF521.457

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JOURNAL PUBMED REFERENCE

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Thoelen, I., Lemey, P., van der Donck, I., Beuselinck, K., Lindberg, M.A. and Van Ranst, M. Direct Submission

Direct Submission

Submitted (12-700-2002) Laboratory of Clinical & Epidemiological Virology, Department of Microbiology and Immunology, Rega Institute for Medical Research, University of Leuven, Minderbroedersstraat 10, Leuven BE-3000, Belgium

Location/Qualifiers
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                                                                                                                            Viruses; ssRNA positive-strand viruses, no DNA stage; picornaviridae; Enterovirus.

1 (bases 1 to 185)
Thoelen,I., Lemey,P., Van Der Donck,I., Beuselinck,K.,
Lindberg,A.M. and Van Ranst,M.
Molecular typing and epidemiology of enteroviruses identified from an outbreak of aseptic meningitis in Belgium during the summer of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Viruses; ssRNA positive-strand viruses, no DNA stage;
plocoravitades; Enterovirus.
1 (base 1 to 185)
Thoelen,I., Lemey,P., Van Der Donck,I., Beuselinck,K.,
Lindberg,A.M. and Van Ranst,M.
Molecular typing and epidemiology of enteroviruses identified from an outbreak of aseptic meningitis in Belgium during the summer of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /isolation_source="patient 43 - zipcode Belgium 9402"
/db_xref="taxon:41846"
<1._.>185
  Human echovirus 30 isolate BE00-43 5' UTR, partial sequence
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partial sequence
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Thoelen, I., Lemey, P., van der Donck, I., Beuselinck, K.,
Lindberg, M.A. and Van Ranst, M.
Theret Submission
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Human echovirus 6 isolate BE00-44 5' UTR,
AF521459
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100.0%; Score 19; DB 13;
Best Local Similarity 100.0%; Pred. No. 9.5;
Matches 19; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               organism="Human echovirus 30"
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12767006
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/isolate="BE00-43"
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                                              AF521458.1 GI:31790800
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                                                                                      Human echovirus 30
Human echovirus 30
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AF521459
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Lindberg, M.A. and Van Ranst, M.
Direct Submission
Direct Submission
Virology, Department of Microbiology and Immunology, Rega Institute
for Medical Research, University of Leuven, Minderbroedersstraat
10, Leuven BB-3000, Balgium
Location/Qualifiers
Virology, Department of Microbiology and Immunology, Rega Institute for Medical Research, University of Leuven, Minderbroedersstraat 10, Leuven BE-3000, Belgium Location/Qualifiers
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                                                                                                                                                  /isolation_source="patient 41 - zipcode Belgium 3390"
/db_xref="taxon:12062"
<1._.>185
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/db_xref="taxon:12062"
<1. .>185
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Human echovirus 6 isolate BE00-42 5' UTR, partial sequence.
AF521457
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Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
I (bases I to 18)
Thoelen, I., Lemey, P., Van Der Donck, I., Beuselinck, K.,
Lindberg, A.M. and Van Ranst, M.
                                                                                                                                                                                                                                                                                                         DB 13; Length 185;
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Pred. No. 9.5;
; Mismatches 0;
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12767006
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/organism="Human echovirus
/virion
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/isolate="BE00-42"
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Best Local Similarity 100.
Matches 19; Conservative
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Best Local
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DEFINITION

RESULT 68 AF521460

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ORGANISM ACCESSION VERSION KEYWORDS SOURCE

REFERENCE AUTHORS

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The Company of the Company of Leney, London of Manager, London of Manager, London of Manach, London of Manach, M.
Lindberg, M.A. and Van Ranst, M.
Lindberg, M.A. and Van Ranst, M.
Direct Submission
Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological
Virology, Department of Microbiology and Immunology, Rega Institute
for Medical Research, University of Leuven, Minderbroedersstraat
10, Leuven BE-3000, Belgium
Location/Qualifiers
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Submitted (12-UTM-2002) Laboratory of Clinical & Epidemiological
Virology, Department of Microbiology and Immunology, Rega Institute
for Medical Research, University of Leuven, Minderbroedersstraat
10, Leuven BE-3000, Belgium
                               Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae; Enterovirus.

1 (bases 1 to 185)
Thoelen,I., Lemey,P., Van Der Donck,I., Beuselinck,K.,
Lindberg,A.M. and Van Ranst,M.
Molecular typing and epidemiology of enteroviruses identified from an outbreak of aseptic meningitis in Belgium during the summer of
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1 (bases 1 to 185)
Thoelen,I., Lemey,P., Van Der Donck,I., Beuselinck,K.,
Lindberg,A.M. and Van Ranst,M.
Molecular typing and epidemiology of enteroviruses identified from an outbreak of aseptic meningitis in Belgium during the summer of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /isolation_source="patient 48 - zipcode Belgium 1770"
/db_xref="taxon:41846"
<1._.>185
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Human echovirus 6 isolate BE00-49 5' UTR, partial sequence.
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Lindberg, M.A. and Van Ranst, M.
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llarity 100.0%; Pred. No. 9.5;
Conservative 0; Mismatches 0;
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/organism="Human echovirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /mol type="genomic RNA"
/isolate="BE00-48"
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/isolate="BE00-49"
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Location/Qualifiers
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                Human echovirus 30
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Human echovirus 6
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Best Local Simi
Matches 19;
              ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AF521460 185 bp RNA linear VRL 17-JUN-2003
Human coxeackievirus B5 isolate BE00-47 5' UTR, partial sequence.
AF521460
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1 (bases 1 to 185)
Thoelen! I., Lemey.P., Van Der Donck,I., Beuselinck,K.,
Lindberg.A.M. and Van Ranst,M.
Molecular typing and epidemiology of enteroviruses identified from an outbreak of aseptic meningitis in Belgium during the summer of
                                                                                                      - zipcode Belgium 1910"
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Human echovirus 30 isolate BE00-48 5' UTR, partial sequence
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Lindberg, M.A. and Van Ranst, M.
Direct Submission
                                                                                                                                                                                                                 DB 13; Length 185;
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/organism="Human echovirus 6"
/virion
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2767006
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                                                    /mol_type="genomic RNA"
/isolate="BE00-44"
/isolation_source="patient
/db_xref="taxon:12062"
                                                                                                                                                                                                                                    Pred. No. 9.5
Mismatches
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100.0%; Pred. No.
:ive 0; Mismatch
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/isolate="BE00-47"
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Human coxsackievirus B5
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Best Local Similarity
Matches 19; Conserv
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Best Local S:
Matches 19
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DEFINITION ACCESSION VERSION

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Thoelen, I., Lemey, P., van der Donck, I., Beuselinck, K., Lindberg, M.A. and Van Ranst, M.

Lindberg, M.A. and van Ranst, M.

Direct Submission

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Ladoratory of Clinical & Epidemiological

Subjology, Department of Microbiology and Immunology, Rega Institute
for Medical Research, University of Leuven, Minderbroedersstraat

10, Leuven BB-3000, Belgium
                                                                                                                                                                                                                              Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological Virology, Department of Microbiology and Immunology, Rega Institute for Medical Research, University of Leuven, Minderbroedersstraat 10, Leuven BE-3000, Belgium
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VRL 17-JUN-2003
Lindberg, A.M. and Van Ranst, M. Molecular typing and epidemiology of enteroviruses identified from an outbreak of aseptic meningitis in Belgium during the summer of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.

1 (bases 1 to 185)
Thoelen,I., Lemey,P., Van Der Donck,I., Beuselinck,K.,
Lindberg,A.M. and Van Ranst,M.
Molecular typing and epidemiology of enteroviruses identified from an outbreak of aseptic meningitis in Belgium during the summer of
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/db_xref="taxon:12062"
<1. .>185
                                                                                                                                                                                                                                                                                                                                                                                                                                                           /isolation_source="patient 51 - zipcode Belgium 3583"
|db_xref="taxon:47501"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AF521465 186 186 bp RNA linear VRL 17-
Human echovirus 6 isolate BE00-52 5' UTR, partial sequence.
AF521465
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                                                                                                                                                           Thoelen, I., Lemey, P., van der Donck, I., Beuselinck, K., Lindberg, M.A. and Van Ranst, M. Direct Submission
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/organism="Human echovirus 13"
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/isolate="BE00-52"
                                                                                                                                                                                                                                                                                                                                                                                                                       /mol_type="genomic RNA"
/isolate="BE00-51"
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Human echovirus 6
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Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological
Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological
Virology, Department of Microbiology and Immunology, Rega Institute
for Medical Research, University of Leuven, Minderbroedersstraat
10, Leuven BE-3000, Belgium
Location/Qualifiers
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Picornaviridae; Enterovirus.
1 (bases 1 to 185)
Thoelen, I., Lemey, P., Van Der Donck, I., Beuselinck, K.,
Lindberg, A.M. and Van Ranst, M.
Molecular typing and epidemiology of enteroviruses identified from
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/db_xref="taxon:12062"
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Human echovirus 13 isolate BE00-51 5' UTR, partial sequence.
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Human echovirus 6 isolate BE00-50 5' UTR, partial sequence
AF521463
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Human echovirus 13
Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviries Enterovirus.
I (Dases 1 to 185)
Thoelen,I., Lemey,P., Van Der Donck,I., Beuselinck,K.,
                                                                                             Length 185;
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                                                                                             100.0%; Score 19; DB 13; 100.0%; Pred. No. 9.5;
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isolate="BE00-50"
    /db_xref="taxon:12062"
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Human echovirus 6
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Best Local Similarity
Matches 19; Conserv
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TITLE JOURNAL

FEATURES

PUBMED REFERENCE

AUTHORS

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Query Match Best Local

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RESULT 72 AF521464 LOCUS

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Thoelen, I., Lemey, P., van der Donck, I., Beuselinck, K., Lindberg, M.A. and Van Ranst, M.
Dindberg, M.A. and Van Ranst, M.
Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological Virolegy, Department of Microbiology and Immunology, Rega Institute for Medical Research, University of Leuven, Minderbroedersstraat 10, Leuven BE-3000, Belgium
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Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological
Virology, Department of Microbiology and Immunology, Rega Institute
for Medical Research, University of Leuven, Minderbroedersstraat
10, Leuven BB-3000, Belgium
Location/Qualifiers
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Human coxsackievirus B5
Viruses; ssRNA positive-strand viruses, no DNA stage;
Viruses; ssRNA positive-strand viruses, no DNA stage;
Dicornaviridae; Enterovirus.

1 (bases 1 to 185)
Thoelen,I., Lemey,P., Van Der Donck,I., Beuselinck,K.,
Mindberg,A.M. and Nanst,M.
Molecular typing and epidemiology of enteroviruses identified from an outbreak of aseptic meningitis in Belgium during the summer of
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5' UTR, partial sequence.
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/db_xref="taxon:12062"
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Thoelen,I., Lemey,P., van der Donck,I., Beuselinck,K.,
Lindberg,M.A. and Van Ranst,M.
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/organism="Human coxsackievirus B5"
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100.0%; Pred. No. 9.5;
vative 0; Mismatches 0;
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Human coxsackievirus B5 isolate BE00-25
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/db_xref="taxon:12074"
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    1. .185
    /organism="Human echovirus"
/virion

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/isolate="BE00-25"
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/isolate="BE00-24"
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Human coxsackievirus B5 isolate BE00-55 5' UTR, partial sequence.
AF521467
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/db_xref="taxon:12074"
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Human echovirus 6 isolate BE00-24 5' UTR, partial sequence.
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Direct Submission
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Picornaviridae; Enterovirus.
1 (bases 1 to 185)
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Picornaviridae; Enterovirus.
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/organism="Human coxsackievirus
                     red. No. 9.5;
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100.0%; Pred. No. 9.5
Live 0; Mismatches
                     Pred. No.
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/isolate="BE00-55"
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Human coxsackievirus B5
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Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological
Virology, Department of Microbiology and Immunology, Rega Institute
for Medical Research, University of Leuven, Minderbroedersstraat
10, Leuven BE-3000, Belgium
Location/Qualifiers
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Human coxeackievirus B5 isolate BE00-29 5' UTR, partial sequence.
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Picornaviridae; Enterovirus.
1 (bases 1 to 185)
Thoelen, I., Lemey, P., Van Der Donck, I., Beuselinck, K.,
Lindberg, A.M. and Van Ranst, M.
Molecular typing and epidemiology of enteroviruses identified from
                                                                                                                                                                   Human coxsackievirus B5
Human coxsackievirus B5
Human coxsackievirus B5
Human span as B8RNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.

1 (bases 1 to 185)
Thoelen, I., Lemey, P., Van Der Donck, I., Beuselinck, K.,
Lindberg, A.M. and Van Ranst, M.
Molecular typing and epidemiology of enteroviruses identified from an outbreak of aseptic meningitis in Belgium during the summer of
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Human echovirus 30 isolate BE00-16 5' UTR, partial sequence.
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Thoslen,I., Lemey,P., van der Donck,I., Beuselinck,K.,
Lindberg,M.A. and Van Ranst,M.
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<1...>185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /mol_type="genomic RNA"
/isolate="BE00-29"
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 14 CCCCTGAATGCGGCTAATC 32
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Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological Virology, Department of Microbiology and Immunology, Rega Institute for Medical Research, University of Leuven, Minderbroedersstraat 10, Leuven BE-3000, Belgium Location/Qualifiers
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Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological
Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiology, Rega Institute
Virology, Department of Microbiology and Immunology, Rega Institute
for Medical Research, University of Leuven, Minderbroedersstraat
10, Leuven BE-3000, Belgium
Location/Qualifiers
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Human echovirus 30

Viruses; saRNA positive-strand viruses, no DNA stage;

Viruses; saRNA positive-strand viruses, no DNA stage;

1 (bases 1 to 185)

Thoelen,I., Lemey,P., Van Der Donck,I., Beuselinck,K.,
Lindberg,A.M. and Van Ranst,M.

Molecular typing and epidemiology of enteroviruses identified from an outbreak of aseptic meningitis in Belgium during the summer of
                                                                                                                                                                                                                     /mol_type="genomic RNA"
/isolate="BE00-16"
/isolation_source="patient 16 - zipcode Belgium 3294"
/db_xref="taxon:41846"
-1. ->185
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/db_xref="taxon:41846"
<1. .>185
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5' UTR, partial sequence.
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Thoelen, I., Lemey, P., van der Donck, I., Beuselinck, K.,
Lindberg, M.A. and Van Ranst, M.
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    1. .185
    /organism="Human echovirus 30"

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/organism="Human echovirus 30"
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Human echovirus 30 isolate BE00-17
AF521475
AF521475.1 GI:31790817
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/isolate="BE00-17"
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Gaps

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Virology, Department of Microbiology and Immunology, Rega Institute for Medical Research, University of Leuven, Minderbroedersstraat 10, Leuven BE-3000, Belgium
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Human coxsackievirus B5 isolate BE00-27 5' UTR, partial sequence.
AF521480
AF521480.1 GI:31790822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
1 (bases 1 to 185)
Thoelen,I., Lemey,P., Van Der Donck,I., Beuselinck,K.,
Lindberg,A.M. and Van Ranst,M.
Molecular typing and epidemiology of enteroviruses identified from an outbreak of aseptic meningitis in Belgium during the summer of
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                                                                                                                                                         - zipcode Belgium 1830"
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                                                                                                                                                /isolation_source="patient 19
/db_xref="taxon:41846"
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/db_xref="taxon:41846"
<1._.>185
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1. .185
/organism="Human echovirus
/virion
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                                                                                                 /mol_type="genomic RNA"
/isolate="BE00-19"
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/isolate="BE00-20"
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Human echovirus 30
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Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological Virology, Department of Microbiology and Immunology, Rega Institute for Medical Research, University of Leuven, Minderbroedersstraat 10, Leuven BB-3000, Belgium
Location/Qualifiers
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Thochen, I. Lemey, P., van der Donck, I., Beuselinck, K.,
Lindberg, M.A. and Van Ranst, M.
Lindberg, M.A. and Van Ranst, M.
Submission
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                VRL 17-JUN-2003
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Lindberg, A.M. and Van Ranst, M.
Molecular typing and epidemiology of enteroviruses identified from
an outbreak of aseptic meningitis in Belgium during the summer of
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Lindberg, A.M. and Van Ranst, M.
Molecular typing and epidemiology of enteroviruses identified from
an outbreak of aseptic meningitis in Belgium during the summer of
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             AF521476 1865 bp RNA linear VRL 17-.
Human echovirus 30 isolate BE00-18 5' UTR, partial sequence
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Human echovirus 30 isolate BE00-19 5' UTR, partial sequence
AF521477
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                                                                                                                                           Human echovirus 30
Human echovirus 30
Viruses, seRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
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Human echovirus 30
Viruses; seRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
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/db_xref="taxon:41846"
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Pred. No. 9.5;
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2767006
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/isolate="BE00-18"
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1 Similarity 100.0%; P:
19; Conservative 0;
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Thoelen, I., Lemey, P., van der Donck, I., Beuselinck, K.,
Lindbarg, M.A. and Van Ranst, M.
Lindbarg, M.A. and Van Ranst, M.
Direct Submission
Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological
Virology, Department of Microbiology and Immunology, Rega Institute
for Medical Research, University of Leuven, Minderbroedersstraat
10, Leuven BE-3009, Belgium
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Molecular typing and epidemiology of enteroviruses identified from an outbreak of aseptic meningitis in Belgium during the summer of
    /isolation_source="patient 72 - zipcode Belgium 3000"
/db_xref="taxon:47504"
<1._.>185
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partial sequence.
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AF521482
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1 (bases 1 to 185)
Thoelen, I., Lemey, P., Van Der Donck, I., Beuselinck, K., Lindberg, A.M. and Van Ranst, M.
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Picornaviridae; Enterovirus.
1 (bases 1 to 185)
                                                                                                      Length 185;
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                                                                                                  Score 19; DB 13;
Pred. No. 9.5;
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/db xref="taxon:47501"
<1. ..185
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Human echovirus 30 isolate BE00-74
AF521483
AF521483.1 GI:31790825
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/isolate="BE00-73"
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ilarity 100.0%;
Conservative 0
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Human echovirus 30
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Human echovirus 13
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Birect Submission

Submitted (12-71N-2002) Laboratory of Clinical & Epidemiological Virology, Department of Microbiology and Immunology, Rega Institute for Medical Research, University of Leuven, Minderbroedersstraat 10, Leuven BE-3000, Belgium

Location/Qualifiers
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1 (bases 1 to 185)
Thoelen,I., Lemey,P., Van Der Donck,I., Beuselinck,K.,
Thoelen,I., Lamey,P., Van Der Donck,I., Beuselinck,K.,
Molecular typing and epidemiology of enteroviruses identified from an outbreak of aseptic meningitis in Belgium during the summer of
                                                                                                                                          Molecular typing and epidemiology of enteroviruses identified from an outbreak of aseptic meningitis in Belgium during the summer of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /isolation_source="patient 27 - zipcode Belgium 9840"
/db_xref="taxon:12074"
<1. .>185
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Human echovirus 16 isolate BE00-72 5' UTR, partial sequence.
AF521481
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Human coxeackievirus BS
Human coxeackievirus BS
Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
Thoelen,I., Lemey,P., Van Der Donck,I., Beuselinck,K.,
Lindberg,A.M. and Van Ranst,M.
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100.0%; Pred. No.
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/isolate="BE00-72"
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/isolate="BE00-27"
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Human echovirus 30
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Human echovirus 30
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                                                                                                                                   Thoelen, I., Lemey, P., van der Donck, I., Beuselinck, K., Lindberg, M.A. and Van Ranst, M. Direct Submission
Direct Submission
Submitted (12-70N-2002) Laboratory of Clinical & Epidemiological Virology, Department of Microbiology and Immunology, Rega Institute for Medical Research, University of Leuven, Minderbroedersstraat 10, Leuven BB-3009, Bolgium
Location/Qualifiers
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Thoelen, I., Lemey, P., van der Donck, I., Beuselinck, K.,
Lindberg, M.A. and Van Ranst, M.
Direct Submission
Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological
Virology, Department of Microbiology and Immunology, Rega Institute
for Medical Research, University of Leuven, Minderbroedersstraat
10, Leuven BE-3000, Belgium
Location/Qualifiers
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Thoelen, I., Lemey, P., Van Der Donck, I., Beuselinck, K.,
Lindberg, A.M. and Van Ranst, M.
Molecular typing and epidemiology of enteroviruses identified from
an outbreak of aseptic meningitis in Belgium during the summer of
2000
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                                                                                                                                                                                                                                                                                                                             /isolation_source="patient 74 - zipcode Belgium 8930"
/db_xref="taxon:41846"
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    zipcode Belgium 7700"

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Human echovirus 16 isolate BE00-75 5' UTR, partial sequence
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Human echovirus 16
Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
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/virion
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/db_xref="taxon:47504"
<1...>185
                                                                                     J. Med. Virol. 70 (3), 420-429 (2003)
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                                                                                                                                                                                                                                                                                                                            'mol type="genomic RNA"
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/isolate="BE00-75"
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AF521484
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SOURCE
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The last i. Lemey. P., van der Donck, I., Beuselinck, K., Lindberg, M.A. and Van Ranst, M. Dindberg, M.A. and Van Ranst, M. Direct Submission

Direct Submitsed (12-70N-2002) Laboratory of Clinical & Epidemiological Submitted (12-70N-2004) Laboratory of Clinical & Epidemiological Virology, Department of Microbiology and Immunology, Rega Institute for Medical Research, University of Leuven, Minderbroedersstraat 10, Leuven BE-3000, Belgium

Location/Qualifiers
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Picornaviridae; Enterovirus.
1 (Dases I to 185)
Thoelen, I., Lemey, P., Van Der Donck, I., Beuselinck, K.,
Lindberg, A.M. and Van Ranst, M.
Molecular typing and epidemiology of enteroviruses identified from
an outbreak of aseptic meningitis in Belgium during the summer of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Viruses; SBRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
I (bases 1 to 185)
Thoelen, I. Lemey, P., Van Der Donck, I., Beuselinck, K.,
Lindberg, A.M. and Van Ranst, M.
Molecular typing and epidemiology of enteroviruses identified from an outbreak of aseptic meningitis in Belgium during the summer of
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/db.xref="taxon:41846"
<1. .>185
                                                        Gaps
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Human echovirus 30 isolate BE00-76 5' UTR, partial sequence.
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partial sequence.
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100.0%; Score 19; DB 13; Length 185; 100.0%; Pred. No. 9.5;
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5' UTR,
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100.0%; Pred. No. 9.5;
Live 0; Mismatches 0;
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/organism="Human echovirus 30"
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                                                     Mismatches
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Human echovirus 30 isolate BE00-77
AF521486
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Thoelen, I., Lemey, P., van der Donck, I., Beuselinck, K., Lindberg, M.A. and Van Ranst, M. Dindberg, M.A. and Van Ranst, M. Direct Submission of University of Clinical & Epidemiological Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological Virology, Department of Microbiology and Immunology, Rega Institute for Medical Research, University of Leuven, Minderbroedersstraat 10, Leuven BB-3000, Belgium
                                                                                                                          AF521488 18-JUN-2003 185 bp RNA linear VRL 17-JUN-2003 Human echovirus 16 isolate BE00-79 5' UTR, partial sequence. AF521488
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l (Dases 1 to 185)
Thoelen,I., Lemey,P., Van Der Donck,I., Beuselinck,K.,
Indberg,A.M. and Van Ranst,M.
Molecular typing and epidemiology of enteroviruses identified from an outbreak of aseptic meningitis in Belgium during the summer of
                                                                                                                                                                                                                                                                          Viruses; ssRNA positive-strand viruses, no DNA stage; picornavitade; Enterovirus.

1 (Dases 1 to 185)
Thoelen,I., Lemey,P., Van Der Donck,I., Beuselinck,K.,
Indoberg,A.M. and Van Ranst,M.
Molecular typing and epidemiology of enteroviruses identified from an outbreak of aseptic meningitis in Belgium during the summer of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /isolation_source="patient 79 - zipcode Belgium 3012"
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<1._.>185
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Human echovirus 6 isolate BE00-81 5' UTR, partial sequence.
AF521490
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Thoelen, I., Lemey, P., van der Donck, I., Beuselinck, K.,
Lindberg, M.A. and Van Ranst, M.
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/organism="Human echovirus 16"
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/isolate="BE00-79"
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CCCCTGAATGCGGCTAATC 32
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Best Local Similarity 100.
Matches 19; Conservative
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JOURNAL
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SOURCE
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                                                           Thoelen, I., Lemey, P., van der Donck, I., Beuselinck, K., Lindberg, M.A. and van Ranst, M. Direct Submission Submission Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological Virology, Department of Microbiology and Immunology, Rega Institute for Medical Research, University of Leuven, Minderbroedersstraat 10, Leuven BE-3000, Belgium
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Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological
Virology, Department of Microbiology and Immunology, Rega Institute
for Medical Research, University of Leuven, Minderbroedersstraat
10, Leuven BE-3000, Belgium
Location/Qualifiers
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Lindberg, A.M. and Van Ranst, M.
Molecular typing and epidemiology of enteroviruses identified from
an outbreak of aseptic meningitis in Belgium during the summer of
                                                                                                                                                                                                                                                                                                                                     /isolation_source="patient 77 - zipcode Belgium 8560"
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<1. .>185
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/db_xref="taxon:47501"
<1. _.>185
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Human echovirus 13 isolate BE00-78 5' UTR, partial sequence
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Thoelen, I., Lemey, P., van der Donck, I., Beuselinck, K.,
Lindberg, M.A. and Van Ranst, M.
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Human echovirus 13
Viruses, seRNA positive-strand viruses, no DNA stage,
Picornaviridae, Enterovirus.
1 (bases 1 to 185)
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    1. .185
    /organism="Human echovirus 30"

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    Med. Virol. 70 (3), 420-429 (2003)
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100.0%; Pred. No. 9.5
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/isolate="BE00-77"
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/isolate="BE00-78"
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Direct Submission
Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological
Virology, Department of Microbiology and Immunology, Rega Institute
for Medical Research, University of Leuven, Minderbroedersstraat
10, Leuven BE-3000, Belgium
Location/Qualifiers
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Direct Submission

Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological Virology, Department of Microbiology and Immunology, Rega Institute for Medical Research, University of Leuven, Minderbroedersstraat 10, Leuven BB-3009, Belgium

Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.

1 (bases 1 to 185)
Thoelen; I., Lemey, P., Van Der Donck, I., Beuselinck, K.,
Lindberg, A.M. and Van Ranst, M.
Molecular typing and epidemiology of enteroviruses identified from an outbreak of aseptic meningitis in Belgium during the summer of
                                                                                                                                                                 /isolation_source="patient 81 - zipcode Belgium 3010"
/db_xref="taxon:12062"
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/db_xref="taxon:41846"
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Human echovirus 30 isolate BE00-83 5' UTR, partial sequence.
AF521492
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100.0%; Score 19; DB 13;
Best Local Similarity 100.0%; Pred. No. 9.5;
Matches 19; Conservative 0; Mismatches 0;
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/isolate="BE00-81"
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/isolate="BE00-83"
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Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological Virology, Department of Microbiology and Immunology, Rega Institute for Medical Research, University of Leuven, Minderbroedersstraat 10, Leuven BR-3000, Belgium
AF521493 185 bp RNA linear VRL 17-JUN-2003
Human coxeackievirus B5 isolate BE00-56 5' UTR, partial sequence.
AF521493
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Human coxsackievirus B5 isolate BE00-57 5' UTR, partial sequence.
AF521494
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Lindberg, M.A. and Van Ranst, M.
Direct Submission
Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological
Virology, Department of Microbiology and Immunology, Rega Institute
for Medical Research, University of Leuven, Minderbroedersstraat
10, Leuven BB-3000, Belgium
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Human coxsackievirus B5
Viruses; saRNA postiive-strand viruses, no DNA stage;
Viruses; saRNA postiive-strand viruses, no DNA stage;
Licornaviridae; Enterovirus.

1 (bases 1 to 185)
Thoselen, I., Lemey, P., Van Der Donck, I., Beuselinck, K.,
Thoselen, I., Lemey Van Der Donck, I., Beuselinck, K.,
Molecular typing and epidemiology of enteroviruses identified from an outbreak of aseptic meningitis in Belgium during the summer of
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Lindberg, A.M. and Van Ranst, M.
Molecular typing and epidemiology of enteroviruses identified from
an outbreak of aseptic meningitis in Belgium during the summer of
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|db_xref="taxon:12074"
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Thochen, I., Lemey, P., van der Donck, I., Beuselinck, K.,
Lindberg, M.A. and Van Ranst, M.
Direct Submission
                                                                                                                                                           Human coxeackievirus B5
Human coxeackievirus B5
Viruses; seRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
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/virion
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Best Local Similarity 100.0%; Pred. No. 9.5;
Matches 19; Conservative 0; Mismatches 0;
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/isolate="BE00-56"
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FEATURES

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Thoelen,I., Lemey,P., van der Donck,I., Beuselinck,K.,
Lindberg,M.A. and Van Ranst.M.
Direct Submission

Direct Submission

Submitted (12-70N-2002) Laboratory of Clinical & Epidemiological

Virology, Department of Microbiology and Immunology, Rega Institute
for Medical Research, University of Leuven, Minderbroedersstraat

10, Leuven BE-3000, Belgium

Location/Qualifiers
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Submitted (12-UTN-2002) Laboratory of Clinical & Epidemiological
Virology, Department of Microbiology and Immunology, Rega Institute
for Medical Research, University of Leuven, Minderbroedersstraat
10, Leuven BE-3000, Belgium
                                                         Viruses, ssRNA positive-strand viruses, no DNA stage, Picornaviridae, Enterovirus.

1 (bases 1 to 185)
Thoelen,I., Lemey,P., Van Der Donck,I., Beuselinck,K.,
Lindberg,A.M. and Van Ranst,M.
Molecular typing and epidemiology of enteroviruses identified from an outbreak of aseptic meningitis in Belgium during the summer of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Viruses; ssRNA positive-strand viruses, no DNA stage;
locomaviridae; Enterovirus.
l (bases 1 to 185)
Thoelen,I., Lemey,P., Van Der Donck,I., Beuselinck,K.,
LidbergyA.M. and Van Ranst,M.
Molecular typing and epidemiology of enteroviruses identified from an outbreak of aseptic meningitis in Belgium during the summer of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /isolation_source="patient 59 - zipcode_Belgium 2300"
/db_xref="taxon:41846"
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Human echovirus 18 isolate BE00-60 5' UTR, partial sequence.
AFS21497
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Thoelen, I., Lemey, P., van der Donck, I., Beuselinck, K.,
Lindberg, M.A. and Van Ranst, M.
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/isolate="BE00-59"
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Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological
Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological
Virology, Department of Microbiology and Immunology, Rega Institute
for Medical Research, University of Leuven, Minderbroedersstraat
10, Leuven BE-300/0, Belgium
Location/Qualifiers
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Picornaviridae; Enterovirus.
I (bases 1 to 185)
Thoelen, I., Lemey, P., Van Der Donck, I., Beuselinck, K.,
Lindberg, A.M. and Van Ranst, M.
Molecular typing and epidemiology of enteroviruses identified from an outbreak of aseptic meningitis in Belgium during the summer of
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/db_xref="taxon:41846"
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Human echovirus 30 isolate BE00-58 5′ UTR, partial sequence.
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                                      organism="Human coxsackievirus B5"
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Direct Submission

Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological Virology, Department of Microbiology and Immunology, Rega Institute for Medical Research, University of Leuven, Minderbroedersstraat 10, Leuven BE-3000, Belgium

Location/Qualifiers
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Human coxsackievirus B5 isolate BE00-62 5' UTR, partial sequence.
AF521499
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/db_xref="Taxon:47506"
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Human echovirus 6 isolate BE00-61 5' UTR, partial sequence.
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Human echovirus 6
Viruses; ssRMA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
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Best Local Similarity 100.0%; Pred. No. 9.5;
Matches 19; Conservative 0; Mismatches 0; Indels
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Human coxsackievirus B5
Viruses; seRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
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Thoelen, I., Lemey, P., van der Donck, I., Beuselinck, K.,
Lindberg, M.A. and Van Ranst, M.
Lindberg, M.A. and Van Ranst, M.
Direct Submission
Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological
Virology, Department of Microbiology and Immunology, Rega Institute
for Medical Research, University of Leuven, Minderbroedersstraat
10, Leuven BB-3000, Balgium
Location/Qualifiers
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                       Thoelen, I., Lemey, P., Van Der Donck, I., Beuselinck, K., inthoberg, A.M. and Van Ranst, M. Molecular typing and epidemiology of enteroviruses identified from an outbreak of aseptic meningitis in Belgium during the summer of
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Sequence 374022, Sequence 1875, Ap Sequence 166, App Sequence 142053, Sequence 142053, Sequence 147022, Sequence 434002, Sequence 274574, Sequence 274574, Sequence 440003,	Sequence 440005, Sequence 3103, App Sequence 3103, App Sequence 3104, App Sequence 34027, A Sequence 34027, A Sequence 34027, A Sequence 49133, A Sequence 295301, Sequence 2172, App Sequence 216541, Sequence 20545, Sequence 20545, Sequence 20545, Sequence 21398, A Sequence 2261, App Sequence 2261, App Sequence 242742, Sequence 242742, Sequence 242742, Sequence 242742, Sequence 242743, Sequence 242743, Sequence 242743, Sequence 242743, Sequence 242743, Sequence 242743, Sequence 242743,	Sequence 257853, Sequence 230356, Sequence 230356, Sequence 719915, Sequence 719915, Sequence 922842, Sequence 927842, Sequence 1670, Ap. Sequence 1670, Ap. Sequence 13777, Ap. Sequence 13777, Ap. Sequence 13318, Sequence 123918, Sequence 123918, Sequence 19151, Ap. Sequence 6222, Ap. Sequence 8622, Ap. Sequence 8624, Ap. Sequence 8624, Ap. Sequence 8624, Ap. Sequence 8160, Ap. Sequence 8161, Ap. Sequence 8161, Ap. Sequence 8162, Ap. Sequence 8162, Ap. Sequence 8162, Ap. Sequence 8161, Ap. Sequence 8161, Ap. Sequence 8161, Ap. Sequence 8161, Ap. Sequence 19151, Ap. Sequence 8161, Ap. Sequence 19151, Ap. Sequence 19151, Ap. Sequence 8161, Ap. Sequence 19151, Ap.	ednence ednence ednence ednence ednence ednence ednence
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; OTHER INFORMATION: Chemically synthesized forward primer for amplifying enteroviral CTHER INFORMATION: RNA
US-10-829-474-16
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APPLICANT: ARMAND, Philippe
APPLICANT: LEFAIRE, Philippe
TITLE OF INVENTION: METHOD FOR CONTROLLING THE MICROBIOLOGICAL QUALITY OF AN AQUEOUS
TITLE OF INVENTION: MEDIUM AND KIT THEREFOR
FILE REFERENCE: 114502
CURRENT APPLICATION WHOBER: US/10/332,123
CURRENT FILING DATE: 2003-09-24
                                                                                                                                                                                                                                  FEATURE:
OTHER INFORMATION: Chemically synthesized forward primer for amplifying enteroviral
OTHER INFORMATION: RNA
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Pred. No. 2.4;
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    TITLE OF INVENTION: ENTEROVIRUS PRIMERS AND PROBES FILE REFERENCE: 043956-0121
CURRENT APPLICATION NUMBER: US/10/829,474
CURRENT FILING DATE: 2004-04-22
NUMBER OF SEQ ID NOS: 57
SOFTWARE: Patentin version 3.2
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APPLICANT: MARLANI, BILLAND.
TITLE OF INVENTION: ENTEROVIRUS PRIMERS AND PROBES
FILE REFERENCE: 043956-0121
CURRENT APPLICATION NUMBER: US/10/829,474
CURRENT FILLING DATE: 2004-04-22
NUMBER OF SEQ ID NOS: 57
SEQ ID NOS: 57
SEQ ID NO 16
LENGTH: 25
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MABILAT, Claude
VACHON, Carrole
LACROIX, Bruno
VERNET, GUY
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Best Local Similarity 100.0%;

Matches 19; Conservative 0
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Best Local Similarity 100.0%;
Matches 19; Conservative (
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                                                                                                                                         SEQ ID NO 15
LENGTH: 20
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APPLICANT:
APPLICANT:
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2.4;
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                                                                                                                                Sequence 1, Application US/10829474
Publication No. US20050239055A1
GENERAL INFORMATION:
APPLICANT: Genetics & IVF
TITLE OF INVENTION: ENTEROVINUS PRIMERS AND PROBES
FILE REFERENCE: 043956-0121
CURRENT APPLICATION NUMBER: US/10/829,474
CURRENT FILING DATE: 2004-04-22
NUMBER OF SEQ ID NOS: 57
SOFTWARE: Patentin version 3.2
SEQ ID NO 1.
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TITLE OF INVENTION: ENTEROVIRUS PRIMERS AND PROBES FILE REPERENCE: 043956-0121
CURRENT APPLICATION NUMBER: US/10/829,474
CURRENT FILING DATE: 2004-04-22
NUMBER OF SEQ ID NOS: 57
SOFTWARE: Patentin version 3.2
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100.0%; Pred. No.
tive 0; Mismatch
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Publication No. US20050239055A1
GENERAL INFORMATION:
APPLICANT: Genetics & IVF
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; Publication No. US20050239055A1
1 CCCTGAATGCGGCTAATC 19
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APPLICANT: MARIANI, Brian D.
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Matches 19; Conservative
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nes 19; Conserva
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Best Local S:
Matches 19
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TITLE OF INVENTION: METHOD FOR CONTROLLING THE MICROBIOLOGICAL QUALITY OF AN AQUEOUS TITLE OF INVENTION: MEDIUM AND KIT THEREFOR FILE REFERENCE: 114502

CURRENT PPLICATION NUMBER: US/10/332,123

CURRENT FILING DATE: 2003-09-24

PRIOR APPLICATION NUMBER: PCT/FR01/02191

PRIOR APPLICATION NUMBER: FR00-08839

PRIOR FILING DATE: 2000-07-06

NUMBER OF SEQ ID NOS: 108

SOFTWARE: PAGENTIN VERSION 3.2

SOFTWARE: PAGENTIN VERSION 3.2

SEQ ID NO 74

LENGTH: 30
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Pred. No. 2.4;
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APPLICANT: Shih, Yu-Hau
APPLICANT: Taai, Chuan-Mei
APPLICANT: Haia, Yih-Weng
APPLICANT: Haiao, Haiung
APPLICANT: Haiao, Haiung
APPLICANT: Haiao, Haiung
APPLICANT: Haiao, Haing
APPLICANT: Wang, Shin-Hwan
TITLE OF INVENTION: BLOWDLECULE-BOUND SUBSTRATES
FILE REFERENCE: 12674-002002
CURRENT FILING DATE: 2003-04-07
PRIOR FILING DATE: 2000-03-09
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO.
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100.0%; Score 19; DB 6;
Best Local Similarity 100.0%; Pred. No. 2.5;
Matches 19; Conservative 0; Mismatches 0
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Publication No. US20040072239A1
GENERAL INFORMATION:
APPLICANT: REMAND. Patricia
APPLICANT: GUILLOT, Emmanuelle
APPLICANT: WABILAT. Claude
APPLICANT: WACHON, Carole
APPLICANT: LACROIX, Bruno
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Publication No. US20030228683A1
GENERAL INFORMATION:
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Best Local Similarity 100.0%;
Matches 19; Conservative 0
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ORGANISM: Echovirus 12
US-10-332-123-74
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APPLICANT: MABILAT, Claude
APPLICANT: MACHON, Carole
APPLICANT: LACROIX, Brunc
APPLICANT: VERNET, Guy
APPLICANT: VERNET, Guy
APPLICANT: LAFRAND, MATLE-ABITIG
APPLICANT: LAFFAIRE, Philippe
TITLE OF INVENTION: MEDIUM AND KIT THEREFOR
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CURRENT APPLICATION NUMBER: US/10/332,123
CURRENT FILING DATE: 2003-09-24
FRIOR APPLICATION NUMBER: PCT/FR01/02191
PRIOR FILING DATE: 2001-07-06
PRIOR FILING DATE: 2000-07-06
NUMBER OF SEQ ID NOS: 108
SOFTWARE: Patentin version 3.2
LENGTH: 30
         PRIOR APPLICATION NUMBER: PCT/FR01/02191
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Publication No. US20040072239A1
GENERAL INFORMATION:
APPLICANT: RENAUD, Patricia
APPLICANT: GULLLOT, Emmanuelle
APPLICANT: MABILAT, Claude
APPLICANT: VACHON, Carole
APPLICANT: VACHON, Carole
APPLICANT: VERNET, GUY
APPLICANT: VERNET, GUY
APPLICANT: ARMAND, Marie-Astrid
                             PRIOR FILING DATE: 2001-07-06
PRIOR APPLICATION WUNDER: FR00-08839
PRIOR FILING DATE: 2000-07-06
NUMBER OF SEQ ID NOS: 108
SOFTWARE: Patentin version 3.2
SEQ ID NO 70
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CRGANISM: Poliovirus type 2
US-10-332-123-70
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ORGANISM: Coxsackievirus A21
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Matches 19; Conservative
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US-10-332-123-74
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APPLICANT: ARMAND, Marie-Astrid
APPLICANT: LAFFAIRE, PHILIPPE
TITLE OF INVENTION: METHOD FOR CONTROLLING THE MICROBIOLOGICAL QUALITY OF AN AQUEOUS
TITLE OF INVENTION: MEDIUM AND KIT THEREFOR
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APPLICANT: WU, TZONG-YUAN
APPLICANT: LE, JIN-CHING
TITLE OF INVENTION: INTERNAL RIBOSOME ENTRY SITES FOR RECOMBINANT PROTEIN
TITLE OF INVENTION: EXPRESSION
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APPLICANT: PRICE, JAMES A.
APPLICANT: HELLYER, TOBIN J.
TITLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID
FILE REFERENCE: 020187.0187PTUS
CURRENT APPLICATION NUMBER: US/10/760,048
CURRENT APPLICATION NUMBER: US/10/760,048
SURPRANS OF SEQ ID NOS: 67
SOFTWARE: PATCHIN VOR: 67
SOFTWARE: PATCHIN VOR: 3.2
SEQ ID NO 67
                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: PCT/FRO1/02191
PRIOR APPLICATION NUMBER: PCT/FR01/02191
PRIOR PILING DATE: 2001-07-06
PRIOR PILING DATE: 2000-07-06
NUMBER OF SEQ ID NOS: 108
SQFTWARE: Patentin version 3.2
SEQ ID NO 55
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CURRENT APPLICATION NUMBER: US/10/332,123
CURRENT FILING DATE: 2003-09-24
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Publication No. US20050112095A1
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Best Local Similarity 100.0%;
Matches 19; Conservative 0
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Best Local Similarity 100.0%;
Matches 19; Conservative 0
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; ORGANISM: Echovirus (X77708)
US-10-332-123-55
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COSBACKievirus B3
US-10-760-048-67
                                                                                                                LACROIX, Bruno
VERNET, Guy
                                                                                        Carole
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APPLICANT:
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                              APPLICANT: ARMAND, MARIE-ABILIDA
APPLICANT: LAFFAIRE, Philippe
TITLE OF INVENTION: METHOD FOR CONTROLLING THE MICROBIOLOGICAL QUALITY OF AN AQUEOUS
TITLE OF INVENTION: METHOD FOR CONTROLLING THE MICROBIOLOGICAL QUALITY OF AN AQUEOUS
TITLE OF INVENTION: MEDICALION NUMBER: US/10/332,123
CURRENT APPLICATION NUMBER: US/10/332,123
CURRENT PILING DATE: 2003-09-24
PRIOR PILING DATE: 2003-09-24
PRIOR FILING DATE: 2000-07-06
NUMBER OF SEQ ID NOS: 108
SOFTWARE: Patentin version 3.2
SEQ ID NO 54
LENGTH: 520
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APPLICANT: VENERT, GLY
APPLICANT: ARMAND, Marie-Astrid
APPLICANT: LAFFALER, FILIAPE
TITLE OF INVENTION: METHOD FOR CONTROLLING THE MICROBIOLOGICAL QUALITY OF AN AQUEOUS
TITLE OF INVENTION: MEDIUM AND KIT THEREFOR
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CURRENT APPLICATION NUMBER: US/10/332,123
CURRENT FILING DATE: 2003-09-24
PRIOR APPLICATION NUMBER: PCT/FR01/02191
PRIOR PELING DATE: 2001-07-06
PRIOR PELING DATE: 2000-07-06
PRIOR PELING DATE: 2000-07-06
NUMBER OF SEQ ID NOS: 108
SOFTWARE: Patentin version 3.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 19; 100.0%; Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 53, Application US/10332123
Publication No. US20040072239A1
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                                                                                                                                                                                                                                                                                                                                                                                    ; TYPE: DNA
; ORGANISM: CoxBackievirus (D00538)
US-10-332-123-54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                386 ccccrcaarccccraarc 404
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VERNET, Guy
THAND, Marie-Astrid
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LACROIX, Bruno
VERNET, Guy
ARMAND, Marie-Astrid
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MABILAT, Claude
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TYPE: DNA
; ORGANISM: Poliovirus (X00595)
US-10-332-123-53
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nes 19; Conservative
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Best Local S
Matches 19
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Sequence 7, Application US/10136819

Subjication No. US20030166593A1

GENERAL INFORMATION:
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TITLE OF INVESTION:
FILE REFERENCE: 6627-PA1198
CURRENT APPLICATION NUMBER: US/10/136,819
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: 60/287,423
PRIOR APPLICATION NUMBER: 60/287,423
PRIOR FILING DATE: 2001-04-30
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin version 3.1
SEQ ID NO 7
LIENGTH: 7399
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Publication No. US20030046716A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Meade, Harry M.
APPLICANT: Blomerneyer, Klaus
TITLE OF INVENTION: GROWTH FACTOR
FILE REFERENCE: 10275-120001
CURRENT FILING DATE: 2001-06-19
FRIOR APPLICATION NUMBER: 60/212,406
PRIOR APPLICATION NUMBER: 60/212,406
PRIOR FILING DATE: 2000-06-19
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 3
LENGTH: 2076
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                                                                                                                                                   Query Match 100.0%; Score 19; DB 8; Length 745; Best Local Similarity 100.0%; Pred. No. 3; Matches 19; Conservative 0; Mismatches 0; Indels
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US-09-884-586A-3
    SEQ ID NO 10
LENGTH: 745
TYPE: DNA
ORGANISM: Poliovirus
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Best Local Similarity
Matches 19; Conserv
                                                                                                      US-10-489-136-10
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US-10-136-819-7
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APPLICANT: Skulachov, Maxim
APPLICANT: Skulachov, Maxim
APPLICANT: Skulachov, Maxim
APPLICANT: Skulachov, Maxim
APPLICANT: Ivanov, Peter
APPLICANT: Ivanov, Peter
APPLICANT: Ivanov, Peter
APPLICANT: Gleba, Yuri
TITLE OF INVENTION: IDENTIFICATION OF EUKARYOTIC INTERNAL RIBOSOME ENTRY SITE (IRES)
FILE REFERENCE: 9286.30
CURRENT APPLICATION NUMBER: US/10/489,136
CURRENT APPLICATION NUMBER: PCT/EPD2/09844
PRIOR APPLICATION NUMBER: DE 101 43 238.0
PRIOR FILING DATE: 2002-09-03
PRIOR FILING DATE: 2001-09-04
NUMBER OF SEQ ID NOS: 41
SOFTWARE: Patentin version 3.2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT JOHN HEACLG
TITLE OF INVENTION: SARS-CORONAVIRUS VIRUS-LIKE PARTICLES
TITLE OF INVENTION: AND METHODS OF USE
FILE REPERENCE: BIOGRAM. 013A
CURRENT APPLICATION NUMBER: US/10/839,729
CURRENT FILING DATE: 2004-05-04
PRIOR APPLICATION NUMBER: 60/468703
PRIOR APPLICATION NUMBER: 60/468703
NUMBER OF SEQ ID NOS: 49
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 21
LENGTH: 743
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; FILE REFERENCE: 08842.0002-00000
; CURRENT APPLICATION NUMBER: US/10/614,283
; CURRENT FILING DATE: 2003-07-08
; PRIOR APPLICATION NUMBER: 60/394,269
; NUMBER OF SEC ID NOS: 1
; SOFTWARE: PatentIn Ver. 3.2
; SOFTWARE: PatentIn Ver. 3.2
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; ORGANISM: Mahoney Strain Poliovirus Type I
US-10-839-729-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 21, Application US/10839729
; Publication No. US20050002953A1
; GENERAL INFORMATION:
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Publication No. US20050014150A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                420 CCCCTGAATGCGGCTAATC 438
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Best Local Similarity 100.
Matches 19; Conservative
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                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Enterovirus 71
US-10-614-283-1
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OTHER INFORMATION: Description of Artificial Sequence: Synthetic US-10-873-573-7
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                                                  APPLICANT: KINGSMAN, et al., Alan John
TITLE OF INVENTION: Vector System
FILE REFERENCE: 674523-2016
CURRENT APPLICATION NUMBER: US/10/408,456
CURRENT FILING DATE: 2003-04-08
PRIOR APPLICATION NUMBER: CGT(GB01/04433
PRIOR FILING DATE: 2001-10-15
PRIOR FILING DATE: 2001-10-15
PRIOR FILING DATE: 2000-10-06
NUMBER OF SEQ ID NOS: 34
SEQ ID NO 34
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APPLICANT: MITRAPHANOUS, KYRI
APPLICANT: MOHLL, JONATHAN
APPLICANT: MISKIN, JAMES
TITLE OF INVENTION: VECTOR SYSTEM
TITLE REFERENCE: 674523-2016.1
CURRENT FILING DATE: 2004-06-21
PRIOR PELICATION NUMBER: 10/408,456
PRIOR PELICATION NUMBER: 10/408,456
PRIOR PELICATION NUMBER: 10/408,456
PRIOR PELICATION NUMBER: 10/408,456
PRIOR PELING DATE: 2001-10-05
PRIOR PILING DATE: 2001-10-05
PRIOR PILING DATE: 2000-10-06
NUMBER OF SEQ ID NOS: 11
SEQ ID NO 7
SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                               ; TYPE: DNA
; ORGANISM: Equine Infectious Anemia Virus
US-10-408-456-34
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; Sequence 10, Application US/10829474
; Publication No. US20050239055A1
; GENERAL INFORMATION:
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Publication No. US20050002907A1
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Best Local Similarity
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                                                                                                                                                                   GENERAL INCOMPATION

GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Oxford Biomedica (UK) Limited

TITLE OF INVENTION: Vector System

TITLE REFERENCE: 674523-2016

CURRENT FILLING DATE: 2003-04-08

PRIOR APPLICATION NUMBER: PCT/GB01/04433

PRIOR PILLING DATE: 2001-10-15

PRIOR PILLING DATE: 2001-10-15

PRIOR PILLING DATE: 2001-10-15

NUMBER OF SEQ ID NOS: 34

SOFTWARE: PatentIn version 3.0
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| Publication No. US20040013648A1
| GENERAL INFORMATION:
| APPLICANT: Oxford Biomedica (UK) Limited
| APPLICANT: Oxford Biomedica (UK) Limited
| TITLE OF INVENTION: Vector System
| TITLE REPERBNCE: 674523-2016
| CURRENT FILING DATE: 2003-04-08
| PRIOR APPLICATION NUMBER: PCT/GB01/04433
| PRIOR PILING DATE: 2001-10-15
| PRIOR PILING DATE: 2001-10-15
| PRIOR PILING DATE: 2001-10-15
| PRIOR PILING DATE: 2001-10-06
| NUMBER OF SEQ ID NOS: 34
| SOFTWARE: PatentIn version 3.0
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; ORGANISM: Equine Infectious Anemia Virus
US-10-408-456-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TYPE: DNA; Guine Infectious Anemia Virus US-10-408-456-5
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                             454 CCCCTGAATGCGGCTAATC 472
1 CCCTGAATGCGGCTAATC 19
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LENGTH: 10448
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LENGTH: 11058
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APPLICANT: Genetics & IVF

; Sequence 34, Application US/10408456; Publication No. US20040013648A1

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                                                 - 3.5 inch, 1.44 Mb storage
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Publication No. US20020160976A1
GENERAL INFORMATION:
APPLICANT: Miles, Vincent J.
Mathews, Michael B.
Katze, Michael G.
Witherell, Gary
Watson, Julia C.
TITLE OF INVENTION: METHOD FOR SELECTIVE INACTIVATION
OP VIRAL REPLICATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
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8.7;
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ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
                                                                                                      SOFTWARE: Word Perfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/802,1108
FILING DATE: 07-Mar-2001
PLING APPLICATION CURKNOWN>
PRIOR APPLICATION NUMBER: CURKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
RPPLICATION NUMBER: US/10/104,611
PLING DATE: 22-Mar-2002
CLASSIFICATION: «UNKNOWI»
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FRAGMENT TYPE: internal
SEQUENCE DESCRIPTION: SEQ ID NO: 105:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      94.7%; Score 18; 100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 10036/2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
                                                                                                                                                                                                                                              ATTORNEY FAGENT INFORMATION:
NAME: Larson, Marina T. REGISTRATION NUMBER: 32,038
REGISTRATION NUMBER: 32,038
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
HYPOTHETICAL: no
                                         MEDIUM TYPE: Diskette - COMPUTER: IBM compatible OPERATING SYSTEM: MS DOS
                                                                                                                                                                                                                                                                                                                                                                                        (970) 468-0104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .
                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 105: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: double
        ZIP: 80435
COMPUTER READABLE FORM:
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Best Local Similarity 100.(
Matches 18; ConBervative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ANTI-SENSE: yes
                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX:
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                                                                                                                                                                                                                           OTHER INFORMATION: Chemically synthesized forward primer for amplifying enteroviral OTHER INFORMATION: RNA
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                                                                                                                                                                                                                                                                                                          94.7%; Score 18; DB 9; Length 18; 100.0%; Pred. No. 8.5;
                                                                                                                                                                                                                                                                                                                                                   0; Indels
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TITLE OF INVENTION: ENTEROVING PRIMERS AND PROBES FILE REFERENCE: 043956-0121
CURRENT APPLICATION NUMBER: US/10/829,474
CURRENT FILING DATE: 2004-04-22
NUMBER OF SEQ ID NOS: 57
SOFTWARE: Patentin version 3.2
SEQ ID NO 10
LENGTH: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: MARIANI, Brian D.
TITLE OF INVENTION: ENTEROVIRUS PRIMERS AND PROBES FILE REFERENCE: 042956-0121
CURRENT APPLICATION NUMBER: US/10/829,474
CURRENT FILING DATE: 2004-04-22
NUMBER OF SEQ ID NOS: 57
SOFTWARE: Patentin version 3.2
SEQ ID NO 11
LENGTH: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 9;
8.5;
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Oppedahl & Larson LLP
STREET: PO Box 5068
CITY: Dillon
STATE: CO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 18;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 105, Application US/09802110B
Publication No. US20030082535A1
GENERAL INFORMATION:
APPLICANT: Leushner, James
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LaCroix, Jean-Michel TITLE OF INVENTION: METHOD, COM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 11, Application US/10829474
Publication No. US20050239055A1
GENERAL INFORMATION:
APPLICANT: Genetics & IVF
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100.0%; Pre
0;
                                                                                                                                                                                                                                                                                                            94.,
100.0%; Pr.
0;
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Dunn, James M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                    TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 100.
Matches 18; Conservative
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Matches 18; Conserva
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US-10-829-474-11
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US-10-829-474-11
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                                                                                                                                       DB 5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FBALSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/112,241
FILING DATE: 28 -Mar-2002
CLASSIFICATION: OF CURROWN>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Watson, Julia C.
TITLE OF INVENTION: METHOD FOR SELECTIVE
OF VIRAL REPLICATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/221,816B
FILING DATE: 01-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: COTUZZI, LAUKA A
REGISTRATION NUMBER: 30,742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 17.4; DE Pred. No. 23; 3; Mismatches
                                                                                                                                     Score 17.4; DI
Pred. No. 23;
3; Mismatches
                     TOPOLOGY: linear

MOLECULE TYPE: RNA
SEQUENCE DESCRIPTION: SEQ ID NO: 31:
US-10-112-547-31
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SEQUENCE DESCRIPTION: SEQ ID NO: 31:
                                                                                                                                                                                                                                                                                                                RESULT 12-241-31

// Sequence 31, Application US/10112241

// Publication No. US20020165194A1

// GENERAL INFORMATION:

// APPLICANT: Miles, Vincent J.

// Mathews, Michael B.

// Katze, Michael G.

// Witherell, Gary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (212) 790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                      457 ccccugaaugcgccuaacc 475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (212) 869-8864
                                                                                                                                                                                                                 1 CCCCTGAATGCGGCTAATC 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 627 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: USA
ZIP: 10036/2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
                                                                                                                                       91.68;
78.98;
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78.9%;
       nucleic acid
                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SECUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: New York
                                                                                                                   Query Match
Best Local Similarity '
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 15; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                            Length 627;
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APPLICANT: Miles, Vincent J.

Mathews, Michael B.

Katze, Michael G.

Witherell, Gary

Watson, Julia C.

TITLE OF INVENTION: METHOD FOR SELECTIVE INACTIVATION

OF VIRAL REPLICATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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                                                                                                                                                                                                                                                                                                                                                                                            91.6%; Scc... 78.9%; Pred. No. 2c., 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
                   APPLICATION NUMBER: US/08/221,816B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/221,816B
                                 FILING DATE: 01-AFR-1994
ATTORNEY/AGENT INFORMATION:
NAME: COUTZ1, Laura A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7960-030
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: COTUZZI, Laura A
REGISTRATION NUMBER: 30,742
REPRERICE/DOCKET NUMBER: 7960-030
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/10/112,547
PILING DATE: 28 Mar-2002
CLASSIFICATION: «UNKNOWN»
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: RNA
SEQUENCE DESCRIPTION: SEQ ID NO: 31:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM Compatible OPERATING SYSTEM: DOS SOFTWARE: Fast SEQ USESION 2.0 CURRENT APPLICATION DATA:
                                                                                                                                                     (212) 790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (212) 790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 31, Application US/10112547
Publication No. US20020160977A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 01-APR-1994
                                                                                                                                                                     TELEFAX: (212) 869-8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         457 CCCCUGAAUGCGGCUAACC 475
                                                                                                                                                                                                                                              LENGTH: 627 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 627 base pairs
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEX: 66141 PENNIE INFORMATION FOR SEQ ID NO: 31: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 33
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: New York
STATE: New York
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                                                                                                                                                       TELEPHONE:
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Best Local Similarity
Matches 15; Conserva
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OTHER INFORMATION: Chemically synthesized forward primer for amplifying enteroviral OTHER INFORMATION: RNA
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; Publication No. US20050239055A1
; GENERAL INFORMATION:
APPLICANT: Genetics & IVF
; APPLICANT: Genetics & IVF
; TITLE OF INVENTION: ENTEROVIRUS PRIMERS AND PROBES
; FILE REPERSINCE: 043956-0121
; CURRENT APPLICATION NUMBER: US/10/829,474
; CURRENT FILING DATE: 2004-04-22
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: Patentin version 3.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 8;
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                                                                                                                                                                                                                      CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/867,798
FILING DATE: 14-Jun-2004
CLASSIFICATION - UNANOWN-
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/10/109,368
FILING DATE: 27-Mar-2002
APPLICATION NUMBER: US/08/221,816
FILING DATE: 01-APR-1994
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 30,742
REGISTRATION NUMBER: 30,742
REGISTRATION INFORMATION:
TELECOMMUNICATION INFORMATION:
               STREET: 1155 Avenue of the Americas CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3; Mismatches
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Pred. No. 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear MOLECULE TYPE: RNA SEQUENCE DESCRIPTION: SEQ ID NO: 31:
                                                                                                                                                            COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 627 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 CCCCTGAATGCGGCTAATC 19
                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                91.68;
78.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA ORGANISM: Artificial Seguence
ADDRESSEE: Pennie
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                                                                                COUNTRY: USA
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Best Local Similarity
Matches 15, Conserva
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Best Local Similarity
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US-10-829-474-6
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LENGTH: 17
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                                                                                                                                                   Witherell, Gary
Watson, Julia C.
TITLE OF INVENTION: METHOD FOR SELECTIVE INACTIVATION
OF VIRAL REPLICATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SELECTIVE INACTIVATION
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GENERAL INFORMATION:
APPLICANT: Miles, Vincent J.
Mathews, Michael B.
Katze, Michael G.
Witherell, Gary
Watson, Julia C.
TITLE OF INVENTION: METHOD FOR SELECTIVE IN
OF VIRAL REPLICATION
                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/10/109,368
FILING DATE: 27-Mar-2002
CLASSIFICATION: «UNKNOWN»
PRIOR APPLICATION DATE: US/08/221,816
FILING DATE: 01-APR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: COLUZZI, Laura A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7960-030
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFFAX: (212) 869-8864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               91.6%; Score 17.4; I
78.9%; Pred. No. 23;
tive 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA
ZIP: 1036/2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ VOSS
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 , MOLECULE TYPE: RNA
, SEQUENCE DESCRIPTION: SEQ ID NO: 31:
US-10-109-368-31
                              Sequence 31, Application US/10109368
Publication No. US20030144226A1
GENERAL INFORMATION:
APPLICANT: Miles, Vincent J.
Mathews, Michael B.
Katze, Michael G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 31, Application US/10867798 Publication No. US20040254140A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 627 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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INFORMATION FOR SEQ ID NO: 31:
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Best Local Similarity
....hes 15; Conservat
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US-10-867-798-31
             US-10-109-368-31
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APPLICANT: Paul, John H.
APPLICANT: Paul, John H.
APPLICANT: Casper, Erica T.
APPLICANT: Casper, Erica T.
TITLE CASPERATION: Materials and Methods for Detection of Enterovirus and Norovirus
FILE REFERENCE: USF-114XC621
CURRENT APPLICATION NUMBER: 10/857,109
PRIOR APPLICATION NUMBER: 10/857,109
PRIOR PELING DATE: 2004-09-10
PRIOR APPLICATION NUMBER: 10/179,082
PRIOR APPLICATION NUMBER: 60/301,218
PRIOR PELING DATE: 2001-06-27
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin Version 3.2
SEQ ID NO 2.
                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: Chemically synthesized forward primer for amplifying enteroviral; OTHER INFORMATION: RNA
US-10-829-474-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
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                                      APPLICANT: MARIANI, Brian D.
TITLE OF INVENTION: ENTROVIRUS PRIMERS AND PROBES
FILE REFERENCE: 043956-0121
CURRENT APPLICATION NUMBER: US/10/829,474
CURRENT FILING DATE: 2004-04-22
NUMBER OF SEQ ID NOS: 57
SOFTWARE: Patentin version 3.2
SEQ ID NO 13
                                                                                                                                                                                                                                                                                                                                                             DB 9;
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Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; OTHER INFORMATION: Primer Ent P2 (JP128)
US-10-938-005-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    89.5%; Score 17;
100.0%; Pred. No.
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Publication No. US20040172684A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                               89.5%; Sco...
100.0%; Pre
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Publication No. US20050048475A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 17; Conservative
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Best Local Similarity 100.0
Matches 17; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: Chemically synthesized forward primer for amplifying enteroviral OTHER INFORMATION: RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: Chemically synthesized forward primer for amplifying enteroviral ; OTHER INFORMATION: RNA
US-10-829-474-9
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      Gaps
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31;
    Indels
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    ö
                                                                                                                                                                                                                                 APPLICANT: Genetics & IVF
APPLICANT: Genetics & IVF
APPLICANT: MARIANI, Brian D.
TITLE OF INVENTION: ENTEROVIRUS PRIMERS AND PROBES
FILE REPERENCE: 043956-0121
CURRENT APPLICATION NUMBER: US/10/829,474
CURRENT FILING DATE: 2004-04-22
NUMBER OF SEQ ID NOS: 57
SOFTWARE: PatentIn version 3.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 9, Application US/10829474
Publication No. US20050239055A1
GENERAL INFORMATION:
APPLICANT: Genetics & IVF
APPLICANT: MARIANI, Brian D.
TITLE OF INVENTION: ENTEROVIRUS PRIMERS AND PROBES
    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
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Mismatches
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100.0%; Pred. No.
tive 0; Mismatch
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CURRENT APPLICATION NUMBER: US/10/829,474
UNINBER OF FILING DATE: 2004-04-22
NUMBER OF SEQ ID NOS: 57
SOFTWARE: Patentin version 3.2
                                                                                                                                                                         Sequence 7, Application US/10829474 Publication No. US20050239055A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 13, Application US/10829474
; Publication No. US20050239055A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: Artificial Sequence
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Best Local Similarity 100.'
Matches 17; Conservative
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Best Local Similarity 100.
  Conservative
17;
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                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO 7
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Matches
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Sequence 33914, Application US/10437963
; Sequence 33914, Application US/10437963
; Publication No. US20040123343A1
; Publication No. US20040123343A1
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Shou, Yihua
; APPLICANT: Wu, Wei
; APPLICANT: Barbazuk, Brad
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 33914
; LENGTH: 110
; OTHER INFORMATION: Chemically synthesized forward primer for amplifying enteroviral ; OTHER INFORMATION: RNA US-10-829-474-12
                                                                                                                                                                                                                                                                    US-10-425-115-173355

US-10-425-115-173355, Application US/10425115

Sequence 173355, Application No. US20040214272A1

FUBLICARIT: LA ROBA, Thomas J.

APPLICANT: La ROBA, Thomas J.

APPLICANT: ADA, Yohua

APPLICANT: Cao, Yongwei

TITLE OF INVENTION: NLCleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants

FILE REFERENCE: 38-21 (53222)

CURRENT APPLICANTON NUMBER: US/10/425,115

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 369326

SEQ ID NO 173355

LENGTH: 359
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                                                                                     Length 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
                                                                                                                            0; Indels
                                                                                   Query Match 84.2%; Score 16; DB 9; Le Best Local Similarity 100.0%; Pred. No. 1.1e+02; Matches 16; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 84.2%; Score 16; DB 8; Lv
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 16; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: Clone ID: MRT4577_89681C.1
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ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Zea mays
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  TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement FILE REPRENCE: 38-21 (3535)B
CURRENT APPLICATION NUMBER: US/10/767,701
CURRENT FILING DATE: 2004-01-29
NUMBER OF SEQ ID NOS: 63128
SEQ ID NO 7988
LENGTH: 1216
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Best Local Similarity 100.0%; Pred. No. 41;
Matches 17; Conservative 0; Mismatches 0; Indels
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US-10-767-701-7988
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Sequence 12, Application US/10829474

Publication No. US20050239055A1

GENERAL INFORMATION:

APPLICANT: Genetics & IVF

TITLE OF INVENTION: EXTEROVIRUS FRIMERS AND PROBES

FILE REFERENCE: 043956-0121

CURRENT APPLICATION NUMBER: US/10/829,474

CURRENT FILING DATE: 2004-04-22

NUMBER OF SEQ ID NOS: 57

SOFTWARE: PatentIn version 3.2

SEQ ID NO 12

LENTIN: 16
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Pred. No. 67;
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                                                                                                                                                                                                                                                                                                                                                                                                   789 CCCTGAÁTGCGGCTAAT 805
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94.4%;
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ORGANISM: Artificial Sequence
FEATURE:
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ORGANISM: artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 86.3
Best Local Similarity 94.4
Matches 17; Conservative
                                                                                                                                                   TYPE: DNA ORGANISM: Sorghum bicolor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CTHER INFORMATION: Primer US-10-911-318-74
                                                                                                                                                                                              FEATURE:
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Sequence 2, Application US/10179082A
Publication No. US20030186222A1
GENERAL INFORMATION:
APPLICANT: Paul, John H
TITLE OF INVENTION: RAPID DETECTION OF ENTEROVIRUSES IN ENVIRONMENTAL SAMPLES BY NASB.
FILE REFERENCE: USP-114XC6
CURRENT APPLICATION NUMBER: US/10/179,082A
CURRENT FILING DATE: 2002-11-04
NUMBER OF SEQ ID NOS: 23
SOFTWARE: Patentin version 3.1
SEQ ID NO 2
                                                            PRIOR FILING DATE: 2000-10-23
PRIOR PELICATION NUMBER: 60/242,578
PRIOR PELICATION NUMBER: 60/253,625
PRIOR PELICATION NUMBER: 60/253,625
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2001-02-09
PRIOR PILING DATE: 2001-02-09
PRIOR PILING DATE: 2001-02-09
PRIOR PILING DATE: 2001-02-06
PRIOR PILING DATE: 2001-02-16
PRIOR PILING DATE: 2001-03-16
PRIOR PILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 83.2%; Score 15.8; DB 7; Length 1326; 89.5%; Pred. No. 1.9e+02; ive 0; Mismatches 2; Indels 0;
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APPLICANT: Berks. Randy M.
APPLICANT: Berks. ID Groth
TITLE OF INVENTION: Methods For Monitoring Multiple Gene
TITLE OF INVENTION: Expression
FILE REFERENCE: 10085.500-US
CURRENT APPLICATION NUMBER: 08/9974,300
CURRENT FILING DATE: 2001-10-05
PRIOR APPLICATION NUMBER: 09/680,598
PRIOR FILING DATE: 2000-10-06
PRIOR FILING DATE: 2001-03-27
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Pred. No. 2.5e+02;
0; Mismatches 1;
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                60/230,347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
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US-10-282-122A-19830
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Best Local Similarity 94.1%;
Matches 16; Conservative
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; ORGANISM: Enterovirus sp.
US-10-179-082A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 17; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With; TITLE OF INVENTION: PLANTE and Uses Thereof for Plant Improvement; PLE REFERENCE: 38-21(5321)B; CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 33913
LENGTH: 127F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Identification of Essential Genes in Microorganisms PILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR PILING DATE: 2004-03-21
PRIOR PILING DATE: 2004-03-321
PRIOR PILING DATE: 2004-03-21
PRIOR PILING DATE: 2004-05-32
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Best Local Similarity 89.5%; Pred. No. 1.9e+02; Matches 17; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: Clone ID: PAT_MRT4530_37980C.1
US-10-437-963-33913
                                                                                                                                                                                                                                                                                                                   Sequence 33913, Application US/10437963
Publication No. US20040123343A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Bukharov, Andrey A.
APPLICANT: Barbazuk, Brad
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-10-282-122A-19830/c
; Sequence 19830, Application US/10282122A
; Publication No. US20040029129A1
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**RAPPLICATION NUMBER: 60/206,848

**RILING DATE: 2000-05-23

**RAPPLICATION NUMBER: 60/207,727

**RELING DATE: 2000-05-26

**RAPPLICATION NUMBER: 60/230,335

**RAPPLICATION NUMBER: 60/230,335

**RILING DATE: 2000-09-06
                                                                                                                                       411 cccricagraccaccraric 393
                                                                                                  1 CCCCTGAATGCGGCTAATC 19
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Zamudio, Carlos
Malone, Cheryl
Haselbeck, Robert
Ohlsen, Kari
Zyskind, Judith
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Carr, Grant
Yamamoto, Robert
Forsyth, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 89.5
Matches 17; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                          RESULT 41
US-10-437-963-33913/c
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Gaps
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; Patent No. US20020132767A1
; GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REPRERENCE: PC009
; CURRENT APPLICATION NUMBER: US/09/764,847
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 2003
; SEQ ID NO 1550
; LENGTH: 32187
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Pred. No. 4e+02;
0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 15.4; DB 3; Length 32187; Pred. No. 4e+02;
                                                                                                                                                           Query Match 81.1%; Score 15.4; DB 9; Length 1943; Best Local Similarity 94.1%; Pred. No. 3.3e+02; Matches 16; Conservative 0; Mismatches 1; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 48
US-10-092-154-1550/c
US-10-092-154-1550/c
Sequence 1550, Application US/10092154
Publication No. US20030054375A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PC009C1
CURRENT APPLICATION NUMBER: US/10/092,154
CURRENT FILING DATE: 2002-03-07
NUMBER OF SEQ ID NOS: 2003
Prior Application removed - See File Wrapper or Palm
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1550
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US-09-764-847-1549/c
; Sequence 1549, Application US/09764847
                                 ; TYPE: DNA; CRGANISM: LACTOBACILLUS RHAMNOSUS
US-10-650-274-73
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ilarity 94.1%;
Conservative
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ilarity 94.1%;
Conservative
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US-10-092-154-1550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-847-1550
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Best Local Similarity
Matches 16; Conserv
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Best Local Similarity
Matches 16; Conserv
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      LENGTH: 1943
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Sequence 561, Application US/0988227

Publication No. US20030158396A1

GENERAL INFORMATION:

APPLICANT: Kleathhous, Harold

APPLICANT: Tomb, Jean-Francois

TITLE OF INVENTION: Encoding No. US20030158396A1e1 Helicobacter Polypeptides in the

TITLE OF INVENTION: Genome

TITLE OF IN
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| Sequence 73, Application US/10650274
| Sequence 73, Application US/10650274
| Publication No. US20050202437A1
| GENERAL INFORMATION:
| APPLICANT: GIERN, MATTHEW
| APPLICANT: HAVUKKALA, ILKKA J
| APPLICANT: LUBBERS, MARK WILLIAM
| APPLICANT: DIBKKER, JAMES
| TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES,
| TITLE OF INVENTION: THEM. |
| TITLE OF INVENTION: THEM. |
| FILE REFERENCE: 11000.1073 |
| CURRENT APPLICATION NUMBER: US/10/650,274 |
| CURRENT PILING DATE: 2003-08-28 |
| NUMBER OF SEQ ID NOS: 187 |
| SOFTWARE: PASTSEQ FOR WINDOWS VERSION 4.0 |
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                                                                                                                                                                                                                                                          Query Match 81.1%; Score 15.4; DB 3; Length 750; Best Local Similarity 94.1%; Pred. No. 3.18+02; Matches 16; Conservative 0; Mismatches 1; Indels C
NUMBER OF SEQ ID NOS: 8481
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5975
LENGTH: 750
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                                                                                                                                                                                                                                                                                                                                                                                             2 CCCTGAATGCGGCTAAT 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Helicobacter pylori
                                                                                                                                TYPE: DNA
CRGANISM: Bacillus clausii
US-09-974-300-5975
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; NAME/KEY: CDS
; LOCATION: (22)...(1593)
US-09-882-227-561
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Best Local Similarity
"...rhes 16; Conservat
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US-09-882-227-561
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APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: Show Yihua
APPLICANT: Zhow Yihua
APPLICANT: Cao Yongwel
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
LENGTH: 197
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Publication No. US20040214272A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: La Rosa, Thomas J.
APPLICANT: APPLICANT: Acvalic, David K.
APPLICANT: APPLICANT: Acvalic, David K.
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(5322) B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 89087
LENGTH: 415
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                                                                                             Gaps
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Pred. No. 5e+02;
0; Mismatches 0;
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100.0%; Pred. No. 4.7e+02;
tive 0; Mismatches 0;
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                                                  DB 9;
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US-10-425-115-89087
                                                                                             Mismatches
                                                    Score 15;
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100.0%; Pre
                                             78.9%; £
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                                             Query Match
Best Local Similarity 100.0
Matches 15; Conservative
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Best Local Similarity 100.
Matches 15; Conservative
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Matches 15; Conservative
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ORGANISM: Glycine max
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US-10-424-599-90608
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    US-10-829-474-8
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                                  APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PC009
CURRENT APPLICATION NUMBER: US/09/764,847
CURRENT PILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper
NUMBER OF SEQ ID NOS: 2003
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1549
LENGTH: 32193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REPERENCE: PC009C1
CURRENT APPLICATION NUMBER: US/10/092,154
CURRENT FILING DATE: 2002-03-07
NUMBER OF SEQ ID NOS: 2003
Prior Application removed - See File Wrapper or Palm
SOFTWARE: Patentin Ver. 2.0
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Publication No. US20030054375A1
GENERAL INFORMATION:
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Best Local Similarity 94.1%;
Matches 16; Conservative
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ORGANISM: Artificial Sequence
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Best Local Similarity 94.17
Best Local 5; Conservative
Patent No. US20020132767A1
                                                                                                                                                                                                                                                                ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-847-1549
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ORGANISM: Homo sapiens
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Best Local Similarity 100.0%; Pred. No. 5.1e+02;
Matches 15; Conservative 0; Mismatches 0;
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Pred. No. 5.2e+02;
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FILE REFERENCE: MMIII10-2
CURRENT APPLICATION NUMBER: US/10/972,079
CURRENT FILING DATE: 2004-10-22
PRIOR APPLICATION NUMBER: US 60/514,333
PRIOR FILING DATE: 2003-10-24
NUMBER OF SEQ ID NOS: 96631
SOFTWARE: PatentIN version 3.1
SOFTWARE: PatentIN version 3.1
LENGTH: 599
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; Sequence 261980, Application US/10027632
; Publication No. US20020198371A1
                                                                                                                                                                                                                                                                                                                                           COTHER INFORMATION: n is any nucleotide US-10-972-079-35873
                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Chicken 19866894262226_1
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APPLICANT: HOLM, Tom
TITLE OF INVENTION: METHODS & SYSTEMS FOR INFERRING TRAITS TO BREED & MANAGE NON-BEER
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CURRENT APPLICATION NUMBER: US/10/282,122A

CURRENT PILING DATE: 2003-02-20

FRIOR PILING DATE: 2000-03-21

PRIOR PILING DATE: 2000-03-21

PRIOR PILING DATE: 2000-03-21

PRIOR PILING DATE: 2000-05-25

PRIOR PILING DATE: 2000-05-26

PRIOR PILING DATE: 2000-05-26

PRIOR PILING DATE: 2000-05-26

PRIOR PLING DATE: 2000-05-26

PRIOR PLING DATE: 2000-05-26

PRIOR PLING DATE: 2000-09-09

PRIOR PLING DATE: 2000-09-09

PRIOR PLING DATE: 2000-10-23

PRIOR PLING DATE: 2001-02-09

PRIOR PLING DATE: 2001-02-09
                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Xu, H. TILLE OF INVENTION: Identification of Essential Genes in Microorganisms
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'... 0; Mismatches
                                                                                         Sequence 20329, Application US/10282122A
Publication No. US20040029129A1
GENERAL INFORMATION:
APPLICANT: Manone, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Oblsen, Kari
APPLICANT: Cyskind, Judith
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GENERAL INFORMATION:
APPLICANT: MAI GENOMICS, INC.
APPLICANT: ROSENFELD, David
APPLICANT: KERR, Richard
APPLICANT: HOLM, TOM
                                                                                                                                                                                                                                                                                                                  Wall, Daniel
Trawick, John
Carr, Grant
Yamamoto, Robert
Forsyth, R.
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US-10-282-122A-20329
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Best Local Similarity
Matches 15; Conserva
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US-10-972-079-35873
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APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108927.129
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TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108927.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
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    Indels
  Mismatches
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PRIOR FILING DATE: 2000-04-20
PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: 2000-02-24
PRIOR PILING DATE: 2000-02-24
PRIOR PILING DATE: 100-02-10-23
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/15/363
PRIOR PLICATION NUMBER: US 60/156,358
PRIOR PLICATION NUMBER: US 60/146,002
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Publication No. US20030204075A9
GENERAL INFORMATION:
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PRICK FILING DATE: 2000-07-12
PRICK APPLICATION NUMBER: US 60/198,676
PRICK APPLICATION NUMBER: US 60/193,483
PRICK PILING DATE: 2000-03-29
PRICK APPLICATION NUMBER: US 60/193,483
PRICK APPLICATION NUMBER: US 60/185,218
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Publication No. US20030204075A9
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PRIOR FILING DATE: 2000-07-12
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APPLICATION NUMBER: US 60/185,218
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APPLICATION NUMBER: US 60/146,002
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                                                                                      81 CTGAATGCGGCTAAT 95
                                             4 CTGAATGCGGCTAAT 18
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SOFTWARE: FastSEQ for Window
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 78.9
Best Local Similarity 100:
Matches 15; Conservative
15; Conservative
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US-10-027-632-261979
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                                      TLE OF INVENTION: Identification and Mapping of Single Nucleotide
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TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
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                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TILE CELLING DATE: FOLYWOLDILENES IN CHE AND TELLE REPRENCE: 10827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR PILING DATE: 2000-07-12
PRIOR PELING DATE: 2000-03-29
PRIOR PILING DATE: 2000-03-29
PRIOR PELING DATE: 2000-02-24
PRIOR PELING DATE: 2000-02-24
PRIOR PELING DATE: 1999-11-23
PRIOR PELING DATE: 1999-11-23
PRIOR PELING DATE: 1999-11-23
PRIOR PELING DATE: 1999-10-24
PRIOR PELING DATE: 1999-09-28
PRIOR PELING DATE: 1999-09-28
PRIOR PELING DATE: 1999-09-28
PRIOR PELING DATE: 1999-09-28
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SCOTMARE: FastSEQ for Windows Version 4.0
SEQ ID NO 261981
LENGTH: 969
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Publication No. US20020198371A1
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Best Local Similarity 100.
Matches 15; Conservative
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Best Local Similarity
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; ORGANISM: Human
US-10-027-632-261981
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TYPE: DNA
ORGANISM: Oryza sativa
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ORGANISM: Homo sapiens
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Best Local Similarity
Matches 15; Conserv
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                                                                                                            78.9%; Score 15; DB 6; Length 969;
100.0%; Pred. No. 5.2e+02;
tive 0; Mismatches 0; Indels
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 261980
LENGTH: 969
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Sequence 38285, Application US/10437963

Publication No. US20040123343A1

GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Ru, Wei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Barbarouk, Brad
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100.0%; Pre
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                                                                                                            Query Match 78.9
Best Local Similarity 100.
Matches 15; Conservative
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Best Local Similarity 100.
Matches 15; Conservative
                                                               ; TYPE: DNA
; ORGANISM: Human
US-10-027-632-261980
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APPLICANT:
APPLICANT:
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APPLICANT:
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TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILE REFERENCE: 38-21(53221) Plant September: 18-21(53221) Plant September: 18-21(53221) Plant September: 18-21(63221) Plant September: 18-21(63221) Plant September: 2003-05-14 NUMBER: OF SEQ ID NOS: 204966 SEQ ID NOS: 204966 LENGTH: 1458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION: (1409)..(2074)
OTHER INFORMATION: 94% homologous to Escherichia coli L-asparagine permease (L-
OTHER INFORMATION: asparagine transport protein), accession number D90785, Smith-
OTHER INFORMATION: Waterman Score=1059.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Hyseq, Inc.
TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
FILE REFERENCE: 790CTB3/US
CURRENT APPLICATION NUMBER: US/10/450,763
CURRENT FILING DATE: 2003-06-11
PRIOR PILING DATE: 2001-03-30
PRIOR PILING DATE: 2000-03-31
PRIOR PILING DATE: 2000-03-31
PRIOR FILING DATE: 2000-08-23
NUMBER OF SEQ ID NOS: 60736
SOFTWARE: Custom
SEQ ID NO 29581
LENGTH: 2780
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TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
TITLE TERERGE: 3288.1
CURRENT APPLICATION NUMBER: US/10/719,900
CURRENT FILING DATE: 2003-11-20
PRIOR APPLICATION NUMBER: 60/427,808
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               78.9%; Score 15; DB 9; Lo
llarity 100.0%; Pred. No. 5.6e+02;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: Clone ID: PAT_MRT4530_41936C.1
US-10-437-963-38285
                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                              78.9%; Score 15; 100.0%; Pred. No.
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Publication No. US20050026164A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 29581, Application US/10450763 Publication No. US20050196754A1 GENERAL INFORMATION:
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Best Local Similarity 100.(
Matches 15, Conservative
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APPLICANT: Leach, Martin D.
APPLICANT: Leach, Martin D.
APPLICANT: Shinkets, Richard A.
APPLICANT: Shinkets, Richard A.
APPLICANT: Shinkets, Richard A.
CURRENT: LEACH NO. US20040009474Alel Human Polynucleotides and Polypeptides EncorILE REFERENCE: 21402-012
CURRENT APPLICATION WINBER: US/09/864,408A
CURRENT FILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: 60/206,690
PRIOR APPLICATION NUMBER: 60/206,690
NUMBER OF SEQ ID NGS: 9068
SOFTWARE: RESESEQ for Windows Version 4.0
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APPLICANT: INVOKO, Hidecoshi
APPLICANT: INVOKO, Hidecoshi
APPLICANT: TAMIYA, Gen
ITILE OF INVENTION: GENE MAPPING METHOD USING MICROSATELLITE
ITILE OF INVENTION: GENETIC POLYMORPHISM MARKERS
FILE REFERENCE: ORIN-003CIP
CURRENT APPLICATION NUMBER: US/10/674,124A
CURRENT APPLICATION NUMBER: US/257,511
PRIOR APPLICATION NUMBER: 10/257,511
PRIOR FILING DATE: 2003-09-07
PRIOR FILING DATE: 2000-10-30
PRIOR PLILING DATE: 2000-10-30
PRIOR APPLICATION NUMBER: JP2002-12699
PRIOR APPLICATION NUMBER: JP2002-383869
PRIOR APPLICATION NUMBER: JP2002-383869
PRIOR APPLICATION NUMBER: JP2002-383869
PRIOR APPLICATION NUMBER: JP2002-383869
PRIOR PILING DATE: 2002-12-09
NUMBER OF SEQ ID NOS: 27110
SEQ ID NO 10734
LENGTH 295
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Pred. No. 6.3e+02;
0; Mismatches 2;
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// LOCATION: (289)

// OTHER INFORMATION: Wherein n may be a, c, g or t

US-09-864-408A-4131
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Publication No. US20040197797A1
                                                      US-09-864-408A-4133/c
; Sequence 4133, Application US/09864408A
; Publication No. US20040009474A1
; GENERAL INFORMATION:
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LOCATION: (286)..(286)
OTHER INFORMATION: Wherein n may
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88.9%;
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Best Local Similarity 88.99
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc_feature
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LENGTH: 293
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Publication No. US20050026169A1
GENERAL INFORMATION:
TITLE OF INVENTION: GENETIC POLYNORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: MYCCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001499
CURRENT APPLICATION NUMBER: US/10/741,600
CURRENT PILING DATE: 2003-12-22
NUMBER OF SEQ ID NOS: 73997
SOFTWARE: FREESE OF WINDOWS Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:

APPLICANT: CARGILL, Michele et al.

TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED MITH

TITLE OF INVENTION: ALZHEIMER'S DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CL001496

CURRENT APPLICATION NUMBER: US/10/719,993

CURRENT PILING DATE: 2003-11-24

NUMBER OF SEQ ID NOS: 55342

SOPTWARE: FactSEQ for Windows Version 4.0
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                                                                                                                                                                                                                            Length 25;
                       NUMBER OF SEQ ID NOS: 982914
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 576555
LENGTH: 25
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Pred. No. 5.3e+02;
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Pred. No. 6.1e+
0; Mismatches
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Publication No. US20040265849A1
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Best Local Similarity 88.9%;
Matches 16; Conservative
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88.9%;
PRIOR FILING DATE: 2002 11 20
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Best Local Similarity 88.9
Matches 16; Conservative
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Best Local Similarity 88.9
Matches 16; Conservative
                                                                                                                       TYPE: DNA
CRGANISM: Mus musculus
US-10-719-900-576555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-719-993-17666
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ORGANISM: Homo sapiens
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US-10-741-600-37330/c
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SEQ ID NO 17666
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LENGTH: 201
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Gaps

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; Sequence 152061, Application US/09925065A; Bodication No. US2005028172A9; Publication No. US20050228172A9; CENERAL INFORMATION:
APPLICANT: Wang, David G.; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome; CURRENT APPLICATION NUMBER: US/09/925,065A; CURRENT FILING DATE: 2001-08-08; PRIOR FILING DATE: 2000-10-24; PRIOR FILING DATE: 2000-10-24; PRIOR FILING DATE: 2000-11-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Williams, Amanda
APPLICANT: Williams, Asseph F.
APPLICANT: Boland, Joseph F.
APPLICANT: Alvarez, Chris
APPLICANT: Alvarez, Chris
APPLICANT: Wetzel, Jon C.
APPLICANT: Scherf, Uwe
APPLICANT: Vockley, Joseph G.
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US-10-240-425-991
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                                                                                                                                                                                                                                                              Length 405;
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                                                                                                                                                                                                                                                         Query Match 77.9%; Score 14.8; DB 7; Best Local Similarity 88.9%; Pred. No. 6.4e+02; Matches 16; Conservative 0; Mismatches 2;
                                                                                                                                                                             ; OTHER INFORMATION: Clone ID: PAT_MRT3847_44988C.1
US-10-424-599-81916
                  ORGANISM: Glycine max
FEATURE:
NAME/KEY: unsure
CCATLON: (1)..(405)
OTHER INFORMATION: unsure at all n locations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILE REFERENCE: 44921-5026
CURRENT APPLICATION NUMBER: US/10/240,425
CURRENT FILING DATE: 2002-09-30
PRIOR APPLICATION NUMBER: PCT/US01/09847
PRIOR FILING DATE: 2001-03-28
PRIOR FILING DATE: 2000-03-31
NUMBER OF SEQ ID NOS: 1588
SOFTWARE: Patentin Ver. 2.1
SOFTWARE: 937
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Sequence 991, Application US/10240425; Publication No. US20040033502A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                         380 CCCCTGAATGGGGCGAAT 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    162 cccreaacececraare 145
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-925-065A-152961/c
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                                                                                                                                                       FEATURE:
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APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: 105/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 64661
LENGTH: 354
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Sequence 81916, Application US/10424599

Publication No. US20040031072A1

GENERAL INFORMATION:

APPLICANT: La Rosa Thomas J

APPLICANT: Zhou Yihua

APPLICANT: Cao Yongwei

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

TITLE OF INVENTION NUMBER: US/10/424,599

CURRENT APPLICATE: 2003-04-28

CURRENT FILING DATE: 2003-04-28

NUMBER OP SEQ ID NOS: 285684

SEQ ID NO 81916
                                        OTHER INFORMATION: Distance between a terminus base of telomere on CTHER INFORMATION: chromosomal short arm and 5'-terminus of this base OTHER INFORMATION: sequence: 112298313
CTHER INFORMATION: bistance between 3'-terminus of neighbour sequence of OTHER INFORMATION: sequence listing upward to telomere on chrosomal short arm and CTHER INFORMATION: 5'-terminus of this base sequence: 96016
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                                                                                                                                                                                                                                                                                    Length 295;
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                                                                                                                                                                                                                                                                                 77.9%; Score 14.8; DB 8;
88.9%; Pred. No. 6.3e+02;
tive 0; Mismatches 2;
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Pred. No. 6.3e+02;
0; Mismatches 2;
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US-10-437-963-66461
OTHER INFORMATION: Located on chromosome 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 66461, Application US/10437963
Publication No. US20040123343A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wo, Wei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Barbazuk, Brad
                                                                                                                                                                                                                                                                                                                                                                                           1 CCCCTGAATGCGGCTAAT 18
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88.9%;
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Best Local Similarity 88.9
Matches 16; Conservative
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Best Local Similarity 88.9
Matches 16; Conservative
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Sequence 112662, Application US/10425115
Publication No. US20040214272A1
GENERAL INFORMATION:
APPLICANT: La Rovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(53222)B
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TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: No. No. 136
TITLE OF INVENTION: NO. 136
CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2001-08-08
PRIOR FILING DATE: 2000-10-24
PRIOR FILING DATE: 2000-11-20
PRIOR FILING DATE: 2000-11-20
PRIOR FILING DATE: 2000-11-60
PRIOR FILING DATE: 2000-11-6
PRIOR FILING DATE: 2000-11-6
PRIOR FILING DATE: 2000-11-6
PRIOR FILING DATE: 2001-01-6
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                                                                                                                                                                                                                                                                                                                                                                Length 595;
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Pred. No. 6.6e+02;
0; Mismatches 2;
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PRIOR FILING DATE: 2000-11-30
PRIOR PILING DATE: 2001-01-16
PRIOR PLING DATE: 2001-01-16
PRIOR PLING DATE: 2001-01-16
PRIOR PLING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
SOFTWARE: FBSESEQ for Windows Version 4.0
LENGTH: 595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      S-09-925-065A-886331/c
Sequence 886331, Application US/09925065A
Publication No. US20050228172A9
GENERAL INPORMATION:
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88.9%;
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Best Local Similarity 88.9
Matches 16; Conservative
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Matches 16; Conservative
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US-09-925-065A-152961
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US-09-925-065A-886331
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US-10-425-115-112682/c
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APPLICANT: I.N.S.B.R.M.

APPLICANT: I.N.S.B.R.M.

TITLE OF INVENTION: Polynucleotides which are of nature B2/D+ A- and which are isolat

TITLE OF INVENTION: B. coli, and biological uses of these polynucleotides and of their

FILE REFERENCE: BLANDING

CURRENT APPLICATION NUMBER: US/10/238,075

CURRENT PILING DATE: 2002-09-10

PRIOR APPLICATION NUMBER: 003145

PRIOR FILING DATE: 2000-03-10

SOFTWARE: Patentin version 3.1

SEQ ID NO 384
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Pred. No. 6.6e+02;
0; Mismatches 2;
                                                                                                                                                                                                                              Score 14.8; DB 8;
Pred. No. 6.6e+02;
0; Mismatches 2;
                                                                                                                                          ; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_34256C.1
US-10-425-115-112682
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 112682
LENGTH: 635
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Publication No. US20040123343A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Wu, Wei
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 384, Application US/10238075
Publication No. US20030148324A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                       527 CCCTGAAAGCGGCTAACC 510
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88.98;
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88.9%;
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Best Local Similarity 88.5.
Lines 16; Conservative
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Best Local Similarity 88.9
Matches 16; Conservative
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US-10-238-075-384
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                                                                                                        TYPE: DNA
ORGANISM: Zea mays
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Gaps

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Sequence 246, Application US/10006285

Publication No. US20030165854A1

GENERAL INFORMATION:

APPLICANT: Mary Jane Cunningham

APPLICANT: Matchew R. Kase RENEWATION:

TITLE OF INVENTION: MARKER GENES RESPONDING TO TREATMENT WITH TOXINS

FILE REFERENCE: PA-0039 US

CURRENT APPLICATION UNMERR: US/10/006,285

CURRENT FILING DATE: 2001-12-05

NUMBER OF SEQ ID NOS: 514

SOFTWARE: PERL Program
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TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
TITLE FERENCE: 108827.128
CURRENT PILING DATE: 2082-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR PILING DATE: 2000-07-12
PRIOR FILING DATE: 2000-04-20
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR PILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/195,218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 14.8; DB 6; Length 719;
Pred. No. 6.6e+02;
0; Mismatches 2; Indels (
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; NambKEX: misc_feature
; OTHER INFORMATION: Incyte ID No. US20030165854A1 211417_Rn.1
US-10-006-285-246
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                  PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR PILING DATE: 1999-09-28
PRIOR PILING DATE: 1999-09-28
PRIOR PILING DATE: 1999-09-28
PRIOR PILING DATE: 1999-09-05
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSEQ for Windows Version 4.0
SOFTWARE: 7199
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         160 CCCTGAATGCGCCTGATC 177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 77.9%;
Best Local Similarity 88.9%;
Matches 16; Conservative (
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                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Human
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Sequence 18639, Application US/10027632

Publication No. US20020138371A1

GENERAL INFORMATION:

APPLICANT: Wang, David G.

TITLE OF INVENTION: Polymorphisms in the Human Genome

FILE REFERENCE: 108827.129

CURRENT APPLICATION NUMBER: US/0027,632

CURRENT FILING DATE: 2000-04-30

PRIOR FILING DATE: 2000-07-12

PRIOR FILING DATE: 2000-07-12

PRIOR FILING DATE: 2000-04-30

PRIOR FILING DATE: 2000-04-30

PRIOR FILING DATE: 2000-04-30

PRIOR FILING DATE: 2000-04-20

PRIOR FILING DATE: 2000-04-24

PRIOR FILING DATE: 1990-03-29

PRIOR FILING DATE: 1999-11-23

PRIOR FILING DATE: 1999-11-23

PRIOR FILING DATE: 1999-11-23

PRIOR FILING DATE: 1999-11-23

PRIOR FILING DATE: 1999-08-08

PRIOR PLING DATE:
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// Sequence 18639, Application US/10027632

// Sequence 18639, Application US/10027632

// Publication No. US20030204075A9

// GENERAL INPORMATION:

// APPLICANT: Wang, David G.

// TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

// TITLE OF INVENTION: Polymorphisms in the Human Genome

// TITLE OF INVENTION: Polymorphisms in the Human Genome

// FILE REFERENCE: 108827.129

// CURRENT FILING DATE: 2002-04-30

// PRIOR FILING DATE: 2000-07-12

// PRIOR FILING DATE: 2000-07-12

// PRIOR APPLICATION NUMBER: US 60/198,676

// PRIOR APPLICATION NUMBER: US 60/193,483

// PRIOR FILING DATE: 2000-03-29

// PRIOR PILING DATE: 2000-03-29
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                                                                                                                                    Query Match 77.9%; Score 14.8; DB 7; Length 714; Best Local Similarity 88.9%; Pred. No. 6.6e+02; Matches 16; Conservative 0; Mismatches 2; Indels (
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Pred. No. 6.6e+02;
0; Mismatches 2; Indels (
                             ; OTHER INFORMATION: Clone ID: PAT_MRT4530_8018C.1
US-10-437-963-80579
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Best Local Similarity
Matches 16; Conserva
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FEATURE:
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DETECTING EXPRESSION OF 10,000 OR MORE
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APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REPERSINCE: 108827.129
CURRENT APPLICATION NUMBER: U5/10/027,632
CURRENT PILING DATE: 2002-04-30
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TITLE OF INVENTION: DETECTION KIT, SUCH AS M TITLE OF INVENTION: ARRAYS, FOR DETECTING ENTITLE OF INVENTION: DROSOPHILA GENES.
TITLE OF INVENTION: DROSOPHILA GENES.
CURRENT FILING DATE: 2005-04-04
FRIOR PRIOR APPLICATION NUMBER: 60/157,832
PRIOR PRIOR APPLICATION NUMBER: 60/161,932
PRIOR PLING DATE: 1999-10-05
PRIOR PLING DATE: 1999-10-19
PRIOR PLING DATE: 1999-11-12
PRIOR FLING DATE: 2000-01-12
PRIOR FLING DATE: 2000-03-23
NUMBER OF SEQ ID NOS: 43008
SOUTHARRE: PRESEQ FOR WINDOWS VERSION 4.0
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PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR FILING DATE: 2000-07-12
PRIOR FILING DATE: 2000-04-20
PRIOR FILING DATE: 2000-04-20
PRIOR PILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/195,218
PRIOR FILING DATE: 2000-03-24
PRIOR FILING DATE: 2000-03-24
PRIOR FILING DATE: 1999-11-23
PRIOR FILING DATE: 1999-11-23
PRIOR FILING DATE: 1999-10-38
PRIOR FILING DATE: 1999-09-80
PRIOR FILING DATE: 1999-09-80
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Publication No. US20020198371A1
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Best Local Similarity 88.9%;
Matches 16; Conservative
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; ORGANISM: DROSOPHILA
US-11-097-143-12548
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US-10-027-632-262260
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APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REPRENCE: 108027.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
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6.7e+02;
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                                                  PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR PILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR PILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: PASSECT OF WINDOWS VERSION 4.0
SEQ ID NO 154375
LENGTH: 810
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Pred. No. 6.
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PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: 2000-02-24
PRIOR FILING DATE: 2000-02-24
PRIOR FILING DATE: 1999-11-23
PRIOR FILING DATE: 1999-10-23
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-09-28
PRIOR PRIOR DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-28
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 154375
LENGTH: 810
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Publication No. US20030204075A9
                              ICATION NUMBER: US 60/167,363
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Publication No. US20050208558A1
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ilarity 88.9%;
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Best Local Similarity 88.9
Matches 16; Conservative
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Best Local Similarity
Matches 16; Conserv
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ORGANISM: Human
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Sequence 262261, Application US/10027632
Publication No. US20030204075A9
GRNERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
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Pred. No. 6.8e+02;
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CURRENT PELLING DATE: 2002-04-30
PRIOR PELLING DATE: 2002-04-30
PRIOR PELLING DATE: 2002-04-30
PRIOR FILING DATE: 2000-07-12
PRIOR PELLING DATE: 2000-07-12
PRIOR PELLING DATE: 2000-04-20
PRIOR PELLING DATE: 2000-03-29
PRIOR PELLING DATE: 2000-03-29
PRIOR PELLING DATE: 2000-03-24
PRIOR PELLING DATE: 2000-03-24
PRIOR PELLING DATE: 2000-03-24
PRIOR PELLING DATE: 1999-109-8
PRIOR PELLING DATE: 1999-109-8
PRIOR PELLING DATE: 1999-09-8
PRIOR PELLING DATE: 1999-09-09-8
PRIOR PELLING DATE: 1999-09-09
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 262260
LENGTH: 926
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Publication No. US20040123343A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Wu, Wei
APPLICANT: Barbaruk, Brad
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Best Local Similarity 88.9%;
Matches 16; Conservative
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Best Local Similarity 88.9
Matches 16; Conservative
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US-10-027-632-262261
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US-10-027-632-262260
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US-10-027-632-262261
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APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
ITILE OF INVENTION: Polymorphisms in the Human Genome
ITILE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US 60/218,006
FRIOR PELING DATE: 2002-04-30
FRIOR PELING DATE: 2000-07-22
FRIOR PELING DATE: 2000-04-20
FRIOR PELING DATE: 2000-04-20
FRIOR PELING DATE: 2000-03-24
FRIOR PELING DATE: 1999-11-23
FRIOR PELING DATE: 1999-11-23
FRIOR PELING DATE: 1999-11-23
FRIOR PELING DATE: 1999-09-28
FRIOR PELING DATE: 1999-08-09
FRIOR PELING DATE: 1999-09-08-09
FRIOR PELING DATE: 1999-09-09-08-09
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TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Oblymorphisms in the Human Genome
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT APPLICATION NUMBER: US 60/218,006
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR PLING DATE: 2000-07-12
PRIOR FILING DATE: 2000-07-12
PRIOR FILING DATE: 2000-04-20
PRIOR PLING DATE: 2000-04-20
PRIOR PLING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR PLING DATE: 2000-03-24
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR PLING DATE: 2000-03-24
PRIOR PLING DATE: 1000-03-24
PRIOR PLING DATE: 1000-02-24
PRIOR PLING DATE: 1000-02-28
PRIOR PLING DATE: 1000-02-28
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                                        2; Indels
    88.9%; Pred. No. 6.8e+02;
tive 0; Mismatches 2
                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 262261, Application US/10027632; Publication No. US20020198371A1; GENERAL INFORMATION:
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                                                                                                                                                                 311 CCCTGAAAGCGGCTTATC 328
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Best Local Similarity 88.9
Matches 16; Conservative
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Best Local Similarity 88.9
Matches 16; Conservative
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US-10-027-632-262261
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TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement; TITLE REFERENCE: 38-21(53221) B; CURRENT APPLICATION NUMBER: US/10/437,963 CURRENT FILING DATE: 2003-05-14 NUMBER OF SEQ ID NOS: 204966 SEQ ID NO 56310 LENGTH: 1551
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Publication No. US2020198371A1
GENERAL INFORMATION:
APPLICANT: WANG, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
PILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027, 632
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Pred. No. 7.1e+02;
0; Mismatches 2; Indels 0
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Pred. No. 7e+02;
0; Mismatches 2;
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US-10-437-963-56310
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PRIOR APPLICATION NUMBER: US 60/218,006

PRIOR FILING DATE: 2000-07-12

PRIOR FILING DATE: 2000-07-12

PRIOR FILING DATE: 2000-04-20

PRIOR PILING DATE: 2000-03-29

PRIOR PILING DATE: 2000-03-29

PRIOR PILING DATE: 2000-03-29

PRIOR PILING DATE: 2000-02-24

PRIOR PILING DATE: 1999-1-23

PRIOR FILING DATE: 1999-09-28

PRIOR FILING DATE: 1999-09-28

PRIOR FILING DATE: 1999-08-09

PRIOR FILING DATE: 1999-08-09

NUMBER OF SEQ ID NOS: 325720

SOFTWARE: FABLESEQ FOR WINDOWS VERSION 4.0

SERVICH: 1929
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88.9%;
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88.9%;
                                                                                                                            La Rosa, Thomas J
Kovalic, David K
Zhou, Yihua
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Best Local Similarity 88.9
Matches 16; Conservative
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Best Local Similarity 88.9
Matches 16; Conservative
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US-10-027-632-257412
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us-10-82;

TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With;
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement;
FILE REPRENCE: 38-21(5321)B
CURRENT APPLICATION WUMBER: 185/10/437,963
CURRENT PILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 56313
LENGTH: 1026
TYPE: NA
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APPLICANT: Ripp, Kevin
APPLICANT: Ripp, Kevin
APPLICANT: Ripp, Revin
APPLICANT: Ripp, Revin
APPLICANT: Ripp, Revin
APPLICANT: Cheng, Peizhong
TITLE OF INVENTION: ORGANELLE
TITLE OF INVENTION: PORMATION ND METHODS OF USE
TITLE OF INVENTION: PORMATION ND METHODS OF USE
FILE REPERENCE: BB1392 US NA
CURRENT APPLICATION NUMBER: US/10/269,441
CURRENT APPLICATION NUMBER: US/09/672,607
PRIOR FILING DATE: 2000-09-28
PRIOR FILING DATE: 2000-09-28
PRIOR FILING DATE: 1999-09-30
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Microsoft Office 97
TENNING 1140
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77.9%; Score 14.8; DB 7; Length 1026;
Best Local Similarity 88.9%; Pred. No. 6.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0
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US-10-437-963-56313
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OTHER INFORMATION: unsure at all n locations
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APPLICANT: Cahoon, Edgar B.
APPLICANT: Coughlan, Sean J.
APPLICANT: Helentjaris, Timothy George APPLICANT: Jung, Rudolf
APPLICANT: Li, Chun Ping
APPLICANT: Nichols, Scott
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; Publication No. US20040123343A1
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Publication No. US20030084475A1
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88.9%;
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Best Local Similarity 88.9°
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Oryza sativa
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US-10-437-963-56310/c
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DEPLICANT: LA CONTRIBUTION:
APPLICANT: LA CONTRIBUTION:
APPLICANT: LA CONTRIBUTION:
APPLICANT: ALOU, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: Wei
APPLICANT: Wei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Boukharov, Andrey A.
APPLICANT: Boukharov, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE REPERENCE: 38-21(5321)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT APPLICATION ADMISS: 204966
SEQ ID NOS: 204966
SEQ ID NOS: 204966
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APPLICANT: Li, Ping
APPLICANT: Li, Ping
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPERENCE: 38-21(53221) B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NOS: 204966
LENGTH: 2508
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77.9%; Score 14.8; DB 7;
Best Local Similarity 88.9%; Pred. No. 7.2e+02;
Matches 16; Conservative 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: Clone ID: PAT_MRT4530_81184C.1
US-10-437-963-81682
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US-10-437-963-68811
                                                                                                                                                                          Sequence 81682, Application US/10437963
Publication No. US20040123343A1
GENERAL INFORMATION:
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Publication No. US20040123343A1
GENERAL INFORMATION:
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APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Gao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Boukharov, Andrey A.
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ORGANISM: Oryza sativa
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ORGANISM: Oryza sativa
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                                Sequence 257412, Application US/10027632

Publication No. US20030204075A9

Fublication No. US20030204075A9

GENERAL INFORMATION:

APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
FILE OF INVENTION: Polymorphisms in the Human Genome
FILE REPERENCE: 108827.129

CURRENT APPLICATION NUMBER: US 60/218,006

FRIOR APPLICATION NUMBER: US 60/218,006

FRIOR APPLICATION NUMBER: US 60/198,676

FRIOR FILING DATE: 2000-04-20

FRIOR FILING DATE: 2000-04-20

FRIOR FILING DATE: 2000-04-20

FRIOR FILING DATE: 2000-03-29

FRIOR FILING DATE: 2000-03-29

FRIOR PRICATION NUMBER: US 60/167,363

FRIOR PRICATION NUMBER: US 60/167,363

FRIOR PRICATION NUMBER: US 60/167,363

FRIOR FILING DATE: 1999-09-28

FRIOR FILING DATE: 1999-09-08

FRIOR FILING DATE: 1999-09-08

FRIOR FILING DATE: 1999-08-08

FRIOR FILING DATE: PARESEQ FOR WINDOWN VERSION 4.0
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Best Local Similarity 88.9
Matches 16; Conservative
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Best Local Similarity 88.9
Matches 16; Conservative
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ORGANISM: Oryza sativa
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US-10-437-963-11634/c
                        US-10-027-632-257412
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APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21 (53221) B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 56314
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TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant, Improvement
FILE REFERENCE: 38-21(5321)B
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                                                                                                           Length 2534;
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Pred. No. 7.2e+02;
0; Mismatches 2; Indels 0
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                                                                                                    Score 14.8; DB 10;
Pred. No. 7.2e+02;
0; Mismatches 2;
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US-10-437-963-56314
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CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 58997
LENGTH: 2775
                                                                                                                                                                                                                                                                                                                                                                        Sequence 56314, Application US/10437963
Publication No. US20040123343A1
GENERAL INFORMATION:
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Publication No. US20040123343A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                   1922 CGCTTGAATGCGGCTAAT 1939
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APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Buckharov, Andrey A.
APPLICANT: Barbazuk, Brad
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Boukharov, Andrey A.
                                                                                                    Query Match 77.9%;
Best Local Similarity 88.9%;
Matches 16; Conservative
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88.9%;
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APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
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Best Local Similarity 88.9
Matches 16; Conservative
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ORGANISM: Oryza sativa
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       ; TYPE: DNA
; ORGANISM: DROSOPHILA
US-11-097-143-35308
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TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFRENCE: 39-21(53221) B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 83164
LENGTH: 2525
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TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
TITLE OF INVENTION: DROSOPHILA GENES.
TITLE OF INVENTION: DROSOPHILA GENES.
TITLE REPERENCE: CLOOO728
CURRENT PILING DATE: 2005-04-04
RELOR APPLICATION NUMBER: 60/157,832
PRIOR APPLICATION NUMBER: 60/161,932
PRIOR APPLICATION NUMBER: 60/161,932
PRIOR FILING DATE: 1999-10-19
PRIOR FILING DATE: 1999-10-28
PRIOR APPLICATION NUMBER: 60/161,932
PRIOR APPLICATION NUMBER: 60/164,769
PRIOR APPLICATION NUMBER: 60/164,769
PRIOR APPLICATION NUMBER: 60/175,693
PRIOR APPLICATION NUMBER: 60/175,693
PRIOR APPLICATION NUMBER: 60/175,693
PRIOR PILING DATE: 2000-01-12
PRIOR APPLICATION NUMBER: 60/115,693
PRIOR APPLICATION NUMBER: 60/115,693
PRIOR PILING DATE: 2000-01-12
PRIOR APPLICATION NUMBER: 60/191,637
PRIOR APPLICATION NUMBER: 60/191,637
PRIOR PILING DATE: 2000-03-23
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Pred. No. 7.2e+02;
0; Mismatches 2; Indels 0
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; OTHER INFORMATION: Clone ID: PAT_MRT4530_86136C.1
US-10-437-963-87164
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SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                              Sequence 87164, Application US/10437963
Publication No. US20040123343A1
GENERAL INFORMATION:
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Publication No. US20050208558A1
GENERAL INFORMATION:
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806 CCTTCAATGCGCTAAT 789
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Boukharov, Andrey A.
Barbazuk, Brad
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Best Local Similarity 88.9%;
Matches 16; Conservative
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APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
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ORGANISM: Oryza sativa
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LENGTH: 2534
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APPLICANT: Li, Ping
TITLE OF INVENTION: FLOW BROCIATED OF THE OF INVENTION: Plants and Uses Thereof for Plant Improvement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Venter, J. Craig
APPLICANT: et al.
TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
TITLE OF INVENTION: DROSOPHILA GENES.
CURRENT FLING DATE: 1005-04-04
PRIOR APPLICATION NUMBER: 60/15/,832
PRIOR APPLICATION NUMBER: 60/160,191
PRIOR FILING DATE: 1999-10-19
PRIOR FILING DATE: 1999-10-28
PRIOR FILING DATE: 1999-11-12
PRIOR FILING DATE: 2000-01-12
PRIOR FILING DATE: 2000-01-12
PRIOR APPLICATION NUMBER: 60/175,693
PRIOR FILING DATE: 2000-01-12
PRIOR APPLICATION NUMBER: 60/194,831
PRIOR P
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Pred. No. 7.38+02;
0; Mismatches 2; Indels 0:
                                                                                                          Length 2775;
                                                                                                                                                                                   2; Indels
                                                                                                          Score 14.8; DB 7;
Pred. No. 7.3e+02;
0; Mismatches 2;
; OTHER INFORMATION: Clone ID: PAT_MRT4530_6047C.1
US-10-437-963-58797
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; Sequence 23474, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Exovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Boukharov, Andrey A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 31342, Application US/11097143 Publication No. US20050208558A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                      974 CCCTTCAATGCGGCTAAT 957
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                                                                                                          Query Match 77.9%;
Best Local Similarity 88.9%;
Matches 16; Conservative
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Best Local Similarity 88.9
Matches 16; Conservative
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; ORGANISM: DROSOPHILA
US-11-097-143-31342
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US-11-097-143-31342
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; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT PILING DATE: 2000-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 23474
; LENGTH: 2848
; TYPE: DNA
; OTHER INFORMATION: Clone ID: PAT_MRT4530_28550C.1
US-10-437-963-23474

Query Match
Best Local Similarity 88.9%; Pred. No. 7.38+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Sequence 33, Appl
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Sequence 2701, Ap
Sequence 38314, A
Sequence 152961,
Sequence 37125, A
Sequence 37125, A
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Sequence 43, Appl
Sequence 45, Appl
Sequence 50, Appl
Sequence 50, Appl
Sequence 57, Appl
Sequence 54, Appl
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Sequence 55,
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Sequence 60,
Sequence 53,
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US-10-939-294A-8358
US-10-939-294A-1620
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US-10-939-294A-2653
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US-10-939-594A-2653
US-10-939-594A-1620
US-10-939-182A-80809
US-10-932-182A-80809
US-10-932-182A-80809
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US-11-112-908-38
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US-09-925-065A-259192
US-10-750-185-50407
US-10-750-623-50407
US-10-750-623-50407
US-10-330-773-413
US-11-114-798-55
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US-09-925-065A-605576
US-09-925-065A-153402
US-09-925-065A-430404
US-09-925-065A-430404
US-10-886-517A-4
US-10-886-517A-6
US-10-886-517A-11
US-10-886-517A-11
US-10-886-517A-39
US-10-886-517A-31
US-10-886-517A-31
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US-10-886-517A-48
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US-11-186-284-17 US-11-186-284-17 US-11-096-568A-33272 US-10-750-185-58770 US-10-750-185-58770 US-10-330-773-58170 US-10-330-773-450 US-10-395-561-13490 US-10-395-561-13490 US-10-395-561-13490 US-10-395-561-13490 US-10-310-310-314-404459 US-10-310-310-314-404459 US-10-310-310-314-404459 US-10-310-314-404459 US-10-310-314A-404459 US-10-310-314-404459 US-10-310-314-404459 US-10-310-314A-404459 US-10-310-314-404459 US-10-310-314A-404459 US-10-310-314A-404459 US-10-310-314A-404459 US-10-310-314A-404459 US-10-312-182A-33573 US-10-312-182A-33573 US-10-312-182A-33573 US-10-314-404459 US-10-312-1849-593942 US-10-312-1849-593942 US-10-312-1849-593943 US-10-312-1849-593943 US-10-312-1849-593943 US-10-312-1849-593943 US-10-312-1849-593943 US-10-312-1849-593943 US-10-995-561-569053 US-10-995-561-54899 US-10-995-665A-19809 US-10-995-665A-198039 US-10-995-665A	6 US-09-925-065A-902048 Sequence US-09-925-065A-495017 Sequence US-09-925-065A-495018 Sequence US-09-925-065A-495018 Sequence US-09-925-065A-19691 Sequence US-09-925-065A-146691 Sequence US-09-925-065A-146691 Sequence US-09-925-065A-14691 Sequence US-09-925-065A-14691 Sequence US-09-925-065A-352368 Sequence US-09-925-065A-352368 Sequence US-09-925-065A-352373 Sequence US-09-925-065A-312186 Sequence US-09-925-065A-312186 Sequence US-09-925-065A-35273 Sequence US-09-925-065A-35283 Sequence US-09-925-065A-35283 Sequence US-09-925-065A-35283 Sequence US-09-925-065A-9568 Sequence
\$ 3205 12 US-11-186-284-17 Sequence       4405 8 US-10-750-623-58770 Sequence       5 1266 12 US-11-124-3674-510 Sequence       5 1268 12 US-10-750-623-58770 Sequence       5 1268 12 US-10-730-623-58770 Sequence       5 1268 12 US-10-124-3674-510 Sequence       5 1268 12 US-10-995-561-13490 Sequence       5 1268 12 US-10-995-561-13501 Sequence       5 1268 12 US-10-995-561-13501 Sequence       5 1268 12 US-10-995-561-13501 Sequence       5 12 US-11-121-086-2394 Sequence       5 12 US-11-121-086-2394 Sequence       5 12 US-10-310-3144-502434 Sequence       5 12 US-11-121-849-593941 Sequence       5 13 US-10-995-561-69053 Sequence       5 14 US-11-121-849-593941 Sequence       5 15 US-10-995-561-69053 Sequence       5 15 US-10-995-561-69053 Sequence       5 15 US-10-995-561-69053 Sequence       5 15 US-10-995-6054-140009 Sequence       5 15 US-10-995-6054-140009 Sequence       5 15 US-10-995-6054-140009 Sequence       5 15 US-10-995-0654-140009 Se	9.5 499 6 US-09-925-055A-902048 Sequence (US-09-925-055A-902048) Sequence (US-09-925-055A-95018) Sequence (US-09-925-055A-95018) Sequence (US-09-925-055A-195018) Sequence (US-09-925-055A-146691 Sequence (US-09-925-055A-912186 Sequence (US-09-925-055A-912186 Sequence (US-09-925-055A-912186 Sequence (US-09-925-055A-95581 Sequence (US-09-925-055A-95581 Sequence (US-09-925-055A-95581 Sequence (US-09-925-055A-95581 Sequence (US-09-925-055A-95681 Sequence (US-09-925-055A-95541 Sequence (US-09-925-055A-95681 Sequence (US-09-925-055A-95681 Sequence (US-09-925-055A-95541 Seque
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70.5 3205 12 US-11-186-284-17 Sequence 70.5 3781 9 US-11-056-2863-3327 Sequence 70.5 3781 9 US-11-056-2863-3327 Sequence 70.5 24488 US-10-756-185-58770 Sequence 70.5 24488 US-10-756-185-58770 Sequence 70.5 24488 US-10-124-3674-510 Sequence 70.5 24488 US-10-124-3674-510 Sequence 70.5 24488 US-10-124-3674-510 Sequence 70.5 24488 US-10-124-3674-510 Sequence 70.5 24488 US-10-124-3674-2900 Sequence 70.5 26182 US-10-124-3674-2913 Sequence 70.5 26182 US-10-295-261-5913 Sequence 70.5 26182 US-10-295-26182 US-10-2	3.2 69.5 499 6 US-09-925-055A-902048 Sequence 69.5 501 6 US-09-925-055A-902048 Sequence 69.5 501 6 US-09-925-055A-95018 Sequence 69.5 501 6 US-09-925-055A-95018 Sequence 69.5 501 6 US-09-925-055A-195018 Sequence 69.5 514 6 US-09-925-055A-146691 Sequence 69.5 514 6 US-09-925-055A-146691 Sequence 69.5 514 6 US-09-925-055A-146691 Sequence 69.5 518 6 US-09-925-055A-13254 Sequence 69.5 531 6 US-09-925-055A-133254 Sequence 69.5 531 6 US-09-925-055A-812186 Sequence 69.5 531 6 US-09-925-055A-812186 Sequence 69.5 531 6 US-09-925-055A-812186 Sequence 69.5 532 6 US-09-925-055A-912186 Sequence 69.5 533 6 US-09-925-055A-912

Sequence 63597, A Sequence 69076, Sequence 49051, A Sequence 49051, A Sequence 41171, A Sequence 69096, A Sequence 69096, A Sequence 69096, A Sequence 48718, A Sequence 14869, A Sequence 724006, Sequence 2499, Ap Sequence 2499, Ap Sequence 2499, Ap Sequence 2499, Ap Sequence 78771, A Sequence 78771, A Sequence 78771, A Sequence 2499, Ap Sequence 2499, Ap Sequence 21, Appl Sequenc	nostics A/B 702/495 Length 20; Indels 0; Gaps 0;
8 US-10-750-623-63597 9 US-11-096-569A-19402 6 US-09-925-065A-669076 8 US-10-750-185-49051 8 US-10-750-185-49051 8 US-10-750-185-49171 8 US-10-750-623-49171 8 US-10-932-182A-78469 7 US-10-932-182A-78469 8 US-10-750-623-48718 8 US-10-750-185-48718 8 US-10-750-185-48718 8 US-10-750-185-78769 9 US-10-750-623-48718 8 US-10-750-185-34268 8 US-10-750-185-34268 8 US-10-750-185-34268 8 US-10-750-185-34268 8 US-10-750-185-34268 8 US-10-750-185-34268 8 US-10-750-185-34268 9 US-10-750-185-34268 10 US-10-932-182A-7877 10 US-10-932-182A-7877 10 US-10-932-182A-7877 10 US-10-932-182A-7877 10 US-10-932-182A-7877 10 US-10-932-182A-78156 10 US-10-932-182A-78156 11 US-11-124-37A-104 12 US-11-124-37A-104 12 US-11-124-37A-104 13 US-11-124-30A-78-59 14 US-10-932-182A-78156 15 US-11-124-020A-1 17 US-11-124-020A-1 18 US-10-330-773-669 11 US-11-124-020A-1 19 US-11-124-020A-1 10 US-10-330-773-669	r Multiplex Diag 19,231 for Enterovirus re 19; DB 12; d. No. 0.34; ismatches 0;
69.5 1503 69.5 151503 69.5 1541 69.5 1541 69.5 1716 69.5 1716 69.5 1744 69.5 1755 69.5 1755 69.5 1755 69.5 1807 69.5 1807 69.5 1916 69.5 1950 69.5 1950 69.5 1950 69.5 1950 69.5 1950 69.5 1950 69.5 1950 69.5 1950 69.5 1950 69.5 1950 69.5 1950 69.5 1950 69.5 1950 69.5 1950 69.5 1950 69.5 1950 69.5 1950 69.5 1950 69.5 1950	n No. US20060003352A1   FORMATION:   Lipkin, W. Ian  : Jingyue, Ju  : Jingyue, Ju  : Jingyue, Ju  : Thomas, Briese
459 4659 13.2 4661 13.2 4662 13.2 4663 13.2 4664 13.2 4668 13.2 4670 13.2 471 13.2 474 473 473 473 473 473 473 473 473 473	Publication No. US20060003352A1 GENERAL INFORMATION: APPLICANT: Lipkin, W. Ian APPLICANT: Thomas, Briese APPLICANT: Thomas, Briese TITLE OF INVENTION: MASS TAG FILE REFERENCE: 0575/71310-A CURRENT APPLICATION NUMBER: US/11/1 CURRENT PILING DATE: 2005-04-28 NUMBER OF SEQ ID NOS: 131 SOFTWARE: Patentin version 3.1 SEQ ID NO 99 IENGTH: 20 TYPE: DNA ORANISM: ARTIFICIAL SEQUENCE FATURE: CHER INFORMATION: Forward Primer i-11-119-231-99 Query Match Best Local Similarity 100.0%; Pre Matches 19; Conservative 0; M
RBS SE	A A A A A A A A A A A A A A A A A A A
Sequence 408502, Sequence 408502, Sequence 408503, Sequence 890322, Sequence 883140, Sequence 813108, Sequence 113598, Sequence 413599, Sequence 643040, Sequence 643040, Sequence 724515, Sequence 191472, Sequence 191472, Sequence 191474, Sequence 191474, Sequence 191476, Sequence 191476, Sequence 603524, Sequence 101476, Sequence 101476, Sequence 101476, Sequence 68831, Sequence 101476, Sequence 101476, Sequence 68831, Sequence 68431, Sequence 18855, Sequence 68429, Sequence 68429, Sequence 68431, Sequence 68431, Sequence 68431, Sequence 68431, Sequence 68431, Sequence 68431, Sequence 68431, Sequence 68431, Sequence 68431, Sequence 1315, App Sequence 68431, Sequence 68431, Sequence 1313, App Sequence 1313, App Sequence 1313, App Sequence 1313, App Sequence 1313, App	Sequence 39690, A Sequence 59520, A Sequence 59520, A Sequence 59520, A Sequence 51539, A Sequence 21639, A Sequence 211, Appl Sequence 75354, A Sequence 47794, A Sequence 716239, Sequence 716239, Sequence 716239, Sequence 8553, A Sequence 64773, A Sequence 63597, A Sequence 63597, A
6 US-09-925-065A-727956 6 US-09-925-065A-408502 6 US-09-925-065A-408503 6 US-09-925-065A-408504 6 US-09-925-065A-801322 6 US-09-925-065A-8013108 6 US-09-925-065A-8013108 6 US-09-925-065A-8013108 6 US-09-925-065A-8013108 6 US-09-925-065A-13598 6 US-09-925-065A-13598 6 US-09-925-065A-131598 6 US-09-925-065A-131603 6 US-09-925-065A-131472 6 US-09-925-065A-131472 6 US-09-925-065A-131472 6 US-09-925-065A-131472 6 US-09-925-065A-13108 6 US-09-925-065A-1317206 6 US-09-925-065A-1317206 6 US-09-925-065A-1317206 6 US-09-925-065A-1313206 6 US-09-925-065A-131206 6 US-09-925-065A-1313206 6 US-09-92	US-10-756-623-39690 US-10-756-623-39690 US-10-756-623-59520 US-10-767-627-8131 US-09-925-065A-21639 US-10-921-234-221 US-10-932-182A-75354 US-10-932-182A-75354 US-10-932-182A-75354 US-10-932-182A-75354 US-10-925-065A-716238 US-09-925-065A-716239 US-09-925-065A-716239 US-09-925-065A-716239 US-09-925-065A-716239 US-09-925-065A-716239 US-09-925-065A-716239 US-09-925-065A-86467 US-09-925-065A-86467 US-09-925-065A-86172 US-09-925-065A-86172 US-09-925-065A-86172 US-09-925-065A-86172 US-09-925-065A-86173 US-09-925-065A-864773 US-10-750-18S-64773 US-11-190-188-64773
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Indels

Length 28;

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Query Match 100.0%; Score 19; DB 7; Length 72; Best Local Similarity 100.0%; Pred. No. 0.39; Matches 19; Conservative 0; Mismatches 0; Indels
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APPLICANT: GROEN, JAN
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING
TITLE OF INVENTION: RHINOVIRUSES
FILE REFERENCE: POCS-003
CURRENT PAPLICATION NUMBER: US/10/886,517A
CURRENT FILING DATE: 2004-07-06
NUMBER OF SEQ ID NOS: 74
SOFTWARE: FABLSEQ for Windows Version 4.0
SEQ ID NO 3
LENGTH: 72
APPLICANT: Jingyue, Ju
APPLICANT: Thomas, Briese
TITLE OF INVENTION: Mass Tag PCR For Multiplex Diagnostics
FILE REFERENCE: 0575/71310-A
CURRENT PEPLICATION NUMBER: US/11/119,231
CURRENT FILING DATE: 2005-04-28
NUMBER OF SEQ ID NOS: 131
SOFTWARE: Patentin version 3.1
SEQ ID NO 95
LENGTH: 28
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CURRENT PAPLICATION NUMBER: US/10/886,517A
CURRENT FILING DATE: 2004-07-06
NUMBER OF SEQ ID NOS: 74
                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 100.0%; Score 19; DB 12; Best Local Similarity 100.0%; Pred. No. 0.35; Matches 19; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: FORWARD PRIMER FOR ENTEROVIRUS US-11-119-231-95

; LOCATION: (28)
; OTHER INFORMATION: n = A, T, C or G
US-10-886-517A-3

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-10-886-517A-3
; Sequence 3, Application US/10886517A
; Publication No. US20060008810A1
; GENERAL INFORMATION:
; APPLICANT: LEE, MING-CHOU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 CCCCTGAATGCGGCTAATC 19
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                                                                                                                                                                                                                                                  TYPE: DNA ORGANISM: ARTIFICIAL SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: LEE, MING-CHOU APPLICANT: KONG, LILLY APPLICANT: GROEN, JAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc_feature
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Fublication No. US20060003352A1
GENERAL INFORMATION:
APPLICANT: Lipkin, W. Ian
APPLICANT: Lipkin, W. Ian
APPLICANT: Thomas, Brises
ITILE OF INVENTION: Mass Tag PCR For Multiplex Diagnostics
FILE REFERENCE: 0575/71310-A
CURRENT APPLICATION NUMBER: US/11/119,231
CURRENT FILING DATE: 2005-04-28
NUMBER OF SEQ ID NOS: 131
SOFTWARE: Patentin version 3.1
SEQ ID NO 47
LENGTH: 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; OTHER INFORMATION: Forward Primer for Enterovirus A/B 702/495
US-11-119-231-98
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                                                                                                                                                            Sequence 98, Application US/11119231
Publication No. US20060003352A1
GENERAL INFORMATION:
APPLICANT: Lipkin, W. Ian
APPLICANT: Thomas, Briese
APPLICANT: Thomas, Briese
TITLE OF INVENTION: Mass Tag PCR For Multiplex Diagnostics
FILE REFERENCE: 0575/71310-A
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                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/11/119,231 CURRENT FILING DATE: 2005-04-28 NUMBER OF SEQ ID NOS: 131 SOFTWARE: PATENTIN VERSION 3.1
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CCCCTGAATGCGGCTAATC 19
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Best Local Similarity 100.0
Matches 19; Conservative
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nes 19; Conservative
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Best Local S
Matches 19
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LENGTH: 25
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; APPLICANT: LEE, MING-CHOU
; APPLICANT: GROEN, JAN
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING; TITLE OF INVENTION: RHINOVIRUSES; FILE REFERENCE: FOCS-003; CURRENT APPLICATION NUMBER: US/10/886,517A; CURRENT FILING DATE: 2004-07-06; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 65
                                                                                                   Sequence 61, Application US/10886517A

Publication No. US20060008810A1

FORERAL INFORMATION:
APPLICANT: LEE, MING-CHOU

APPLICANT: KONG, LILLY

TITLE OF INVENTION: RETHOOURUSES

FILE REFERENCE: PCCS-003

CURRENT APPLICATION UNMER: US/10/886,517A

CURRENT FILING DATE: 2004-07-06

NUMBER OF SEQ ID NOS: 74

SOFTWARE: FASTERQ for Windows Version 4.0

SEQ ID NO 61
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Publication No. US20060008810A1
GENERAL INFORMATION:
APPLICANT: LEE, MING-CHOU
APPLICANT: GROEN, JAN
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING
TITLE OF INVENTION: RETHOUSES
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Best Local Similarity 100.0
Matches 19; Conservative
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US-10-886-517A-61
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Best Local Similarity
Matches 19; Conserv
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Sequence 49, Application US/10886517A

Publication No. US20060008810A1

GENERAL INFORMATION:

APPLICANT: LEE, MING-CHOU

APPLICANT: KONG, LILLY

APPLICANT: GROEN, JAN

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING

TITLE OF INVENTION: RHINOVIRUSES

TITLE OF INVENTION: RHINOVIRUSES

CURRENT APPLICATION NUMBER: US/10/886,517A

CURRENT PILING DATE: 2004-07-06

NUMBER OF SEQ ID NOS: 74

SOFTWARE: FastSEQ for Windows Version 4.0

LENGTH: 117
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| Sequence 59, Application No. US20060008810A1
| GENERAL INFORMATION:
| APPLICANT: LEE, MING-CHOU
| APPLICANT: KONG, LILLY
| APPLICANT: GROEN, JAN
| TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING
| TITLE OF INVENTION: RHINOVIRUSES
| FILE REFERENCE: FOCS-003
| CURRENT APPLICATION NHERS: US/10/886,517A
| CURRENT FILING DATE: 2004-07-06
| NUMBER OF SEQ ID NOS: 74
| SOFTWARE: FASELSEQ for Windows Version 4.0
| SEQ ID NO 59
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                                                                                                                                                      Query Match 100.0%; Score 19; DB 7; Length 117; Best Local Similarity 100.0%; Pred. No. 0.41; Matches 19; Conservative 0; Mismatches 0; Indels
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SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                   TYPE: DNA ORGANISM: human rhinovirus
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ORGANISM: human rhinovirus
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Matches 19; Conserva
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                    SEQ ID NO 41
LENGTH: 117
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Publication No. US20060008810A1
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; GENERAL INFORMATION:
; APPLICANT: LEE, MING-CHOU
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                                           1 CCCCTGAATGCGGCTAATC 19
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Best Local Similarity 100.0%;
Matches 19; Conservative 0
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Best Local Similarity 100.
Matches 19; Conservative
     19; Conservative
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APPLICANT: LEE, MING-CHOU
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US-10-886-517A-66
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US-10-886-517A-67
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Bublication No. US20060008810A1

GENERAL INFORMATION:

APPLICANT: LEE, MING-CHOU

APPLICANT: GROEN, LILLY

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING

TITLE OF INVENTION: RHINOVIRUSES

FILE REFERENCE: FOCS-003

CURRENT FAPILICATION NUMBER: US/10/886,517A

CURRENT FILING DATE: 2004-07-06

NUMBER OF SEQ ID NOS: 74

SOFTWARE: PASES for Windows Version 4.0

SEQ ID NO 64

LENGTH: 118
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Publication No. US20060008810A1
GENERAL INFORMATION:
APPLICANT: LEE, MING-CHOU
APPLICANT: KONG, LILLY
APPLICANT: GROEN, JAN
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING
TITLE OF INVENTION: RHINOVIRUSES
FILE REFERENCE: FOCS-003
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               CURRENT APPLICATION NUMBER: US/10/886,517A;
CURRENT FILING DATE: 2004-07-06;
NUMBER OF SEQ ID NOS: 74
; SEQ ID NO 62;
LENGTH: 118
; TYPE: DNA
; ORGANISM: enterovirus
US-10-886-517A-62
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CURRENT FILING DATE: 2004-07-06
NUMBER OF SEQ ID NOS: 74
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 118
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100.0%; Score 19;
Best Local Similarity 100.0%; Pred. No. (
Matches 19; Conservative 0; Mismatche
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FILE REFERENCE: FOCS-003
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CORGANISM: enterovirus
US-10-886-517A-64
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Matches 19; Conserv
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Best Local Similarity
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US-10-886-517A-63
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| Sequence 67, Application US/10886517A
| Publication No. US20060008810A1
| GENERAL INFORMATION:
| APPLICANT: LEE, MING-HOU
| APPLICANT: KONG, LILLY
| APPLICANT: GROEN, JAN
| TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING
| TITLE OF INVENTION: METHODS (STITLE OF INVENTION: PHILE REFERENCE: FOCS-003
| CURRENT APPLICATION NUMBER: US/10/886,517A
| CURRENT FILING DATE: 2004-07-06
| NUMBER OF SEQ ID NOS: 74
| SEQ ID NO 67
| LENGTH: 118
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                                                                                                                                                                                                                                                                                                                                                      APPLICANT: KONG, LILLY
APPLICANT: KONG, LILLY
APPLICANT: GROEN, JAN
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING
TITLE OF INVENTION: RHINOVIRUSES
FILE REFERENCE: FOCS-003
CURRENT PAPLICATION NUMBER: US/10/886,517A
CURRENT FILLING DATE: 2004-07-06
NUMBER OF SEQ ID NOS: 74
SOFTHARE: PASLEEQ for Windows Version 4.0
SEQ ID NO 66
LENGTH: 118
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US-10-886-517A-70
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| Sequence 70, Application US/10886517A
| Publication No. US20060008810A1
| GENERAL INFORMATION:
| APPLICANT: LDE, MING-CHOU
| APPLICANT: KONG, LILLY
| APPLICANT: GROEN, JAN
| TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING
| TITLE OF INVENTION: RHINOVIRUSES
| TITLE OF INVENTION: THINOVIRUSES:
| UNREBRY FILLING DATE: 2004-07-06
| NUMBER OF SEQ ID NOS: 74
| SOFTWARE: FastSEQ for Windows Version 4.0
| SEQ ID NO 70
| LENGTH: 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 69, Application US/10886517A; Sequence 69, Application US/10886517A; Bublication No. US20060008810A1; GENERAL INFORMATION:

APPLICANT: LEE, MING-CHOU
APPLICANT: GROEN, JAN
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING; TITLE OF INVENTION: RHINOVIRUSES; FILE REFERENCE: FOCS-003; CURRENT APPLICATION NUMBER: US/10/886,517A; CURRENT FILING DATE: 2004-07-06; NUMBER OF SEQ ID NOS: 74; SOFTWARE: FastSEQ for Windows Version 4.0; TEMPLY 100 69; SEQ ID NO 69; TEMPLY 100 60; TEMPLY 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 100.0%; Score 19; DB 7; Length 118; Best Local Similarity 100.0%; Pred. No. 0.41; Matches 19; Conservative 0; Mismatches 0; Indels
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APPLICANT: KONG, LILLY
APPLICANT: GROEN, JAN
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING
TITLE OF INVENTION: METHODYRUSES
FILE REFERENCE: FOCS-003
CURRENT APPLICATION NUMBER: US/10/886,517A
CURRENT FILING DATE: 2004-07-06
NUMBER OF SEQ ID NOS: 74
SOFTWARE: FABELSEQ for Windows Version 4.0
SEQ ID NO 68
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; ORGANISM: enterovirus
US-10-886-517A-68
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Best Local Similarity
Matches 19; Conserv?
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Sequence 137, Application US/11155478A

Sequence 137, Application US/20060014140A1

Sequence 137, Application NO. US20060014140A1

SEQUENCE 101 VOLUERSTRON:

APPLICANT: Boivin, Guy

APPLICANT: Boivin, Guy

TITLE OF INVENTION: RESPIRATORY VIRUSES

TITLE OF INVENTION: RESPIRATORY VIRUSES

TITLE OF INVENTION: RESPIRATORY VIRUSES

TITLE OF INVENTION: UNMBER: US/11/155,478A

CURRENT FILING DATE: 2005-06-20

PRIOR PAPLICATION NUMBER: CA 2,411,264

PRIOR PAPLICATION NUMBER: CA 2,411,264

PRIOR PAPLICATION NUMBER: CA 2,418,004

PRIOR PAPLICATION NUMBER: CA 2,418,004

PRIOR PAPLICATION NUMBER: PT/CA2003/001994

PRIOR PILING DATE: 2003-10-24

PRIOR PILING DATE: 2003-10-24

PRIOR FILING DATE: 2003-10-24

PRIOR PILING DATE: 2003-10-24

PRIOR FILING DATE: 2003-12-19

NUMBER OF SEQ ID NOS: 174

SEQ ID NO 137

LENGTH: 810
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Publication No. US20060008810A1

GENERAL INFORMATION:
APPLICANT: EAST MING-CHOU

APPLICANT: GROEN, JILLY

TITLE OF INVENTION: RHINOVIRUSES

TITLE OF INVENTION: RHINOVIRUSES

FILE REFERENCE: FOCS-003

CURRENT APPLICANTE: 2004-07-06

NUMBER OF SEQ ID NOS: 74

SEQ ID NO 71

LENGTH: 118
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                    100.0%; Score 19; DB 7; Length 118; 100.0%; Pred. No. 0.41;
                                                                          0; Mismatches
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; OTHER INFORMATION: human Enterovirus
; OTHER INFORMATION: strain Coxakievirus B1
; OTHER INFORMATION: accession number m16560
US-11-155-478A-137
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Query Match
Best Local Similarity 100.v
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Gaps
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US-10-886-517A-5
Sequence 5, Application US/10886517A
Publication No. 1220060008810A1
SEGUENT STATEM OF SEQUENCE STATEM OF SEGUENCE SEGUENCE STATEM OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING STATEM OF SEGUENCE FOCS-003
CURRENT APPLICATION NUMBER: US/10/886,517A
CURRENT APPLICATION NUMBER: US/10/886,517A
CURRENT FILING DATE: 2004-07-06
NUMBER OF SEGUENCE STATEM OF SEGUENC
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94.7%; Score 18; DB 7; Length 73;
Best Local Similarity 94.7%; Pred. No. 1.5;
Matches 18; Conservative 0; Mismatches 1; Indels
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LOCATION: (65)...(65)
OTHER INFORMATION: n = A or C
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LOCATION: (69)...(69)
OTHER INFORMATION: n = A or G
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! LOCATION: (70)...(70)
! OTHER INFORMATION: n = C or G
US-10-886-517A-4
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OTHER INFORMATION: n = A or T
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OTHER INFORMATION: n = C or T
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OTHER INFORMATION: n = C or
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THER INFORMATION: n = C
             NAME/KEY: misc_feature
LOCATION: (59)...(59)
OTHER INFORMATION: n = C
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THER INFORMATION: n = T
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LOCATION: (66) ... (66)
OTHER INFORMATION: n =
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NAME/KEY: misc_feature
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NAME/KEY: misc_feature
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LOCATION: (11)...(11)
OTHER INFORMATION: n =
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ORGANISM: enterovirus
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Sequence 4, Application US/10886517A

GENERAL INFORMATION:

APPLICANT: LEE, MING-CHOU

APPLICANT: GROEN, JAN

TITLE OF INVENTION: METHODS AND COMPOSITIONS POR DETECTING

TITLE OF INVENTION: METHOD AND COMPOSITIONS POR DETECTING

TITLE OF INVENTION AND COMPOSITIONS POR DETECTION AND COMPOSITIONS P
Query Match
Best Local Similarity 100.0%; Pred. No. 0.51;
Matches 19; Conservative 0; Mismatches 0; Indels (
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MIHER INFORMATION: n = A, T, C, or G
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OTHER INFORMATION: n = A, C, or G
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HER INFORMATION: n = G or C
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THER INFORMATION: n = G or A
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ORGANISM: human rhinovirus
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SR INFORMATION: n = C
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OTHER INFORMATION: n = T
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GCATION: (19)...(19)
THER INFORMATION: n = T
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LOCATION: (33)...(33)
OTHER INFORMATION: n = G
FEATURE:
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R INFORMATION: n = C
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THER INFORMATION: n = T
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OTHER INFORMATION: n = G
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FEATURE:

MAME/KEY: misc_feature

LOCATION: (28)...(28)

OTHER INFORMATION: n = A, T, C or
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LOCATION: (67)...(67)
OTHER INFORMATION: n = A or G
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OTHER INFORMATION: n = G or T
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LOCATION: (33)...(33)
OTHER INFORMATION: n = A or G
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LOCATION: (30)...(30)
OTHER INFORMATION: n = A or
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NAME/KEY: misc_feature
LOCATION: (66)...(66)
OTHER INFORMATION: n = C or
                                                     FEATURE:
NAME/KEY: misc_feature
LOCATION: (14) ... (14)
OTHER INFORMATION: n = T
FEATURE:
NAME/KEY: misc_feature
LOCATION: (15) ... (15)
OTHER INFORMATION: n = A
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OTHER INFORMATION: n = T
NAME/KEY: misc_feature
LOCATION: (12)...(12)
OTHER INFORMATION: n = C
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LOCATION: (65)...(65)
OTHER INFORMATION: n = C
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LOCATION: (68)...(68)
OTHER INFORMATION: n = C
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LOCATION: (69)...(69)
OTHER INFORMATION: n = G
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LOCATION: (16)...(16)
OTHER INFORMATION: n = T
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LOCATION: (19)...(19)
OTHER INFORMATION: n = A
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LOCATION: (59)...(59)
OTHER INFORMATION: n = T
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OTHER INFORMATION: n = C
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Sequence 6, Application US/10886517A;
Publication No. US20060008810A1;
GENERAL INFORMATION:
APPLICANT: CROMS, LILLY
APPLICANT: GROEN, JAN
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING;
TITLE OF INVENTION: RHINOVIRUSES;
FILE REFERENCE: FOCS-003;
CURRENT APPLICATION NUMBER: US/10/886,517A;
CURRENT APPLICATION NUMBER: US/10/886,517A;
CURRENT FILING DATE: 2004-07-06;
NUMBER OF SEQ ID NOS: 74
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 6;
LENGTH: 73
TYPE: DNA
TYPE: DNA
REATTHE.
Score 18; DB 7; Length 73;
Pred. No. 1.5;
                                         1; Indels
                                           0; Mismatches
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LOCATION: (15)...(15)
OTHER INFORMATION: n = T, C or G
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LOCATION: (33)...(33)
OTHER INFORMATION: n = T, G or C
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OTHER INFORMATION: n = A, G or C
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OTHER INFORMATION: n = A, C or G
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                                                                                                             42 CCCTGAATGCGGCTAANC 60
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LOCATION: (12)...(12)
OTHER INFORMATION: n = C or T
Query Match
Best Local Similarity 94.7%;
Matches 18; Conservative (
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OTHER INFORMATION: n = A,
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OTHER INFORMATION: n = A,
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OTHER INFORMATION: n = A,
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OTHER INFORMATION: n = A,
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OTHER INFORMATION: n = G
FEATURE:
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OTHER INFORMATION: n =
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US-10-886-517A-6
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AME/KEY: misc feature OCATION: (28) ... (28) THER INFORMATION: n = A, T, C or
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THER INFORMATION: n = A, C or G
INFORMATION: n = G or C
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THER INFORMATION: n = G or A
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THER INFORMATION: n = A or C
                                                       OCATION: (12)...(12)
THER INFORMATION: n = C or
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OCATION: (68)...(68)
THER INFORMATION: n = C or
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THER INFORMATION: n = A or
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OCATION: (15)...(15)
THER INFORMATION: n = C
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THER INFORMATION: n = G
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THER INFORMATION: n = A
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THER INFORMATION: n = G
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OCATION: (59)...(59)
THER INFORMATION: n = C
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INFORMATION: n = T
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THER INFORMATION: n = T
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INFORMATION: n =
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LOCATION: (67)...(67)
THER INFORMATION: n =
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OCATION: (19)...(19)
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OTHER INFORMATION: n =
                                     AME/KEY: misc_feature
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AME/KEY: misc_feature
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JOCATION: (16)...(16)
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NAME/KEY: misc_feature
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APPLICANT: GROEN, JAN
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING
TITLE OF INVENTION: RHINOVIRUSES
FILE REPERENCE: FOCS-003
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CURRENT FILING DATE: 2004-07-06
NUMBER OF SEQ ID NOS: 74
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 11
LENGTH: 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 11, Application US/10886517A Publication No. US20060008810A1 GENERAL INFORMATION:
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LOCATION: (65)...(65)
OTHER INFORMATION: n = A or C
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NAME/KEY: misc feature
LOCATION: (69)...(69)
OTHER INFORMATION: n = A or G
FEATURE:
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                                                                                                                                                                     NAME/KEY: misc feature
LOCATION: (62)...(62)
THER INFORMATION: n = A or T
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LOCATION: (68)...(68)
OTHER INFORMATION: n = C or T
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Best Local Similarity 94.7%;
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                              AME/KEY: misc feature
ACATION: (66)...(66)
WHER INFORMATION: n = A, G,
                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: misc feature
LOCATION: (67) ... (67)
OTHER INFORMATION: n = T, G
                                   LOCATION: (59)...(59)

OTHER INFORMATION: n = A, C
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ORGANISM: human rhinovirus
                                                                                                             ION: (61)...(61)
INFORMATION: n = A,
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LOCATION: (5)...(5)
OTHER INFORMATION: n = T
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LOCATION: (61)...(61)
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LOCATION: (11)...(11)
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Sequence 30, Application US/10886517A

Publication No. US2006008810A1

GENERAL INFORMATION:

APPLICANT: IEEE, MING-CHOU

APPLICANT: GROEN, JAN

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING

TITLE OF INVENTION: RHINOVIRUSES

FILE REFERENCE: POCS-003

CURRENT APPLICATION NUMBER: US/10/886,517A

CURRENT FILIAGO BATE: 2004-02'-06

NUMBER OF SEQ ID NOS: 74

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 30
                                                                                                                                                                                                                                                                                       | Sequence 29, Application US/10886517A |
| Sequence 29, Application US/10886517A |
| Publication No. US20060008810A1 |
| APPLICANT: LEE, MING-CHOU |
| APPLICANT: EEE, MING-CHOU |
| APPLICANT: GROEN, JAN |
| TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING |
| TITLE OF INVENTION: RHINOVIRUSES |
| FILE REFERENCE: FOCS-003 |
| FILE REFERENCE: EOCS-003 |
| CURRENT APPLICATION NUMBER: US/10/886,517A |
| CURRENT FILING DATE: 2004-07-06 |
| NUMBER OF SEQ ID NOS: 74 |
| SOFTWARE: FASTERQ for Mindows Version 4.0 |
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                               Indels
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Best Local Similarity 78.9%; Pred. No. 3.2; Matches 15; Conservative 3; Mismatches
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                                                                                                                            41 CCCCUGAAUGCGGCUAACC 59
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                                                                                         1 CCCCTGAATGCGGCTAATC 19
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Best Local Similarity 94.7%;
Matches 18; Conservative
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CRGANISM: human rhinovirus
US-10-886-517A-29
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ORGANISM: human rhinovirus
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Matches 18; Conservative
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Sequence 1, Application US/10886517A;
Publication No. US20060008810A1
SERNERAL INFORMATION:
APPLICANT: LEE, MING-CHOU
APPLICANT: KONG, LILLY
ITILE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING
ITILE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING
TITLE OF INVENTION: RHINOVIRUSES
TITLE OF INVENTION: RHINOVIRUSES
CURRENT APPLICATION NUMBER: US/10/886,517A
CURRENT FILING DATE: 2004-07-06
NUMBER OF SEQ ID NOS: 74
SOFTWARE: FABELSEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 72
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publication No. US20060008810A1

GENERAL INPOWARTON:
APPLICANT: LEB. MINO-CHOU
APPLICANT: GORN, JAM
TITLE OF INVENTION: RHINOVIRUSES
FILE REFERENCE: FOCS-003
CURRENT APPLICATION NUMBER: US/10/886,517A
CURRENT FILING DATE: 2004-07-06
NUMBER OF SEQ ID NOS: 74

SOFTWARE: PASSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 72
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Pred. No. 3.2;
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                                                            94.7%; Score 18; DB 7; Length 73; 94.7%; Pred. No. 1.5; ive 0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
NAME/KEY: misc_feature
LOCATION: 28
COTHER INFORMATION: n = A,T,C or G
US-10-886-517A-1
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; LOCATION: (28)...(28)
; OTHER INFORMATION: n = A,U,C or G
US-10-886-517A-2
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ORGANISM: Artificial Sequence
                                                            Query Match
Best Local Similarity 94.7
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 94.7
Matches 18; Conservative
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ORGANISM: human rhinovirus
   US-10-886-517A-11
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                                                                 Score 17.4; DB 7; Length 118; Pred. No. 3.4; 0; Mismatches 1; Indels
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APPLICANT: KONG, LILLY
APPLICANT: KONG, LILLY
APPLICANT: GROEN, JAN
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING
TITLE OF INVENTION: RHINOVIRUSES
FILE REFERENCE: FOCS-003
CURRENT APPLICATION NUMBER: US/10/886,517A
CURRENT FILING DATE: 2004-07-06
NUMBER OF SEQ ID NOS: 74
SOFTWARE: FASTESQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING TITLE OF INVENTION: RHINOVIRUSES FILE REFERENCE: POCS-003 CURRENT APPLICATION NUMBER: US/10/886,517A CURRENT FILING DATE: 2004-07-06
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Pred. No. 3.4;
0; Mismatches
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Pred. No. 3.
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 36
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; Sequence 36, Application US/10886517A
; Publication No. US20060008810A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 37, Application US/10886517A Publication No. US20060008810A1 GENERAL INFORMATION:
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                                                             Query Match
Best Local Similarity 94.7%;
Matches 18; Conservative
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94.7%;
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ilarity 94.7%;
Conservative
    ; ORGANISM: human rhinovirus
US-10-886-517A-34
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ORGANISM: human rhinovirus
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Best Local Similarity 94.7
Matches 18; Conservative
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                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: KONG, LILLY APPLICANT: GROEN, JAN
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Best Local Similarity
Matches 18; Conserv
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APPLICANT: LEE, MING-CHOU
APPLICANT: ERE, MING-CHOU
APPLICANT: RONG, LILLY
APPLICANT: RONG, LILLY
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING
TITLE OF INVENTION: RAINOVIRUSES
FILE REFERENCE: FOCS-003
CURRENT APPLICATION NUMBER: US/10/886,517A
CURRENT FILING DATE: 2004-07-06
NUMBER OF SEQ ID NOS: 74
SOFTWARE: FastSEQ for Windows Version 4.0
                               APPLICANT: GROSH, JAN
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING
TITLE OF INVENTION: METHODYRUSES
FILE REPERRANCE: POCS-003
FURENT APPLICATION NUMBER: US/10/886,517A
CURRENT FILING DATE: 2004-07-06
NUMBER OF SEQ ID NOS: 74
SOFTWARE: FASTSEQ for Windows Version 4.0
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Publication No. US20060008810A1
GENERAL INFORMATION:
APPLICANT: LEE, MINO-CHOU
APPLICANT: GROEN, JAN
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING
FILE REFERENCE: FOCS-003
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Pred. No. 3.
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Pred. No. 3.
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CURRENT FILING DATE: 2004-07-06
NUMBER OF SEQ ID NOS: 74
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 34
LENGTH: 118
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Best Local Similarity 94.7%;
Matches 18; Conservative
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US-10-886-517A-31
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; ORGANISM: human rhinovirus
US-10-886-517A-33
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Best Local Similarity 94.7
Matches 18; Conservative
LEE, MING-CHOU
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LENGTH: 118
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APPLICANT:
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1 CCCCTGAATGCGGCTAATC 19
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| Sequence 35. Application No. US2006000810A1
| GENERAL INFORMATION:
| APPLICANT: LEE, MING-CHOU
| APPLICANT: KONG, LILLY
| APPLICANT: GROSN, LILLY
| TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING
| TITLE OF INVENTION: RHINOVIRUSES
| FILE REFERRICE: FOCS-003
| CURRENT FILLING DATE: 2004-07-06
| NUMBER OF SEQ ID NOS: 74
| SOFTWARE: FastSEQ for Windows Version 4.0
| SEQ ID NO 35
| LENGTH: 119
US-10-886-517A-28
; Sequence 28, Application US/1086517A
; Dublication Vo. US20060008810A1
; GENERAL INFORMATION:
; APPLICANT: LEE, MING-CHOU
; APPLICANT: GROEN, JAN
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING
; TITLE OF INVENTION: MINGRES
; FILE REFERENCE: FOCS-ON
; FILE REPERENCE: FOCS-ON
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PSSESEQ for Windows Version 4.0
; SEQ ID NO 28
; LENGTH: 119
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Pred. No. 3.4;
0; Mismatches 1; Indels C
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Pred. No. 3.4;
0; Mismatches 1; Indels (
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Publication No. US20060008810A1
GENERAL INFORMATION:
APPLICANT: KONG, LILLY
APPLICANT: KONG, LILLY
APPLICANT: GROEN, JAN
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING
TITLE REFERENCE: FOCS-003
FILLE REFERENCE: FOCS-003
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Best Local Similarity 94.7%;
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 94.7%;
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                             ; TYPE: DNA; ORGANISM: human rhinovirus
US-10-886-517A-28
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Publication No. US20060008810A1

SERERAL INFORMATION:
APPLICANT: KONG, LILLY
APPLICANT: GROSN, JAN
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING
TITLE OF INVENTION: RHINOVIRUSES
FILE REFERENCE: FOCS-003
CURRENT FILING DATE: 2004-07-06
NUMBER OF SEQ ID NOS: 74
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 17.4; DB 7; Length 119;
Pred. No. 3.4;
0; Mismatches 1; Indels 0
                                                                                                                                                                                                                                                                                                                                                                        Sequence 42, Application US/10886517A

Sequence 42, Application US/10886517A

Publication No. US20060008810A1

GENERAL INFORMATION:

APPLICANT: LEE, MING-CHOU

APPLICANT: GROEN, JAN

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING

TITLE OF INVENTION: RHINOVIRUSES

FILE REPERENCE: FOCS-003

CURRENT FILING DATE: 2004-07-06

NUMBER OF SEQ ID NOS: 74

SOFTWARE: FASTERO for Windows Version 4.0

SEQ ID NO 42.
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                                                                                                                                              Score 17.4; DB 7; Length 119;
Pred. No. 3.4;
0; Mismatches 1; Indels
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SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 39 LENGTH: 119
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Best Local Similarity 94.7%;
Matches 18; Conservative (
                                                                                                                                                     Query Match 91.6%;
Best Local Similarity 94.7%;
Matches 18; Conservative
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                                                                TYPE: DNA ORGANISM: human rhinovirus
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Matches 18; Conservative
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91.6%;
94.7%;
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Best Local Similarity 94.7°
Matches 18; Conservative
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CRGANISM: human rhinovirus
US-10-886-517A-56
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Best Local Similarity 94.77
Matches 18, Conservative
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ORGANISM: human rhinovirus
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Best Local Similarity
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Pred. No. 3.4;
0; Mismatches 1; Indels
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                                                                                                                                                                                                                       TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING TITLE OF INVENTION: RHINOVIRUSES FILE REPERBRUE: FOCS-003 CURRENT APPLICATION NUMBER: US/10/886,517A CURRENT FILING DATE: 2004-07-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 55. Application US/10886517A
Publication No. US20060008810A1
GENERAL INFORMATION:
APPLICANT: LEE, MING-CHOU
APPLICANT: KONG, LILLY
APPLICANT: GROEN, JAN
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING
TITLE OF INVENTION: RETHONVIRUSES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: LEE, MING-CHOU
APPLICANT: KOG, LILLY
APPLICANT: GROEN, JAN
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING
FILE REPERENCE: FOCS-003
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Pred. No. 3.4;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 74
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                     Sequence 47, Application US/10886517A Publication No. US20060008810A1
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62 CCCCTGAATGCGGCTAACC 80
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Best Local Similarity 94.7%;
Matches 18; Conservative
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Best Local Similarity 94.7%;
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA ORGANISM: human rhinovirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TYPE: DNA; ORGANISM: human rhinovirus
US-10-886-517A-51
                                                                                                                                       GENERAL INFORMATION:
APPLICANT: LEE, MING-CHOU
APPLICANT: KONG, LILLY
APPLICANT: GROEN, JAN
                                                                               US-10-886-517A-47
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LENGTH: 119
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| Sequence 56, Application US/10886517A
| Publication No. US2006000810A1
| GENERAL INFORMATION:
| APPLICANT: LEE. MING-CHOU
| APPLICANT: GROSE, LILLY
| APPLICANT: GROSE, LILLY
| TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING
| TITLE OF INVENTION: RHINOVIRUSES
| TITLE OF INVENTION: RHINOVIRUSES
| TITLE OF INVENTION: RHINOVIRUSES
| TITLE OF INVENTION: WITHOUT US/10/886,517A
| CURRENT APPLICATION NUMBER: US/10/866,517A
| CURRENT FILING DATE: 2004-07-06
| NUMBER OF SEQ ID NOS: 74
| SOFTWARE: FastSEQ for Windows Version 4.0
| SEQ ID NO 56
| LENGTH: 119
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APPLICANT: GROEN, JAN
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING
TITLE OF INVENTION: RHINOVIRUSES
FILE REFERENCE: FOCS-003
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Pred. No. 3.4;
0; Mismatches
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0; Mismatches
FILE REFERENCE: FOCS-003
CURRENT APPLICATION NUMBER: US/10/886,517A
CURRENT FILING DATE: 2004-07-06
NUMBER OF SEQ ID NOS: 74
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 55
LENGTH: 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 58, Application US/10886517A Publication No. US20060008810A1 GENERAL INFORMATION:
APPLICANT: LEE, MING-CHOU
                                                                                                                                                                                                                                                                                                                                                                                             1 CCCCTGAATGCGGCTAATC 19
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94.7%;
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TYPE: DNA
ORGANISM: human rhinovirus
FERATURE:
NAME/KEY: misc feature
LOCATION: 61, 135, 136, 137, 138, 139, 167, 203, 224, 225, 231, 232,
LOCATION: 284, 336, 390
OTHER INFORMATION: n = A,T,C or G
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Pred. No. 4;
0; Mismatches 1; Indels (
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Publication No. US20050265975A1
GENERAL INPORMATION:
APPLICANT: Miles, Vincent J.
APPLICANT: Mathews, Michael B.
APPLICANT: Witherell, Gary
APPLICANT: Witherell, Gary
TITLE OF INVENTION: METHOD FOR SELECTIVE INACTIVATION
TITLE OF INVENTION: OF VIRAL REPLICATION
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
                            APPLICANT: GROEN, JAN
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING
TITLE OF INVENTION: RHINOVIRUSES
FILE REFERENCE: FOCS-003
CURRENT APPLICATION NUMBER: US/10/886,517A
CURRENT FILING DATE: 2004-07-06
NUMBER OF SEQ ID NOS: 74
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 21
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STATE: New York

COUNTY: USA
ZIP: 10036/2711

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette

COMPUTER: Estabable Form:
MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSEQ Version 2.0

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/11/195,109

FILING DATE: 01-Aug-2005

CLASSIFICATION NUMBER: US/10/109,368

FILING DATE: 14-Jun-2004

APPLICATION NUMBER: US/10/109,368

FILING DATE: 37-Mar-2002

APPLICATION NUMBER: US/10/109,368

FILING DATE: 17-Mar-2002

APPLICATION NUMBER: US/10/109,368

FILING DATE: 17-Mar-2002

APPLICATION NUMBER: US/10/109,368

FILING DATE: US/NGWATION:
NAME: OF-APR-1994
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STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Coruzzi, Laura A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7960-030
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              297 ¢cccrcaarccccraacc 315
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Best Local Similarity 94.7%;
Matches 18; Conservative (
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(212) 869-8864
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                                                                                                                                                                                                                                                                                    Sequence 60, Application US/1086517A;
Sequence 60, Application US/1086517A;
Publication No. US20060008810A1;
GENERAL INFORMATION:
APPLICANT: KONG, LILLY
APPLICANT: KONG, LILLY
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING;
TITLE OF INVENTION: RHINOVIRUSE
FILE REFERENCE: FOCS-003
CURRENT APPLICATION NUMBER: US/10/886,517A
CURRENT APPLICATION NUMBER: 2004-07-06
NUMBER OF SEQ ID NOS: 74
SOFTWARE: FESTERE 2004-07-06
SEQ ID NO 60
LENGTH: 119
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| Sequence 53, Application US/10886517A
| Publication No. US20060008810A1
| GENERAL INPOWATION:
| APPLICANT: LEE, MING-CHOU
| APPLICANT: KONG, LILLY
| APPLICANT: KONG, LILLY
| TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING
| TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING
| TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING
| TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING
| TITLE OF INVENTION: MANBER: US/10/886,517A
| CURRENT APPLICATION NUMBER: US/10/886,517A
| WUMBER OF SEQ ID NOS: 74
| SOFTHARE: FREEERENCY
| SOFTHARE: FREEERENCY
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1; Indels
   0; Mismatches
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GENERAL INFORMATION: APPLICANT: LEE, MING-CHOU
                                                                       1 CCCCTGAATGCGGCTAATC 19
                                                                                                                                        ccccreaargcggcraacc 80
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Best Local Similarity 94.7%;
Matches 18; Conservative
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ORGANISM: human rhinovirus
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ORGANISM: human rhinovirus
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Matches 18; Conservative
   18; Conservative
                                                                                                                                                                                                                                            RESULT 44
US-10-886-517A-60
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US-10-886-517A-21
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   Matches
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DB 7; Length 73;
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Publication No. US20060008810A1
GENERAL INFORMATION:
APPLICANT: LEE, MING-CHOU
APPLICANT: KONG, LILLY
APPLICANT: GROEN, JAN
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING
TITLE OF INVENTION: RHINOVIRUSES
FILE REFERENCE: PCCS-003
CURRENT APPLICATION NUMBER: US/10/886,517A
CURRENT FILING DATE: 2004-07-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   199.5%; Score 17; DB ilarity 89.5%; Pred. No. 5.5; Conservative 0; Mismatches
                                                                                                                                                                                                                                    LOCATION: (52)...(52)
OTHER INFORMATION: n = A,C,T or G
                                                                                                                                                   LOCATION: (33)...(33)
OTHER INFORMATION: n = T, C or G
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INFORMATION: n = T, G or C
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LOCATION: (62)...(62)
OTHER INFORMATION: n = A or
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          INFORMATION: n = A,
                                                                        CCATION: (31)...(31)

THER INFORMATION: n = A,
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COCATION: (66)...(66)
THER INFORMATION: n = A,
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OTHER INFORMATION: n = A,
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OTHER INFORMATION: n = A,
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LOCATION: (65)...(65)
OTHER INFORMATION: n = A
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OTHER INFORMATION: n = C
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INFORMATION: n = A
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LOCATION: (59)...(59)
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LOCATION: (61)...(61)
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LOCATION: (68)...(68)
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Best Local Similarity
Matches 17; Conserva
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                                                                                                                                                                                                            Score 17.4; DB 12; Length 627; Pred. No. 4.1; 3; Mismatches 1; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 7, Application US/10886517A
Fublication No. US20060008810A1
GENERAL INFORMATION:
APPLICANT: LEE, MING-CHOU
APPLICANT: GROEN, LILLY
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING
TITLE OF INVENTION: MHINOVIRUSES
CURRENT FPLICATION NUMBER: US/10/886,517A
CURRENT FILING DATE: 2004-07-06
NUMBER OF SEQ ID NOS: 74
SOFTWARE: FRAEER FREED for Windows Version 4.0
SEQ ID NO 7
LENGTH: 73
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OTHER INFORMATION: n = A,C,T or G
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OTHER INFORMATION: n = T, C or G
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INFORMATION: n = A, T or G
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THER INFORMATION: n = G or C
TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 627 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: RNA
US-11-195-109-31
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INFORMATION: n = C or
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Best Local Similarity 78.9
Matches 15; Conservative
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LOCATION: (14)...(14)
OTHER INFORMATION: n = A,
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OTHER INFORMATION: n = A,
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LOCATION: (5)...(5)
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LOCATION: (30)...(30)
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NUMBER OF SEQ ID NOS: 74
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 12
LENGTH: 73 VAME/KEY: misc feature CCATION: (23)...(29) THER INFORMATION: n = A,T,C or G LOCATION: (52)...(52)

THER INFORMATION: n = A,T,C or G LOCATION: (14)...(14)
OTHER INFORMATION: n = A, C or G FEATURE:

NAME/KEX: misc\_feature
LOCATION: (65)...(65)

OTHER INFORMATION: n = A or C NAME/KEY: misc\_feature LOCATION: (16)...(16) OTHER INFORMATION: n = G or A FEATURE:
NAME/KEY: misc\_feature
LOCATION: (11)...(11)
OTHER INFORMATION: n = G or COCATION:  $(12)^{-}$ ...(12)OTHER INFORMATION: n = C or LOCATION: (62) ... (62) OTHER INFORMATION: n = A or TYPE: DNA ORGANISM: human rhinovirus FEATURE:
NAME/KEY: misc\_feature
LOCATION: (19) ... (19)
OTHER INFORMATION: n = T NAME/KEY: misc\_feature LOCATION: (15)\_..(15) OTHER INFORMATION: n = C FEATURE:
NAME/KEY: misc\_feature
LOCATION: (5)...(5)
OTHER INFORMATION: n = T NAME/KEY: misc feature LOCATION: (59)...(59) OTHER INFORMATION: n = C NAME/KEY: misc\_feature CCCATION: (30)...(30) THER INFORMATION: n = T LOCATION:  $(31)^{-}$ ...(31)OTHER INFORMATION: n = GNAME/KEY: misc\_feature LOCATION: (33)...(33) THER INFORMATION: n = G LOCATION: (61)...(61) OTHER INFORMATION: n = T FEATURE:
NAME/KEY: misc\_feature
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US-10-866-517A-48

Sequence 48, Application US/10865517A
Sequence 48, Application US/10865517A
Publication No. US20060008810A1
GENERAL INFORMATION:
APPLICANT: ELE, MING-CHOU
APPLICANT: GROEN, JAN
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING
TITLE OF INVENTION: RHINOVIRUSES
FILE REFERENCE: FOCS-003
CURRENT APPLICATION NUMBER: US/10/886,517A
CURRENT PILLING DATE: 2004-07-06
NUMBER OF SEQ ID NOS: 74
SOFTWARE: FRAESEQ for Windows Version 4.0
SEQ ID NO 48
LENGTH: 118
                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 89.5%; Score 17; DB 7; Length 73; Best Local Similarity 89.5%; Pred. No. 5.5; Matches 17; Conservative 0; Mismatches 2; Indels
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Sequence 32, Application US/10886517A

Publication No. US20060008810A1

GENERAL INFORMATION:
APPLICANT: LEE, MING-CHOU

APPLICANT: GROEN, JAN

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING

TITLE OF INVENTION: METHODY NEW DETECTING

FILE REFERENCE: FOCS-003
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| NAME/KEY: misc feature
| LOCATION: 78, 89, 92, 110
| CTHER INFORMATION: n = A,T,C or G
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NAME/KEY: misc feature
LOCATION: (70)...(70)
CTHER INFORMATION: n = C or G
US-10-886-517A-12
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OTHER INFORMATION: n = A or G
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ORGANISM: human rhinovirus
                                                                                                                                                        LOCATION: (68) ... (68)
OTHER INFORMATION: n = C FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: n = C
                                                                LOCATION: (67)...(67)
OTHER INFORMATION: n = C
                                              NAME/KEY: misc_feature
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NAME/KEY: misc_feature
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DB 7; Length 118;
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TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING
FILE REFERENCE: FOCS-030
CURRENT APPLICATION NUMBER: US/10/886,517A
CURRENT FILING DATE: 2004-07-06
NUMBER OF SEQ ID NOS: 74
SOFTWARE: FASISEQ for Windows Version 4.0
SEQ ID NO 43
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APPLICANT: LEE, MING-CHOU
APPLICANT: KONG, LILLY
APPLICANT: GROEN, JAN
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING
TITLE OF INVENTION: RHINOVIRUSES
FILE REFERENCE: FOCS-003
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Pred. No. 29;
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CURRENT FILING DATE: 2004-07-06
NUMBER OF SEQ ID NOS: 74
SEQ ID NO 45
LENGTH: 118
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                                                                                                                                                                   Sequence 43, Application US/10886517A Publication No. US20060008810A1
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Publication No. US20060008810A1
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Best Local Similarity 89.5%;
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: human rhinovirus
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GENERAL INFORMATION
APPLICANT: LEE, MING-CHOU
APPLICANT: KONG, LILLY
APPLICANT: GROEN, JAN
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APPLICANT: LEE, MING-CHOU
APPLICANT: KONG, LILLY
APPLICANT: GROEN, JAN
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING
TITLE OF INVENTION: RHINOVIRUSES
FILE REFREENCE: FOCS-003
CURRENT APPLICATION NUMBER: US/10/886,517A
CURRENT PILING DATE: 2004-07-06
NUMBER OF SEQ ID NOS: 74
SOFTWARE FASESEQ for Windows Version 4.0
SEQ ID NO 40
LENGTH: 118
                                                                                                                                                                                                        DB 7; Length 118;
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APPLICANT: GROEN, JAN
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING
TITLE OF INVENTION: HAINOVIRUSES
FILE REFERENCE: POCS-003
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Pred. No. 29;
0; Mismatches
                                                                                                                                                                                                                                             0; Mismatches
CURRENT APPLICATION NUMBER: US/10/886,517A
CURRENT FILING DATE: 2004-07-06
NUMBER OF SEQ ID NOS: 74
SEQ ID NO 32
LENGTH: 118
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                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 38, Application US/10886517A Publication No. US20060008810A1
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Sequence 40, Application US/10886517A
Publication No. US20060008810A1
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89.5%;
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Best Local Similarity 89.5%;
Matches 17; Conservative
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                                                                                                                     TYPE: DNA
CORGANISM: human rhinovirus
US-10-886-517A-32
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US-10-886-517A-40
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US-10-886-517A-38
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Best Local Similarity 89.5
Matches 17; Conservative
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GENERAL INFORMATION:
APPLICANT: LEE, MING-CHOU
APPLICANT: GOESH, JAM
TITLE OF INVENTION: MATHODS AND COMPOSITIONS FOR DETECTING
TITLE OF INVENTION: RHINOVIRUSES
FILE REFERENCE: FOCS-003
CURRENT APPLICATION NUMBER: US/10/886,517A
CURRENT FILING DATE: 2004-07-06
NUMBER OF SEQ ID NOS: 74
SOFTWARE: PASESEQ for Windows Version 4.0
SEQ ID NO 50
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Publication No. US20060008810A1

GENERAL INFORMATION:
APPLICANT: LEE. MING-CHOU
APPLICANT: RONG, LILLY
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING
TITLE OF INVENTION: RHINOVIRUSES
TITLE OF INVENTION: RHINOVIRUSES
CURRENT FILLING DATE: 2004-07-06
NUMBER OF SEQ ID NOS: 74

SOFTWARE: PRESENCE: 2004-07-06
SOFTWARE: PRESENCE: 2004-07-06
SEQ ID NO SE
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           TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING TITLE OF INVENTION: RHINOVIRUSES FILE REFERENCE: FOCS-003
CURRENT APPLICATION NUMBER: US/10/886,517A
CURRENT FILING DATE: 2004-07-06
NUMBER OF SEQ ID NOS: 74
SOFTWARE: FASESEQ for Windows Version 4.0
LENGTH: 118
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89.5%; Pred. No. 29
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Pred. No. 29
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Best Local Similarity 89.5
Matches 17; Conservative
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US-10-886-517A-52
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nes 17; Conservative
GROEN, JAN
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US-10-886-517A-50
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US-10-886-517A-52
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SEQUENCE 57, Application US/1088517A

Publication No. US20060008810A1

APPLICANT: LEE, MING-CHOU

APPLICANT: GROSH, LILLY

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING

TITLE OF INVENTION: MHINOVIRUSES

FILE REFERENCE: FOCS-003

CURRENT APPLICATION NUMBER: US/10/886,517A

CURRENT FILING DATE: 2004-07-06

NUMBER OF SEQ ID NOS: 74

SOFTWARE: FASTSEQ for Windows Version 4.0

SEQ ID NO 57

LENGTH: 118
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Publication No. US20060008810A1

GENERAL INFORMATION:

APPLICANT: LEE, MING-CHOU

APPLICANT: EEE, MING-CHOU

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING

TITLE OF INVENTION: RHINOVIRUSES

FILE REPERENCE: POCS-003

CURRENT APPLICATION NUMBER: US/10/886,517A

CURRENT FILING DATE: 2004-07-06

NUMBER OF SEQ ID NOS: 74

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 54
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Pred. No. 29;
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                    DB 7; Length 118;
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                  Score 15.8; I
Pred. No. 29;
                                                          0; Mismatches
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Pred. No. 29;
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US-10-886-517A-57
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                                                                                              1 CCCCTGAATGCGGCTAATC 19
                                                                                                                      CCCCTGAATGTGGCTAACC 79
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89.5%;
                  83.2%;
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Best Local Similarity 89.5%;
Matches 17; Conservative
Query Match
Best Local Similarity 89.5%
Local Similarity 89.5%
Local Similarity 89.5%
Conservative
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Best Local Similarity
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TITLE OF INVENTION: Methods for identifying target nucleic acid molecules FILE REFERENCE: 19603/4121 (CRF D-2995-02)
CURRENT APPLICATION NUMBER: US/10/939,294A
CURRENT FILING DATE: 2004-09-10
PRIOR PILING DATE: 2003-09-12
NUMBER OF SEQ ID NOS: 38895
SEQ ID NO 20728
LENGTH: 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Barany, Francis
APPLICANT: Turner, Daniel
APPLICANT: Turner, Daniel
APPLICANT: Pingle, Maneesh
APPLICANT: Pingle, Mathods for identifying target nucleic acid molecules
FILE REFERENCE: 19603/4121 (CRF D-2995-02)
CURRENT APPLICATION NUMBER: 0204-09-10
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Publication No. US20050266417A1
GENERAL INFORMATION:
APPLICANT: Barany, Francis
APPLICANT: Turner, Daniel
APPLICANT: Pingle, Maneesh
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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Pred. No. 94;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                          ; OTHER INFORMATION: oligonucleotide probe US-10-939-294A-332
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PRIOR FILING DATE: 2003-09-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 332, Application US/10939294A Publication No. US20050266417A1 GENERAL INFORMATION:
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SOFTWARE: Patentin version 3.3
SEQ ID NO 332
LENGTH: 48
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Best Local Similarity 88.9%;
Matches 16; Conservative
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Best Local Similarity 88.9
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA ORGANISM: Artificial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Artificial
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Publication No. US20050266417A1

GENERAL INFORMATION:
APPLICANT: Barany, Francis
APPLICANT: Turner, Daniel
APPLICANT: Pingle, Maneseh
APPLICANT: WARNER: US/10/939,294A
CURRENT APPLICATION NUMBER: US/10/939,294A
CURRENT PILING DATE: 2004-09-10
PRIOR PILING DATE: 2003-09-12
NUMBER OF SEQ ID NOS: 38895
SEQ ID NOS: 38895
LENGTH: 32
LENGTH: 32
                                                                                                                                                      APPLICANT: POULSEN, TIM S.

APPLICANT: POULSEN, KIRSTEN V.

TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES FILE REPERENCE: 091398.6000-00000

CURRENT APPLICATION NUMBER: US/11/121,086

CURRENT FILING DATE: 2005-05-04

NUMBER OF SEQ ID NOS: 107

SOFTWARE: PATENTI VERSION 3.3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 15.4; DB 12;
Pred. No. 1.1e+02;
0; Mismatches 1;
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; Sequence 20728, Application US/10939294A
; Publication No. US20050266417A1
                                                                     Sequence 55, Application US/11121086
Publication No. US20050266459A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   93734 CCCTGAATGCGGGTAAT 93718
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 94.1%;
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 77.9
Best Local Similarity 88.9
Matches 16; Conservative
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APPLICANT: Turner, Daniel
APPLICANT: Pingle, Maneesh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Homo sapiens
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ORGANISM: Artificial
                                                                                                                                       GENERAL INFORMATION:
APPLICANT: POULSEN,
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LENGTH: 175673
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LENGTH: 64
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| Sequence 2701, Application US/10939294A |
| Sequence 2701, Application US/10939294A |
| Sequence 2701, Application US/20050266417A1 |
| GENERAL INPORMATION: US-20050266417A1 |
| APPLICANT: Barany, Francis |
| APPLICANT: Pincle, Maneeth |
| PILER REFERENCE: 19603/4121 (CRF D-2995-02) |
| CURRENT APPLICATION NUMBER: US/10/939,294A |
| PRIOR FILING DATE: 2004-09-10 |
| PRIOR FILING DATE: 2003-09-12 |
| NUMBER OF SEQ ID NOS: 38895 |
| SEQ ID NO 2701
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APPLICANT: Turner, Daniel
APPLICANT: Turner, Daniel
APPLICANT: Pingle, Mannesh
APPLICANT: Pingle, Mannesh
TITLE OF INVENTION: Methods for identifying target nucleic acid molecules
FILE REPERENCE: 19603/4121 (GRF D-2995-02)
CURRENT APPLICATION NUMBER: 02/10/939,294A
CURRENT FILING DATE: 2004-09-10
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                                                                                                                                                                                                                                                                                     Query Match 77.9%; Score 14.8; Dest Local Similarity 88.9%; Pred. No. 98; Matches 16; Conservative 0; Mismatches
                                                                                                                                                                                                        ; OTHER INFORMATION: oligonucleotide probe US-10-939-294A-1620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ) OTHER INFORMATION: Oligonucleotide probe US-10-939-294A-2653
PRIOR APPLICATION NUMBER: US 60/502/731
PRIOR FILING DATE: 2003-09-12
NUMBER OF SEQ ID NOS: 38895
SEQ ID NO 1620
LENGTH: 48
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PRIOR FILING DATE: 2003-09-12
NUMBER OF SEQ ID NOS: 38895
SEG ID NO 2653
LENGTH: 64
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; Publication No. US20050266417A1
; GENERAL INFORMATION:
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                                                                                                                                                  TYPE: DNA ORGANISM: Artificial
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US-10-939-294A-2653/c
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Sequence 38314, Application US/10995561
Publication No. US20050272054A1
GENERAL INFORMATION:
TUTLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
TITLE OF INVENTION: DETECTION AND USES THEREOF
TITLE OF INVENTION: UNDER: US/10/995,561
CURRENT FILING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 85702
SEQ ID NOS: 85702
SEQ ID NO 38314
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Publication No. US20040181048A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
FILE REFERENCE: 108827.133
CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2001-08-08
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                                                                                                                                                           Query Match 77.9%; Score 14.8; DB 8; Length 64; Best Local Similarity 88.9%; Pred. No. 1e+02; Matches 16; Conservative 0; Mismatches 2; Indels
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PRIOR APPLICATION NUMBER: US 60/243, 096

PRIOR FILING DATE: 2000-10-24

PRIOR PILING DATE: 2000-11-20

PRIOR PILING DATE: 2000-11-20

PRIOR PILING DATE: 2000-11-20

PRIOR PILING DATE: 2000-11-30

PRIOR FILING DATE: 2000-11-6

PRIOR FILING DATE: 2001-01-6

PRIOR FILING DATE: 2001-01-6

PRIOR FILING DATE: 2001-01-6

PRIOR FILING DATE: 2001-01-6

PRIOR FILING DATE: 2001-05-09

NUMBER OF SEQ ID NOS: 957086

SEQ ID NO 152961

LENGTHARE: PASESEQ for Windows Version 4.0

SEQ ID NO 152961
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                                                    ; FEATURE:
; OTHER INFORMATION: oligonucleotide probe
US-10-939-294A-2701
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ORGANISM: Homo sapiens
TYPE: DNA
ORGANISM: Artificial
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Best Local Similarity
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; ORGANISM: Homo sa
US-09-925-065A-152961
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                                                     Gaps
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| Sequence 886331, Application US/09925065A
| Publication No. US20040181048A1
| GENERAL INFORMATION:
| APPLICANT: Wang, David G.
| TITLE OF INVENTION: Identification and Mapping of Single
| TITLE OF INVENTION: Identification and Mapping of Single
| TITLE OF INVENTION: UNCLEOCINGE POLYMOCPHISMS in the Human Genome
| FILE REFERENCE: 108827.135
| CURRENT APPLICATION NUMBER: US 60/243,096
| PRIOR APPLICATION NUMBER: US 60/252,147
| PRIOR APPLICATION NUMBER: US 60/250,092
| PRIOR PILING DATE: 2000-11-20
| PRIOR PILING DATE: 2001-01-16
| PRIOR APPLICATION NUMBER: US 60/261,766
| PRIOR PILING DATE: 2001-01-16
| PRIOR PILING DATE: 2001-01-16
| PRIOR APPLICATION NUMBER: US 60/289,846
| PRIOR SEQ ID NOS: 9570086
| SOFTWARE: FASTSEQ FOR Windows Version 4.0
| LUMBER OF SEQ ID NOS: 9570086
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    Score 14.8; DB 6; Length 595;
Pred. No. 1.3e+02;
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APPLICANT: PANTIN, Dennis
TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
FLE REFERENCE: WMI1100-2
CURRENT APPLICATION NUMBER: US/10/750,185
CURRENT FILING DATE: 2003-12-31
PRIOR PPLICATION NUMBER: US 60/437,482
PRIOR PLING DATE: 2002-12-31
                                                     Indels
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Pred. No. 1.3e+
0; Mismatches
                                                     0; Mismatches
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                                                                                                                                       433 CACTGAATGGGGCTAATC 416
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US-10-750-185-37125
                                                                                              2 CCCTGAATGCGGCTAATC 19
    77.9%;
88.9%;
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88.9%;
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SOFTWARE: Patentin version 3.1
SEQ ID NO 37125
LENGTH: 1946
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APPLICANT: MMI GENOMICS, INC.
APPLICANT: DeNISE, Sue K.
APPLICANT: KERR, Richard
APPLICANT: ROSENFELD, David
Query Match 77.9
Best Local Similarity 88.9
Matches 16; Conservative
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Best Local Similarity 88.9°
Matches 16; Conservative
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ORGANISM: Homo sapiens
US-09-925-065A-886331
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US-09-925-065A-886331/c
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                                             Gaps
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APPLICANT: NAKAMURA, NORIHISA
APPLICANT: KODAWA, YUKIKO
APPLICANT: KODAWA, YUKIKO
APPLICANT: KODAWA, TOMOKKO
APPLICANT: ASHIKAKI, TOSHIHIKO
TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
FILE REPRENEUR: 030685-043
CURRENT APPLICATION NUMBER: US/10/932,182A
CURRENT FILING DATE: 2004-09-02
NUMBER OF SEQ ID NOS: 197023
SOFTWARE: PATENTIN VERSION 3.3
SEQ ID NO 80809
LENGTH: 2139
                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: BATES, Stephen
APPLICANT: FANTIN, Dennis
TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
PILE REPERENCE: MMI1100-1
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    Length 1946;
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    ; DB 8;
1.5e+02;
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    Score 14.8; DE
Pred. No. 1.5e+
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/10/750,623
CURRENT FILING DATE: 2003-12-31
PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR FILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
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; Sequence 80809, Application US/10932182A
; Publication No. US20060046253A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                           Sequence 37125, Application US/10750623
Publication No. US20050287531A1
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                                                                                                                          933 CCCTGAATGCGCCTTATC 916
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; ORGANISM: Bovine 19866880769791
US-10-750-623-37125
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                                                                                 2 CCCTGAATGCGGCTAATC 19
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SEQ ID NO 37125
LENGTH: 1946
  ch 77.9%;
1 Similarity 88.9%;
16; Conservative
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Query Match
Best Local Similarity
Matches 16; Conserv
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Best Local Similarity
Matches 16; Conserv
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Pred. No. 2.4e+02;
0; Mismatches 2;
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Pred. No. 2.4e+02;
0; Mismatches 2;
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Publication No. US20050260659A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Harris, Cole
APPLICANT: Davis, Lisa M.
TITLE OF INVENTION: Breast Cancer Biomarkers
FILE REFERENCE: 04-164-US
CURRENT FILING DATE: 2005-04-22
PRIOR APPLICATION NUMBER: US 60/564,758
PRIOR FILING DATE: 2004-04-23
PRIOR FILING DATE: 2004-06-01
PRIOR FILING DATE: 2004-06-01
PRIOR FILING DATE: 2004-06-01
PRIOR FILING DATE: 2004-06-01
PRIOR FILING DATE: 2004-11-30
PRIOR FILING DATE: 2004-1-30
PRIOR FILING DATE: 2004-11-30
PRIOR SPEING APPLICATION NUMBER: US 60/631,826
PRIOR FILING DATE: 2004-11-30
PRIOR SEQ ID NOS: 511
SOFWHARE: Patentin Version 3.3
                TITLE OF INVENTION: Breast Cancer Biomarkers FILE REFERENCE: 04-164-US
CURRENT FILING DATE: 2005-04-22
PRIOR APPLICATION NUMBER: US/11/112,908
CURRENT FILING DATE: 2006-04-22
PRIOR APPLICATION NUMBER: US 60/564,758
PRIOR APPLICATION NUMBER: US 60/575,978
PRIOR FILING DATE: 2004-06-01
PRIOR APPLICATION NUMBER: US 60/631,702
PRIOR FILING DATE: 2004-11-30
PRIOR FILING DATE: 2004-11-30
PRIOR FILING DATE: 2004-12-07
NUMBER OF SEQ ID NOS: 511
SOFTWARE: PARENTIN VERSION 3.3
SEQ ID NO 37
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88.9%;
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Best Local Similarity 88.9%;
Matches 16; Conservative
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Best Local Similarity 88.9 Matches 16; Conservative
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ORGANISM: Homo sapiens
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| LOCATION: (1)...(137935)

| THER INDEMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-

US-10-995-561-13278
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US-10-995-561-13278, Application US/10995561
| Sequence 13.278, Application No. US20050272054A1
| GENERAL INFORMATION:
| APPLICANT: CARGILL, Michele et al. APPLICANT: CARGILL, MICHELE et al. TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF TITLE OF INVENTION: DETECTION AND USES THEREOF TITLE OF INVENTION: DETECTION AND USES THEREOF CURRENT APPLICATION NUMBER: US/10/995, 561
| CURRENT APPLICATION NUMBER: US/10/995, 561
| NUMBER OF SEQ ID NOS: 85702 |
| SEQ ID NO 13278
                                                                                          US-10-932-182A-80809/C
US-10-932-182A-80809/C
Sequence 80809, Application US/10932182A
PULICARIN NO. US20060046253A1
GENERAL INFORMATION:
APPLICANT: NAKAO, YOSHIHIRO
APPLICANT: NAKANCRA, NORIHISA
APPLICANT: NAKANCRA, NORIHISA
APPLICANT: APPLICANT: ASHIFARI, TOSHHIKO
APPLICANT: ASHIFARI, USCHHIKO
APPLICANT: ASHIFARI, USCHHIKO
APPLICANT: ASHIFARI, TOSHHIKO
APPLICANT: ASHIFARI, TOSHHIKO
APPLICANTENT ASHIFARI, TOSHHIKO
APPLICANT FILING DATE: 2004-09-02
NUMBER OF SEQ ID NOS: 197023
APPLICANTENT PALENCHIN VERSION 3.3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 77.9%; Score 14.8; DB 7; Length 2139; Best Local Similarity 88.9%; Pred. No. 1.5e+02; Matches 16; Conservative 0; Mismatches 2; Indels 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA ORGANISM: Saccharomyces pastorianus
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408 CCCTGAATGCGGCAGATC 391
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Matches 16; Conservative
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ORGANISM: Homo sapiens
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US-11-112-908-37/c
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LENGTH: 2139
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75.8%; Score 14.4; DB 8; Length 1638; 93.8%; Pred. No. 2.5e+02;
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APPLICANT: FAWIN, Dennis
TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
FILE REFERENCE: MAIL100-2
CURRENT APPLICATION NUMBER: US/10/750,185
CURRENT FILING DATE: 2003-12-31
PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR FILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
SOFTWARE: PATENTIN VETSION 3.1
SEQ ID NO 50407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 14.4; DB 6;
Pred. No. 2.2e+02;
0; Mismatches 1;
                                                                         PRIOR PELICATION NUMBER: US 60/252,147
PRIOR FILING DATE: 2000-11-20
PRIOR PELICATION NUMBER: US 60/250,092
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR PILING DATE: 2001-01-16
PRIOR PLING DATE: 2001-05-09
NUMBER: PRIOR PLING DATE: 2001-05-09
SOPTWARE: FASISEQ for Windows Version 4.0
SEQ ID NO 692313
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Publication No. US20050260603A1
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; ORGANISM: Bovine 19866880379342
US-10-750-185-50407
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93.8%;
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APPLICANT: MMI GENOMICS, INC.
APPLICANT: DENISE, Sue K.
APPLICANT: KERR, Richard
APPLICANT: ROSENFELD, David
APPLICANT: HOLM, TOM
                                                            1000-10-24
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GENERAL INFORMATION:
APPLICANT: MMI GENOMICS, INC.
APPLICANT: DeNISE, Sue K.
APPLICANT: KERR, Richard
APPLICANT: ROSENFELD, David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 93.8
Matches 15; Conservative
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Best Local Similarity 93.8
Matches 15; Conservative
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US-09-925-065A-692313
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Fublication No. US20040181048A1
GENERAL INFORMATION:
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: UNCLEOCIDE POLYMOCIPHISMS in the Human Genome
FILE REFERENCE: 108827.135
CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT APPLICATION NUMBER: US 60/243,096
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR FILING DATE: 2000-11-20
PRIOR PRILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR PRILING DATE: 2001-01-16
PRIOR PRILING DATE: 2001-01-16
PRIOR PRILING DATE: 2001-01-16
PRIOR PRILING DATE: 2001-05-09
PRIOR PRILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
SOFTWARE: FastSEQ for Windows Version 4.0
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GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
TITLE OF INVENTION: 1088-7-135
TITLE OF INVENTION: 1088-7-135
                                                                                                                                                                                                                                                                                                                                                                                                 DB 7; Length 358847;
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TITLE OF INVENTION: Novel Compositions and Methods in Cancer FILE REFERENCE: 529452001300
CURRENT APPLICATION UNDER: US/10/330,773
CURRENT FILING DATE: 2002-12-27
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Pred. No. 2.6e+02;
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93.8%; Pred. No. 2.2¢
tive 0; Mismatches
                                                                                               NUMBER OF SEQ ID NOS: 981
SOFTWARER: FastSEQ for Windows Version 4.0
SEQ ID NO 305
LENGTH: 358847
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Publication No. US20040181048A1
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                                                                                                                                                                                                                                                                   | NAME/KEY: misc_feature
| LOCATION: (1) ... (358847)
| OTHER INFORMATION: n = A,T,C or G
US-10-330-773-305
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Best Local Similarity 88.9%;
Matches 16; Conservative
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US-09-925-065A-692313/c
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                                                                                                                                                                                                    TYPE: DNA
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Length 585;

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NUMBER OF SEQ ID NOS:
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LENGTH: 182303
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Publication No. US20660035246A1
GENERAL INFORMATION:
APPLICANT: WINA
APPLICANT: WARQUEZ, ABBEY
TITLE OF INVENTION: CHROMOGENIC IN SITU HYBRIDIZATION METHODS, KITS, AND
TITLE OF INVENTION: COMPOSITIONS
FILE REFERENCE: 0618.011.0004
CURRENT FILING DATE: 2005-044-26
PRIOR FILING DATE: 2005-044-26
PRIOR FILING DATE: 2005-06-17
PRIOR FILING DATE: 2001-06-17
PRIOR FILING DATE: 2001-09-14
                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                APPLICANT: FANTIN, DEFINISTICANT: FANTIN, DEFINISTICANT: FANTIN, DEFINISTICANT: FANTIN, DEFINISTICANT: FANTINO.1

FILE REFERENCE: MMII100-1

CURRENT APPLICATION NUMBER: US/10/750,623

CURRENT FILING DATE: 2003-12-31

PRIOR FILING DATE: 2003-12-31

NUMBER OF SEQ ID NOS: 64922

SOFTWARE: PACENTIN VERSION 3.1

SEQ ID NO 50407

LENGTH: 1638
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 413, Application US/10330773
; Sequence 413, Application US/10330773
; Publication No. US20060040262A1
; GENERAL INFORMATION:
; APPLICANT: David W. Morris
; APPLICANT: Marc Malandro
; TITLE OF INVENTION: Novel Compositions and Methods in Cancer; FILE REPRENENCE: $29452001300
; CURRENT APPLICATION NUMBER: US/10/330,773
; CURRENT FILING DATE: 2002-12-27
; NUMBER OF SEQ ID NOS: 981
; SEQ ID NO 413
; SEQ ID NO 413
; LENGTH: 70549
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                                                                                                                                                                                                                                                                                                                                                                 Query Match
75.8%; Score 14.4; DB 8; Length 1638;
Best Local Similarity 93.8%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0
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NAME/KEY: misc_feature
LOCATION: (1)...(70549)

OTHER INFORMATION: n = A,T,C or G
US-10-330-773-413
                                                                                                                                                                                                                                                                           ; TYPE: DNA
; ORGANISM: Bovine 19866880379342
US-10-750-623-50407
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Best Local Similarity 93.87
These 15; Conservative
BATES, Stephen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-10-330-773-413/c
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APPLICANT:
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US-11-121-086-45

Sequence 45, Application US/11121086

Sequence 45, Application US/11121086

Sequence 45, Application US/11121086

GENERAL INFORMATION:

APPLICANT: POULSEN, KIRSTEN V.

TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES

FILE REFERENCE: 09138.6000-00000

CURRENT APPLICATION NUMBER: US/11/121,086

CURRENT PILIAG DATE: 2005-05-04

PRIOR HILING DATE: 2005-05-04

NUMBER: OF SEQUENCE OF SEQU
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                                                                                                                                                                                                                                           CTHER INFORMATION: Description of Artificial Sequence: Synthetic; OTHER INFORMATION: nucleotide sequence
US-11-114-798-55
                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 75.8%; Score 14.4; DB 9; Length 173120; Best Local Similarity 93.8%; Pred. No. 4.1e+02; Matches 15; Conservative 0; Mismatches 1; Indels 0;
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93.8%; Pred. No. 4.1e+02;
tive 0; Mismatches 1;
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                                                                                                                     TYPE: DNA
ORGANISM: Artificial Sequence
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Best Local Similarity 93.00
The 15; Conservative
SOFTWARE: Patentin Ver.
SEQ ID NO 55
LENGTH: 173120
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SEQ ID NO 380735
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TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
FILE BEPERBRUE: 108827.135
CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/233,096
PRIOR FILING DATE: 2000-10-24
PRIOR FILING DATE: 2000-11-20
PRIOR PILING DATE: 2000-11-20
PRIOR PLING DATE: 2000-11-30
PRIOR PLING DATE: 2000-11-6
PRIOR PLING DATE: 2001-01-6
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                                                                                                                                                                                                                                                                                           Length 451;
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Pred. No. 2.8e+02;
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Pred. No. 2.8e+02;
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                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
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; Sequence 740536, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
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Publication No. US20040181048A1
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Best Local Similarity 84.2%;
Matches 16; Conservative
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Best Local Similarity 84.2%;
Matches 16; Conservative
                                                                                           TYPE: DNA
CORGANISM: Homo sapiens
US-09-925-065A-84313
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; ORGANISM: Homo sapiens
US-09-925-065A-740536
SEQ ID NO 84313
LENGTH: 451
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Gaps
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TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Mucleotide Polymorphisms in the Human Genome
FILE REFERENCE: 108827.135
CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT APPLICATION NUMBER: US 60/243,096
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR FILING DATE: 2000-10-24
PRIOR FILING DATE: 2000-11-20
PRIOR PAPLICATION NUMBER: US 60/252,147
PRIOR PAPLICATION NUMBER: US 60/250,092
PRIOR FILING DATE: 2000-11-30
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                                                                                                                                              Length 534;
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Pred. No. 2.9e+02;
); Mismatches 3; Indels
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                                                                                                                                            Score 14.2; DB 6;
Pred. No. 2.9e+02;
                                                                                                                                                                           0; Mismatches
PRIOR FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
SOFTWARE: PSELSEQ for Windows Version 4.0
SEQ ID NO 84290
LENGTH: 534
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Publication No. US20040181048A1
                                                                                                                                                                                                                                265 CCTTGAATGCAGCTATTC 283
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                                                                                                                                            74.78;
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Best Local Similarity 84.2%;
Matches 16; Conservative
                                                                                                                             Query Match
Best Local Similarity 84.2.
Best Local 16; Conservative
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; ORGANISM: Homo sapiens
US-09-925-065A-380735
                                                                               ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-84290
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RESULT 94
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Publication No. US20040181048A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nuclectide Polymorphisms in the Human Genome
FILE REFERENCE: 1087-1135
CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR APPLICATION NUMBER: US 60/252,147
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 535;
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84.2%; Pred. No. 2.9e+02;
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PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/289,846
PRIOR FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 605576
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 84.2
Best Local 6; Conservative
                                                                                                                                                                                                                                                                                                                         ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-605576
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ORGANISM: Homo sapiens
US-09-925-065A-153402
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-09-925-065A-153402/c
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US-09-925-065A-430404
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APPLICANT: Alexandrov, Nickolai et al.
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
TITLE OF INVENTION: Therby
TITLE OF INVENTION: Therby
FILE REFERENCE: 2750-1592PUS2
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT FILING DATE: 2005-04-01
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GENERAL INFORMATION:

TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
FILE REFERENCE: 108827.135

CURRENT APPLICATION NUMBER: US/09/925,065A

CURRENT APPLICATION NUMBER: US 60/243,096

PRIOR PELING DATE: 2000-10-24

PRIOR PELING DATE: 2000-11-20

PRIOR PELING DATE: 2000-11-30

PRIOR PELING DATE: 2000-11-30

PRIOR PELING DATE: 2001-01-6

PRIOR APPLICATION NUMBER: US 60/250,092

PRIOR PELING DATE: 2001-13-0

PRIOR PELING DATE: 2001-13-0

PRIOR PELING DATE: 2001-13-0

PRIOR PELING DATE: 2001-01-6

PRIOR PELING DATE: 2001-01-6

SOFTWARE: FASELED NOS: 957086

SOFTWARE: FASELED FOR Windows Version 4.0

LENGTH: 548
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Pred. No. 2.9e+02;
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PRIOR FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR FILING DATE: 2000-11-30
PRIOR FILING DATE: 2001-01-6
PRIOR PILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
SOFTWARE: PASISEQ for Windows Version 4.0
SEQ ID NO 430404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 430405, Application US/09925065A Publication No. US20040181048A1 GENERAL INFORMATION:
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84.2%;
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Best Local Similarity 84.2'
Matches 16; Conservative
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                                                                                                                                                                                                                                                                                   TYPE: DNA
CORGANISM: Homo sapiens
US-09-925-065A-430404
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Best Local Similarity
Matches 16; Conserv
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APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
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APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: NUCLEOLIDE POLYMOTPHISMS in the Human Genome
FILE REFERENCE: 108827.135
CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243,096
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 14.2; DB 6; Length 587;
Pred. No. 2.9e+02;
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Pred. No. 2.9e+02;
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CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR PILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR PILING DATE: 2000-11-30
PRIOR FILING DATE: 2000-11-6
PRIOR FILING DATE: 2001-01-16
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   PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR FILING DATE: 2000-11-30
PRIOR PLING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR PILING DATE: 2001-01-16
PRIOR PILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
SOFTWARE: PASLESC for Windows Version 4.0
SEQ ID NO 740537
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F Sequence 361613, Application US/09925065A
Publication No. US20040181048A1
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74.7%;
Best Local Similarity 84.2%;
Matches 16; Conservative
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; ORGANISM: Homo sapiens
US-09-925-065A-123839
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Best Local Similarity
Matches 16; Conserv
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Fublication No. US2004018A1
FILE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: UNCLEOCING POLYMORPhisms in the Human Genome
FILE REFERENCE: 108827.135
CURRENT APPLICATION NUMBER: US 60/255,065A
CURRENT FILING DATE: 2000-10-24
FRIOR PRILING DATE: 2000-11-20
FRIOR PRILING DATE: 2000-11-20
FRIOR PRILING DATE: 2000-11-30
FRIOR PRILING DATE: 2000-11-30
FRIOR PRILING DATE: 2001-01-16
FRIOR APPLICATION NUMBER: US 60/261,766
FRIOR APPLICATION NUMBER: US 60/261,766
FRIOR PRILING DATE: 2001-01-16
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TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
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Pred. No. 2.9e+02;
                                                                                                                                                                                                                                                                                                                                                                     Length 573;
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                                                                                                                                                                                                                                                                                                                                                                 Score 14.2; DB 9;
Pred. No. 2.9e+02;
                                                                                                                                                                                             NAME/KEY: misc_feature
i LOCATION: (1)..(573)
i THER INCRMATION: Ceres Seq. ID no. 15225718
US-11-096-568A-8418
                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
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CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR PILING DATE: 2000-11-20
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NUMBER OF SEQ ID NOS: 957086
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 442742
LENGTH: 577
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84.28;
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Best Local Similarity 84.2%;
Matches 16; Conservative
NUMBER OF SEQ ID NOS: 34471
SEQ ID NO 8418
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US-09-925-065A-442742
                                                                                                   TYPE: DNA ORGANISM: Glycine max
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Best Local Similarity
Matches 16; Conserv
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                                                                 LENGTH: 573
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GENERAL INFORMATION:

TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
FILE REPERENCE: 108827.135
CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2001-08-08
PRIOR PELING DATE: 2000-10-24
PRIOR PILING DATE: 2000-11-24
PRIOR PILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: US 60/250,147
PRIOR PILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR PELING DATE: 2001-01-16
PRIOR PILING DATE: 2001-01-16
PRIOR PILING DATE: 2001-01-16
PRIOR PILING DATE: 2001-01-6
PRIOR PILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 361614
LENGTH: 609
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TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
FILE REFERENCE: 108827.135
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                                                                                                                                                                                                                                                                                                                                                                                                                  Score 14.2; DB 6; Length 609; Pred. No. 2.9e+02;
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            PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR FILING DATE: 2000-11-20
PRIOR FILING DATE: 2000-11-30
PRIOR FILING DATE: 2000-11-30
PRIOR FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR PILING DATE: 2001-01-16
PRIOR PILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
SOPTWARE: PABECEQ for Windows Version 4.0
SEQ ID NO 361613
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US-09-925-065A-361614/c
i, Sequence 361614, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
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Publication No. US20040181048A1
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84.2%; Pred
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FILING DATE: 2000-10-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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US-09-925-065A-361613
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US-09-925-065A-361614
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Best Local Similarity
Matches 16; Conserva
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; CURRENT APPLICATION NUMBER: US/09/925,065A
; PURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR PILING DATE: 2000-10-24
; PRIOR FILING DATE: 2000-10-24
; PRIOR PILING DATE: 2000-11-30
; PRIOR PILING DATE: 2000-11-30
; PRIOR PILING DATE: 2000-11-30
; PRIOR PILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR PILING DATE: 2001-01-16
; PRIOR PILING DATE: 2001-01-06
; PRIOR PILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 390368
; LENGTH: 648
; LENGTH: 648
; ORGANISM: Homo sapiens
US-09-925-065A-390368

Query Match

Query Match

Query Match

Query Match

LCCCTGAATGCGCTAATC 19

Query Match

DD 232 CCCCAGAAAGCGGCTAATC 214

Search completed: March 9, 2006, 01:18:52
Job time: 428.942 secs
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BZ718658 PUCEX69TD CX698810 ydb82g09. CX698884 ydd56d01. CX691884 ydd56d01. CX592600 yd683d07. CC751823 ZMMBBD013 CC753964 ZMMBBD013	BEOOGA16 MRO-BNOOT AU17457 AU17457 BEA6512 BAR69912 BJ466992 BJ466992 BJ473149 BJ7774105 CA657673 WIMO.DKO3 AV774105 CC47389 CH240_296 DN183756 HOL61138 AV774105 CC47389 CH240_296 DN183756 HOL67138 AW585068 W311264	CLO25506 BST00444  CLO25506 BST00444  BJ468271 BJ468271  AL004093 F. rubripe BJ478716 BST479716  CR037253 40442rsic  CR037253 40442rsic  CR037253 40442rsic  CR212741 OML03954  CR212741 OML03021  BR403208 WHE0426 F BG907934 Talr1163H  CX625718 GAN006111  CX625118 GAN006111  CC954381 573rsice  CA255155 SCEPFL417  CD876322 AZO3.109F  BM155186 WHE0454  CR680958 OSJURE665  DN178545 HO33CGS	AV933787 AV933787 CW312739 104 802_1 BJ469064 BJ469064 CB6565403 OSJNEC10L BJ472468 BJ472488 BJ469669 BJ469669 AJ422460 AJ432460 AV933115 AV933115 CA744325 Wrils.pko CD054348 HO01L09T BJ41067 BJ471067 BJ411067 BJ471067 BJ411067 BJ471067 CD054348 HO01L09T CA744325 Wrils.pko CD054348 HO01L09T CA744326 CB66690 CD054348 HO01L09T CC054348 HO01L09T CC064348 HO01COT CC064346 OSJNECIZK CC664104 OSJNECIZK CC664104 OSJNECIZK CC664104 OSJNECIZK CC664104 OSJNECIZK	
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BU911821 AGENCOURT AC895518 183868 TO CL099115 ISBN-32E3 BH717566 BOMJVB3TR DN78352 93003109 CL285172 ZMMBBD062 CC30774 TAM32-18J AL279811 Tetraodon AL056061 Drosophil AL335370 Tetraodon AL0748 Drosophil AL07481 Drosophil AL07481 Drosophil DR046059 FP-8_H06. BQ277749 AGENCOURT CC200990 CH261-134 DN65524 CFW14-F07 BN65524 CFW14-F07 BN655917 CEC43-B10 AK087319 Mus muscu AK087199 Mus muscu AK08919 Mus muscu AK08919 Mus muscu CL949051 OSIFSB002 AK089301 Mus muscu AK089301 Mus muscu CL949651 OSIFSB002 AK089301 Mus muscu CL949651 OSIFSB002 AK01948 Mus muscu CL94065 BNS1-0094G CL1229038 ZMBBE014 CD140350 MG1-0094G CD196399 MS1-0094G CB636844 OSINEA02M	H51561 Y034a03.81 AAA13768 EXT5506.8 AW955727 EST367797 AQ027634 CIT-H8P-2 AQ0659063 AU069063 CB803847 AWGNUUC:S BF588142 FM1 38 CO CG955510 MBEGKT35TR AQ697140 HS 5528 A BP895692 BP895692 AA771056 VA85699.r CW185416 104 603.1 CW185416 104 603.1 AUT79238 AU179238 BJ054677 BJ054677 AL37661 BG105280 C83726 C83726 rabb B41428 H5-1053-B1- AA784934 S36041.f BZ177144 CH230-397 AL247644 Tetraodon AQ412625 RPCI-110-1 BB700363 BB700363 AG967565 Drosephil BM48142 533681 MA CB719375 AL34764 Tetraodon AQ412625 RPCI-110-1 BM70823 BB700363 BZ122180 CH230-461 BM48142 533681 MA CB77371 MA3-0001U AZ193345 SP 10034 CB719879 AMGNUC-U BIGT225 KE134NC.x CD192055 MS1-0074T CC192055 MS1-0074T CC192053 BQ804135 PLAEST198
975 5 BU911821 977 10 AG867779 988 10 C2995518 1028 9 BH717566 9 1052 9 BH717566 9 1055 10 CL099115 1061 9 DRY83532 9 1055 10 CL285772 1067 10 CNS0487A 9 1067 11 CNS0487A 9 1101 10 CNS04613 1101 10 CNS04613 1101 10 CNS04613 1103 8 BN6653574 9 1156 8 DNC46133 1171 8 DNC46136 1171 8 DNC46133 1171 8 DNC46133 1171 8 DNC46133 1171 8 DNC46138 1171 8 DNC46133 1171 8 DNC46133 117	8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8
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Best Local Similarity 100.0
Matches 18; Conservative
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/clone lib="AM2"
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Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoideae, Andropogoneae, Saccharum, Saccharum officinarum
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S Vettore, A.L., da Silva, F.R., Kemper, E.L. and Arruda, P. The libraries that made SUCEST
The libraries that made SUCEST
Genet. Mol. Biol. 24 (1-4), 1-7 (2001)
Contact: Arruda P
Centro de Biologia Molecular e Engenharia Genetica
Universidade Estadual de Campinas
Caixa Postal 6010, 13083-970, Campinas SP, Brazil
Tel: 55 19 3788 1137
Rax: 55 19 3788 1137
Rax: 55 19 3788 1137
Rax: 55 19 3788 1137
Ray: 55 19 3788 1089
Email: parruda@unicamp.br
Clone distribution: clone distribution information can be found through the Brazilian Clone Collection Center (BCCC) at http://www.bcccenter.fcav.unesp.br
http://www.bcccenter.fcav.unesp.br
Plate: 029 row: D column: 06
Seq primer: T7 Promoter Primer.
Location/Qualifiers
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SCEQRT2029D06.g RT2 Saccharum officinarum cDNA clone SCEQRT2029D06
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/clone lib="RT2"
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/westor: pSportl; Site 1: Sall; Site 2: Not1; An unidirectional cDNA library generated from [Root
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Seg primer: T7 Promoter Primer.
Location/Qualifiers
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CA138671.1 GI:35029882
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Saccharum officinarum
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Lillopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Saccharum; Saccharum officinarum
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5', mENA sequence.
CA187742
tips(0.3cm-long) from adult plants]. cDNA was prepared from polyA+ mRNA using SuperSoript Planamid System Kit (Invitrogen). The double-strand cDNAs were fractionated in a sepharose CL-2B 40cm-columns and fragments sizing
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Clone distribution: clone distribution information can be found
through the Brazilian Clone Collection Center (BCCC) at
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Vettore, A.L., da Silva, F.R., Kemper, E.L. and Arruda, P. The libraries that made SUCEST
Contact: Arruda P 24 (1-4), 1-7 (2001)
                                                                                                                                                                                                                                                                                                                                Length 613;
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100.0%; Pred. No. 1e+02;
ive 0; Mismatches 0; Indels
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Universidade Estadual de Campinas
Caixa Poetal 6010, 13083-970, Campinas SP, Brazil
Tel: 55 19 3788 1137
Fax: 55 19 3788 1089
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Plate: 130 row: H column: 04
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us-10-829-474-1.rst

RESULT 4 CA104389/c DEFINITION

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ORGANISM

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AUTHORS TITLE JOURNAL COMMENT

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//LIDIALITE TANA / Apical meristem and tissues surrounding of immature plants; Vector: pSport1; Site_1: Sal1; Site_2: Not1; An unidirectional cDNA library generated from [Apical meristem and tissues surrounding of immature plants]. cDNA was prepared from polyA+ mRNA using SuperScript Plasmid System Kit (Invitrogen). The double-strand cDNAs were fractionated in a sepharose CL-2B 40cm-columns and fragments sizing between 0.8 and 1.5 Kb were directionally cloned into the vector. Details of each source of RNA and library construction can be obtained at http://sucest.lad.ic.unicamp.br/public"
                      Saccharum officinarum
Saccharum officinarum
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Saccharum; Saccharum officinarum
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: parruda@unicamp.br
Clone distribution: clone distribution information can be found
through the Brazilian Clone Collection Center (BCCC) at
http://www.bcccenter.fcav.unesp.br
Plate: 093 row: D column: 05
Seq primer: SP6 Promoter primer.
Location/Qualifiers
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Mardis/Goldman/Sil Genomic Resources for Histoplasma Sequencing
Washington University School of Medicine
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_AL-aaa07f02.b1 Hc6AS_M Ajellomyces capsulatus cDNA 3', mRNA
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Bukaryota; Rungi; Ascomycota; Pezizomycotina; Burotiomycetes;
Onygenales; Ajellomycetaceae; Ajellomyces.

1 (bases i to 589)
Magrini, V., Sil, A., Goldman, W. and Mardis, R.
Genomic Resources for Histoplasma Sequencing Mardis/WashU
Unpublished (2004)
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Vettore, A.L., da Silva, F.R., Kemper, E.L. and Arruda, P. The libraries that made SUCEST
Genet. Mol. Biol. 24 (1-4), 1-7 (2001)
Contact: Arruda P
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Caixa Postal 6010, 13083-970, Campinas SP, Brazil
Tel: 55 19 3788 1137
Fax: 55 19 3788 1089
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Saccharum officinarum"
/mol_type="mRNA"
/do_tref="texaon.4547"
/clone="SGJFHR1033A07"
/lab_host="DH10B"
/clone|lib="HR1"
/note="Gorgan: seedlings inoculated with Herbaspirilum
rubrisubablicans; Vector: pSport1; Site 1: Sal1; Site_2:
NotI; An unidirectional CDNA library generated from
[seedlings inoculated with Herbaspirilum
rubrisubablicans] cDNA was prepared from poly4-mRNA
using SuperScript Plasmid System Kit (Invitrogen). The
double-strand cDNAs were fractionated in a sepharose
CL-28 40cm-columns and fragments sizing between 0.8 and
1.5 Kb were directionally cloned into the vector. Details
of each source of RNA and library construction can be
obtained at http://sucest.lad.ic.unicamp.br/public"
                                                                                                                                                                             656 bp mRNA linear EST 23-SEP-2003
SCUPHRIO33A07.g HR1 Saccharum officinarum cDNA clone SCUPHRIO33A07
S', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Centrode Biologia Molecular e Engenharia Genetica
Universidade Estadual de Campinas
Caixa Poetal 6010, 13083-970, Campinas SP, Brazil
Tel: 55 19 3788 1137
Fax: 55 19 3788 1089
Email: partuda@unicamp.br
Clone distribution: clone distribution information can be found through the Brazilian Clone Gollection Center (BCCC) at http://www.bcccenter.fcav.unesp.br
Plate: 033 row: A column: 07
Plate: 17 Promoter Primer.
Seq primer: T7 Promoter Primer.
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Saccharum; Saccharum officinarum
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Vettore, A.L., da Silva, F.R., Kemper, E.L. and Arruda, P. The libraries that made SUCEST
Genet. Nol. Biol. 24 (1-4), 1-7 (2001)
Contact: Arruda P
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                                                        349 CCCTGAATGCGGCTAATC 332
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                         2 CCCTGAATGCGGCTAATC 19
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CA085581
CA085581.1 GI:34938888
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Saccharum officinarum
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: vmagrini@watson.wustl.edu
Contact Vincent Magrini (vmagrini@watson.wustl.edu) for further information relating to organism, libraries, or clone availability.
Seq primer: M13_reverse.
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Sequences have been trimmed to exclude PolyA, vector and regions
below Phred quality 16. The threshold for highest quality sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sorghum bicolor
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoideae, Andropogoneae, Sorghum.
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An EST database from Sorghum: water-stressed plants
Unpublished (2000)
Contact: Cordonnier-Pratt MM
Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Fax: 706 583 0210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 (bases 1 to 320)
Cordonnier-Pratt, M.-M., Gingle, A., Marsala, C., Sudman, M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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                                                                                                                                                                                                                                                                                                                                        'organism="Ajellomyces capsulatus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          db_xref="taxon:5037"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /dev_stage="Mycelia"
/lab_host="GC10"
/clone_lib="Hc6AS_M"
                                                                                                                                                                                                                                                                      cocation/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                           mol type="mRNA"
strain="G186A-S"
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BG933318.1 GI:14328450
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Best Local Similarity 94.7
Matches 18; Conservative
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/clone lib="Water-stressed 1 (WS1)"
/note="Organ: Mix of 5-week old plants on days 7 & 8 after water was withheld; Vector: Lambda Zap; Site 1: Xho1; Site 2: ECORI; The library was made from poly-A RNA in the cloning vector lambda ZAP II. Clones to be sequenced were prepared by mass excision."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: mmpratt@uga.edu
Library constructed at Texas Tech University by Deshui Zhang in the
Laboratory of Dr. Henry Nguyen. Sequencing was done in the
Laboratory for Genomics and Bioinformatics, University of Georgia.
Sequence ends have been trimmed to exclude vector and regions below
Phred quality 16. Three-prime sequences are presented as their
reverse complement and have been trimmed to exclude polyA.
Seg primer: T7 (TAATACGACTACTATAGGG)
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/note="Organ: Leaf; Vector: pBlueScriptSK-; Site_1: XhoI;
Site_2: EcoRi; The library was prepared from polyA+ RNA
from leaves harvested from pre-flowering, drought-etressed
Sorghum bicolor, cv. TX7000. Double-stranded cDNA was
cloned unidirectionally using the Unizap system from
Stratagene. After amplification, the library was
subtracted by re-association hybridization. Inserts can be
excised with XhoI and EcoRI."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CF771460

392 bp mRNA linear EST 20-OCT-2003
DSBF1_19_G07.g1_A010 Drought-stressed before flowering Sorghum
bicolor cDNA clone DSBF1_19_G07_A010 3', mRNA sequence.
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Sorghum.

1 (bases 1 to 392)

Cordonnier-Pratt, M. - M., Zhang, D., McCartor, K., Nguyen, H.T. and
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Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Cordonnier-Pratt MM
Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Fax: 706 583 0210
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                                                                                                                                                                                                                                                                                                                                                                                                  Length 320;
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|Chon="DSBF1_19 GOT_A010"
|dev atage="PFe-flowering"
|lab_host="BlectroMax DH10B (BRL)"
                                                                                                                                                                                                                                                                                                                                                                                               89.5%; Score 17; DB 2; Le
100.0%; Pred. No. 3.3e+02;
ive 0; Mismatches 0;
1. .320
/organism="Sorghum bicolor"
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                                                           /mol_type="mRNA"
/db_xref="taxon:4558"
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/cultivar="Tx7000"
                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.0%; Pr
Matches 17; Conservative 0;
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525 CCCTGAATGCNGCTAATC 542
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Saccharum officinarum Saccharum officinarum
                                                                                                              (bases 1 to 590)
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Best Local Similarity 94.4
Matches 17; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone lib="Water-stressed 1 (WS1)" /clone lib="Water-stressed 1 (WS1)" /note="Organ: Mix of 5-week old plants on days 7 & 8 after water was withheld; Vector: Lambda Zap; Site 1: XhoI; Site 2: EcoRI; The library was made from poly-A RNA in the cloning vector lambda ZAP II. Clones to be sequenced were prepared by mass excision."
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CA104476
EST.
                                                                                                                                                                                                                               HG933077 554 bp mRNA linear EST 07-JUN-2001
WSL 3 H09.bl_A002 Water-stressed 1 (WSl) Sorghum bicolor cDNA, mRNA
sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: mmpratt@uga.edu
Sequences have been trimmed to exclude PolyA, vector and regions
below Phred quality 16. The threshold for highest quality sequence
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Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoideae, Andropogoneae, Sorghum.
                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Fax: 706 583 0210
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Cordonnier-Pratt, M.-M., Gingle, A., Marsala, C., Sudman, M. and
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An BST databage from Sorghum: water-stressed plants
                                    89.5%; Score 17; DB 6; Length 392;
100.0%; Pred. No. 3.4e+02;
ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  organism="Sorghum bicolor"
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High quality sequence stop: 543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /mol_type="mRNA"
/db_xref="taxon:4558"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (2000)
Contact: Cordonnier-Pratt MM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                          Sorghum bicolor (sorghum)
                                                                                                                                      167 CCCTGAATGCGGCTAAT 183
                                                                                                                                                                                                                                                                                                   BG933077
BG933077.1 GI:14328209
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                                                                                                            2 CCCTGAATGCGGCTAAT 18
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Best Local Similarity 100.
Matches 17; Conservative
                                                    Best Local Similarity 100.
Matches 17; Conservative
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                                   Query Match
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SEPERANCE MACATOR STREET, AND STREET, AND
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Score 17; DB 1; Le
Pred. No. 3.6e+02;
                                                                                                                                                                                                                                                        /organism="Sorghum bicolor"
/mol_type="mRNA"
/db xref="taxon:4558"
                                                                                                                                                                                                                                                                                                                                                                                                                                                  prepared by mass excision."
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Class: transposon insertion site.
Location/Qualifiers
                                                                                                                   Seq primer: T7
High quality sequence start: 71
High quality sequence stop: 696
POLYR=Yes.
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Conservative 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                269 CCCTGAATGCGGCTAAT 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CZ476191.1 GI:62970314
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Fax: 510 486 6798
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CZ476191/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone="ETH12" B02 A002"
/lab_host="ETH12" B02 A002"
/lab_host="DH10B-TI" phage-resistant B. coli"
/clone lib="Ethylene-treated seedlings"
/clone lib="Ethylene-treated seedlings"
/note="Vector: pWE18S-FL3; Site_1: XhoI; Site_2: XhoI; The
library was prepared from poly4+ RNA from seedlings grown
in hydroponic culture. At 8 days of age, medium was
supplemented with 0.5 mM 1-aminocyclopropane-1-carboxylic
acid (ACC) to induce endogenous ethylene (ETH) production.
Roots and shoots were harvested after 27 and 72 hr and
material from both time points was combined prior to RNA
isolation. Double-stranded cDNA was cloned
unidirectionally into different Drall sites of the
pWE18S-FL3 vector (5-prime Drall site is CACTGTCTG,
3-prime_Drall site is CACCATGTG). XhoI excises the cDNA
                                                                                                                                                   Email: mmpratt@uga.edu
Library constructed by Dr. Yutaka Suzuki and Dr. Sumio Sugano in
Library constructed by Dr. Yutaka Suzuki and Dr. Sumio Sugano in
the Human Genome Center, University of Tokyo Institute of Medical
Science; plant material and RNA prepared at Texas A & W University,
sequencing done in the Laboratory for Genomics and Bioinformatics,
University of Georgia. Sequence ends have been trimmed to exclude
vector and regions below Phred quality 16. Three-prime sequences
are presented as their reverse complement and have been trimmed to
exclude polyA.
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WS1 3 H09.gl_A002 Water-stressed 1 (WS1) Sorghum bicolor cDNA, mRNA
sequence.
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Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoldeae, Andropogoneae, Sorghum.
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Contact: Cordonnier-Pratt MM
Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
                                      Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Fax: 706 583 0210
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Cordonnier-Pratt, M.-M., Gingle, A., Marsala, C., Sudman, M. and
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An BST database from Sorghum: water-stressed plants
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                                                                                                                                                                                                                                                                                                                                                              Seq primer: Sug3 (CGACCTGCAGCTCGAGCACA)
POLYA=Yes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'organism="Sorghum bicolor"
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  Other_EST8: ETH1_2_B02.g1_A002
Contact: Cordonnier-Pratt_MM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         db_xref="taxon:4558"
                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /mol_type="mRNA"
/cultivar="BTx623"
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Sorghum bicolor
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COMMENT
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Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Eukaryota, Metazoa, Arthropoda, Hexapoda; Insecta, Pterygota;
Bukaryota, Metazoa, Arthropoda, Hexapoda; Insecta, Pterygota;
Bukaryota, Badopterygota, Diptera, Brachycera, Muscomorpha,
Ephydroidea, Drosophilidae, Drosophila.

I (bases 1 to 118)
Thibault, S. T., Singer, M. A., Miyazaki, W. Y., Milash, B., Dompe, N. A.,
Singh, C. M., Buchholz, R., Demsky, M., Fawcett, R., Francis-Lang, H. L.,
Ryner, L., Cheung, L. M., Chong, A., Erickson, C., Fisher, W. W.,
Greer, K., Hartouni, S. R., Howie, E., Jakkula, L., Joo, D., Killpack, K.,
Laufer, A., Mazzotta, J., Smith, R. D., Stevens, L. M., Stuber, C.,
Swimmer, C., Kopczynski, C., Duyk, G., Winberg, M. L. and Margolis, J.
A complementary transposon tool kit for Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone lib="Water-stressed 1 (WS1)"
/note="Organ: Mix of 5-week old plants on days 7 & 8 after water was withheld; Vector: Lambda Zap; Site 1: XhOI; Site 2: BCORI, The library was made from poly-A RNA in the clonIng vector lambda ZAP II. Clones to be sequenced were
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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Fax: 706 583 0210
Email: mmpratt@uga.edu
Sequences have been trimmed to exclude PolyA, vector and regions
below Phred quality 16. The threshold for highest quality sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           L18 bp DNA linear GSS 29-APR-20 d08347-5prime Exelixis P element XP insertions Drosophila melanogaster genomic Sequence recovered from 5' end of P element, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The P element insertion position is 111 in the 118 bases. This insertion position refers to the first base of the 8 base target
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Sequence orientation is forward strand relative to 5' end of P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gape
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Lawrence Berkeley National Laboratory
Malistop 64-121, One Cyclotron Road, Berkeley, CA 94720, USA
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Gaps

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/note=_organ: Leaf roll from field grown adult plants
(large insert library); Vector: pSport1; Site 1: Sal1;
Site 2: Not1; An unddirectional cDNA library generated
from [Leaf rol] from field grown adult plants (large
insert library)]. cDNA was prepared from polyA+ mRNA
using SuperScript Plasmid System Kit (Invitrogen). The
double-strand cDNAs were fractionated in a sepharose
CL-2B 40cm-columns and fragments sizing between 0.8 and
1.5 KD were directionally cloned into the vector. Details
of each source of RNA and library construction can be
obtained at http://sucest.lad.ic.unicamp.br/public"
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JGI XZT32869.rev NIH XGC_tropTad5 Xenopus tropicalis cDNA clone
CX410223
                                                                                                                                                                                               SCCCLR1C10E02.g LR1 Saccharum officinarum cDNA clone SCCCLR1C10E02 CA190230
                                                                                                                                                                                                                                                                                                                                                                                                                                               Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoideae, Andropogoneae, Saccharum, Saccharum officinarum
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ubases 1 to 569)
Vettore, A.L., da Silva, F.R., Kemper, B.L. and Arruda, P. The libraries that made SUCEST
The libraries that made SUCEST
Contact: Arruda P
Centro de Biologia Molecular e Engenharia Genetica
Universidade Estadual de Campinas
Caixa Postal 6010, 13083-970, Campinas SP, Brazil
Fex: 55 19 3788 1089
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ch 86.3%; Score 16.4; DB 6; Length 569; 1 Similarity 94.4%; Pred. No. 7.6e+02; 17; Conservative 0; Mismatches 1; Indels C
     Indels
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/organism="Saccharum officinarum"
/mol_type="mRNA"
/db_xref="taxon:4547"
/clone="ScCCLRICLOBO2"
/lab_host="DH108"
        1;
     Mismatches
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Seq primer: T7 Promoter Primer.
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                                                     1 CCCCTGAATGCGGCTAAT 18
                                                                                                                                                                                                                                                                                                                                           CA190230.1 GI:35134178
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Saccharum officinarum
                                                                                                         500 ccccrcaardcccracr
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CA190230/c
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     Matches
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                                                                                           /u_arist_uarkonii/zz/
/clone lib="Exelizis P element XP insertions"
/note="Vector: P element XP (GenBank accession number
AY31519), An isogenic w- Drosophila melanogaster strain
was mutagenized by remobilization of transposable
elements. For the P element XP, we selected an easily
mobilized ammunition element among inserts hopped onto the
Binsinscy balancer. New insertions were collected in vials
from dysgenic females using the standard chromosomal
source of transposase, delta2-3. All lines were mapped to
a chromosome by standard genetic methods, examined for
homozygous viability and used for recovery of flanking
genomic sequence by inverse PCR."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Viridiplantae; Chlorophyta; Prasinophyceae; Mamiellales;
Mamiellaceae; Ostreococcus.
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Derelle, E., Ferraz, C., Lagoda, P., Eychenie, S., Cooke, R., Regad, F., Rahau. X.. Courties, C., Delseny, M., Demaille, J., Picard, A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone lib="Ostreococcus tauri genomic shotgun library"
/note="Vector: Bluescript; Site_1: EcoRV; Site_2: EcoRV;
Shotgun library prepared after sonication of the genomic
DNA. Blut ligation in EcoRV site of Bluescript. Size
selection of the inserts after agarose electrophoresis
between 1 and 3 Kb."
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Pred. No. 6.18+02;
0; Mismatches 1; Indels 0;
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CNRS UMR 7628
BP 44, Avenue Fontaule, 66651 Banyuls sur mer, France
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organism="Drosophila melanogaster"
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                        /mol_type="genomic DNA"
/strain="isogenic w- strain"
/db_xref="taxon:7227"
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Contact: Moreau H
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/mol_type="genomic DNA"
/strain="OTTH0595"
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/clone="ota04c08.g"
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94.4%;
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KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS JOURNAL

COMMENT

TITLE

DEFINITION ACCESSION

BH899915

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FEATURES

VERSION KEYWORDS

AUTHORS REFERENCE

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/lab host="DH108"
/clone lib="LR1"
/clone lib="Lag"
/clone libert library); Vector: pSport1; Site_1: SalI;
Site_2: NotI; An unidirectional cDNA library generated
from [Leaf roll from field grown adult plants (large
insert library)]. cDNA was prepared from polyA+ mRNA
using SuperScript labsmid System Kit (Invitrogen). The
double-strand cDNAs were fractionated in a sepharose
CL-28 40cm-collumns and fragments sizing between 0.8 and
1.5 Kb were directionally cloned into the vector. Details
of each source of RNA and library construction can be
obtained at http://sucest.lad.ic.unicamp.br/public"
                                                                               Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoideae, Andropogoneae, Saccharum, Saccharum officinarum
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BX867956 tcba Oncorhynchus mykiss cDNA clone tcba0023c.o.02 5prim,
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: parrida@unicamp.br
Clone distribution: clone distribution information can be found
through the Brazilian Clone Collection Center (BCCC) at
http://www.bcccenter.fcav.unegp.br
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleost.
Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
1 (bases 1 to 760)
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Construction and primary characterization of normalized cDNA
libraries in rainbow trout, Oncorhynchus mykiss
Unpublished (2003)
Contact: Guiguen Y
INRA - SCRIBE
                                                                                                                                                                                                                  Kemper, E.L. and Arruda, P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 690;
                                                                                                                                                                                                       Vettore, A.L., da Silva, F.R., Kemper, E.L. and Arruda
The libraries that made SUCEST
Genet. Mol. Biol. 24 (1-4), 1-7 (2001)
Contact: Arruda P
Centro de Biologia Molecular e Engenharia Genetica
                                                                                                                                                                                                                                                                                                                                               Universidade Bstadual de Campinas
Caixa Postal 6010, 13083-970, Campinas SP, Brazil
Tel: 55 19 3788 1137
Fax: 55 19 3788 1089
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Saccharum officinarum"
/mol_type="mRNA"
/db_xref="taxon:4547"
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Pred. No. 7.8e+02;
0; Mismatches 1;
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Seg primer: T7 Promoter Primer
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                                                         Saccharum officinarum
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Matches 17;
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: cdnadjgi-psf.org
Tissue Procurement: Richard M. Harland Laboratory, University of
California, Berkeley: http://tropicalis.berkeley.edu/home
California, Berkeley
of California, Berkeley
DNA Sequencing: DOE Joint Genome Institute: http://www.jgi.doe.gov
http://image.lln.gov
Naming Conventions: EST name is generated by the concatenation of
the Joint Conventions: EST name is generated by the concatenation of
the Joint Conventions of a generated by the concatenation of
indicates a reverse sequencing read of the insert. It does not
necessarily reflect the orientation of the insert.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone="IMAGE:7609044"
/tissue_type="whole embryo"
/tesue_type="whole embryo"
/dev tagage=Tradpole (sr. 36-41)"
/lab_host="E. coli XL1-Blue derivative, Stratagene
Blectrofen-Blue"
/clone_lib="NIH XGC tropTad5"
/note="Vector: pCs108; Site_1: Sal1; Site_2: Not1; Tadpole
/note="Vector: pCs108; Site_1: Sal1; Site_2: Not1; Tadpole
library constructed by Russell B. Fletcher in R. Harland's
lab using poly A RNA and oligo dT primers (Invitrogen
SuperScript Plasmid System for cDNA Synthesis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cloning). SalI (5' end) -NotI (3' end) cDNA was inserted into vector pCS108 (http://mcb.berkeley.edu/labs/harland/pages/plasmids.html)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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SCRLLR1110E08.g LR1 Saccharum officinarum cDNA clone SCRLLR1110E08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Poly.A. Based upon the presence of a run of 14 or more T residues at the beginning of the sequence, this clone was polyadenylated. The resulting Poly-T sequence has been removed. High quality sequence stop: 503 PolYA-Yes.
                                                                    Renopus tropicalis

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus; Silurana.

[ bases 1 to 655)

Richardson, P., Lucas, S., Rokhsar, D., Detter, J.C., Ng, D.C.,
Brokstein, P. and Lindquist, E.A.

DOE Joint Genome Institute Xenopus tropicalis EST project
Unpublished (2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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Pred. No. 7.7e+02;
0; Mismatches 1; Indels (
                                                                                                                                                                                                                                                                                                            Other EST8: JGI XZT32869.fwd
Contact: Lindquist,E.A., Richardson,P.
DOB Joint Genome Institute
2800 Mitchell Drive, Walnut Creek, CA 94598, USA
Tel: 925 296 5500
Fax: 925 296 5710
                                                   (enopus tropicalis (western clawed frog)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Xenopus tropicalis"
|mol_type="mRNA"
|db_xref="taxon:8364"
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GI:57190925
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CA125729
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FEATURES

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Contact: Stephen Richards
    /chromosome="1"
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Matches 17; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hayashi,S., Ito,K., Sado,Y., Taniguchi,M., Akimoto,A., Takeuchi,H., Ajgaki,T., Matsuzaki,F., Nakagoshi,H., Tanimura,T., Ueda,R., Uemura,T., Yoshihara,M. and Goto,S. GETDB, a database compiling expression patterns and molecular locations of a collection of Gal4 enhancer traps Genesis (2002) in press
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                                                                    Email: Yann.Guiguen@beaulieu.rennes.inra.fr
Seguence cleaned of vector, adaptator and repetitions. Contact us
at sigenasupport@jouy.inra.fr to obtain the chromatogram of this
                                                                                                                                                                                                                                                                                                                                                              /dev stage="from embryos to adults"
/lab_host="DH10B"
/clone_lib="tcba"
/note="Vector: pT7T3D-pac; Rainbow trout multi-tissues -normalized + 1 subtraction; Clone distribution : AGENAE Resource centre. Francois PIUMI,
Francois.Piumi@jouy.inra.fr, INRA, CEA Radiobiologie et Etude du genome (LREG), Domaine de Vilvert, 78352, Jouy-en-Josas cedex, FRANCE, +33 (0) 1.34.65.28.02, +33 (0) 1.34.65.22.73"
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Bukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,
Ephydroidea, Drosophilidae, Drosophila.
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86.3%; Score 16.4; DB 5; Length 760;
Best Local Similarity 94.4%; Pred. No. 7.9e+02;
Matches 17; Conservative 0; Mismatches 1; Indels (
Campus de beaulieu, RENNES cedex, 35042, France
Tel: 02.23.48.50.09
Fax: 02.23.48.50.20
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                                                                                                                                                                                                                                                    /organism="Oncorhynchus mykiss"
                                                                                                                                                                                                                                                                                               /db_xref="taxon:8022"
/clone="tcba0023c.o.02"
/tissue_type="multi-tissues"
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/strain="NP5046"
                                                                                                                                          sequence.
Plate: 0023 row: o column: 2
Seq primer: M13R.
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Lorsophila pseudoobscus.
Lorsophila pseudoobscus.
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Boptaroidea; Drosophilade; Drosophila.
Ephydroidea; Drosophilade; Drosophila.
Ephydroidea; Drosophilade; Drosophila.
Enchards, S., Liu, Y., Bettencourt, B.R., Hradecky, P., Letovsky, S., Nielsen, R., Thoriton, K., Hubisz, M.J., Chen, R., Meisel, R. R.,
Couronne, O., Hua, S., Smith, M.A., Zahang, P., Liu, J., Bussemaker, H.J., van Batenburg, M.F., Howells, S.L., Scherer, S.E., Sodergren, E., Matthews, B.B., Crosby, M.A., Schroeder, A.J., Oritz-Barriantos, D., Rives, C.M., Metzker, M.L., Muzny, D.M., Scott, G., Steffen, D., Mheeler, D.A., Worley, K.C., Havilton, K.J., Egan, A., Gill, R., Hume, J., Morday, M. B., Miner, G., Hamilton, C., Huang, Y., Waldron, L., Verduzco, D., Clerc-Blankenburg, K.P., Dubchak, I., Noor, M.A., Anderson, W., White, K.P., Clark, A.G., Schaeffer, S.W., Comparative genome sequencing of Drosophila pseudoobscura: chromosomal, gene, and cis-element evolution
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DR126636 1104 bp mRNA linear EST 15-JUN-2005 49290467 Drosophila pseudoobscura embryonic cDNA library Drosophila pseudoobscura cDNA clone A19 5', mRNA sequence.
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                                                                                                                                                                                                                                                          Gaps
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/clone_lib="Drosophila pseudoobscura embryonic cDNA
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/map="5C4"
/clone="NP5046-3-1"
/note="flanking P{GaWB} transposon insertion"
                                                                                                                                                                                       Length 800;
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                                                                                                                                                                            Query Match 86.3%; Score 16.4; DB 10;
Best Local Similarity 94.4%; Pred. No. 7.9e+02;
Matches 17; Conservative 0; Mismatches 1;
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Baylor College of Medicine
One Baylor Plaza, Houston, TX 77030, USA
Tel: 713-798-6667
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NCBI Trace Archive: 226715407
Insert Length: 1750 Std Error: 0.25.
Location/Qualifiers
1. .1104
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/db_xref="taxon:7237"
/clone="A19"
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BZ718658 54-FEB-2003 PUCEY69TD ZM_0.6_1.0_KB Zea mays genomic clone ZMMBTal31K17,
Contact: Bharti,A.K.
Dr.Joachim Messing's lab
The Plant Genome Initiative at Rutgers, Waksman Institute, Rutgers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Lillopsida, Poales, Poaceae, PACCAD
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/clone="zMMBTal31K17"
/clone=lib="zM=06.1.0 KB"
/note="Vector: pCR4-T0PO; Site_1: EcoRI; 0.6-1.0 kb high
CoT selected genomic DNA library"
                                                                                                                                                                                                                                                                                                                                    /db.cree="racon:4577"
/clone="ZMMBBb0422D13"
/lab_host="E. coli DH10B"
/clone llb="ZMMBBb (HindIII)"
/note="Vector: pCUG1; Site_1: HindIII; Site_2: HindIII"
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11 (bases 1 to 547)
12 (bases 1 to 547)
13 (bases 1 to 547)
14 (bases 1 to 547)
15 (bases 1 to 547)
16 (bases 1 to 547)
17 (bases 1 to 547)
18 (bases 1 to 547)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 84.2%; Score 16; DB 10; Length 527; Best Local Similarity 100.0%; Pred. No. 1.2e+03; Matches 16; Conservative 0; Mismatches 0; Indels
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                                                                             190 Freilinghuysen Road, Piscataway, NJ 08854, USA Tel: 732 445 5801
Fax: 732 445 5735
Famail: bharti@waksman.rutgers.edu
Seq primer: SP6
Class: BAC ends
High quality sequence start: 94.
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                                                                                                                                                                                                                                                                                                   /mol_type="genomic DNA"
/cultivar="B73"
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/strain="B73"
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 genomic survey sequence.
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Contact: Cathy Whitelaw
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Fax: 301-838-0208
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Zea mays
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                                                              CC751821 485 bp DNA linear GSS 25-JUN-2003
ZMMBBb0133A01.r ZMMBBb Zea mays genomic clone ZMMBBb0133A01 3',
                                                                                                                                                                                                            Zea mays

Makaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
I (bases 1 to 485)
Yu, Y. Kim, H.R., Hatfield, J., Soderlund, C., Bharti, A.K., Messing, J.
and Wing, R.
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1 (bases 1 to 527)
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/note="Vector: pBeloBAC11; Site_1: HindIII; Site_2:
HindIII; Zea mays L. ssp. mays"
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                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Rod Wing,
Arizona Genomics Institute
University of Arizona
Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ
85721-0088, USA
Tel: 520 626 3967
Fax: 520 621 9288
Email: rwing@genome.arizona.edu
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ZMMBBb0422D13r ZMMBBb (HindIII) Zea mays genomic clone
ZMMBBb0422D13 3', genomic survey sequence.
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/cultivar="B73"
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/clone="ZMMBBb0133A01"
/lab_host="DH10B"
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organism="Zea mays"
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CC751821.1 GI:32211287
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CL414924.1 GI:45273060
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Best Local Similarity 100.0
Matches 16; Conservative
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Class: BAC ends.
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Zea mays
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CL414924/c
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Matches 16; Conservative
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/note="Vector: pCMVSport6.1 (Invitrogen); Site 1: Not1;
Site 2: Smal; Arrayed normalized library of full-length
cDNAs representing blastula stage transcriptome of the sea
urchin Strongylocentrotus purpuratus, cloned into the
vector pCMVSport6.1 (Invitrogen)"
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                                                                                                                                                          EST 19-JAN-2005
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                                                                                                                                                                                                                                                                                                                                                  Strongylocentrotidae; Strongylocentrotus.
1 (bases 1 to 595)
Coffman.J.A., Robertson.A.J., Clifton,S., Pape,D., Hillier,L.,
Martin,J., Wylie,T., Dante,M., Meyer,R., Theising,B., Bowers,Y.,
Gibbons,M., Ronko,I., Tsagareishvili,R., Ritter,E., Kennedy,S. and
                                                                                                                                                                              purpuratus cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: est@watson.wustl.edu
DNA sequencing by: Washington University Genome Sequencing Center
Seq primer: -28RPDOT
High quality sequence stop: 595.
Location/Qualifiers
                                                                                                                                                      CX698830 Partin EST 19-JAN-2 linear EST 19-JAN-2 Ydb82909.72 Sea urchin EST Libl. Strongylocentrocus purpuratus ci clone ydb82909 5' similar to TR:Q94532 Q94532 PUTATIVE TYPE III ALCOHOL DEHYDROGENASE. [1] ;, mRNA sequence.
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Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
Echinoidea; Euechinoidea; Echinacea; Echinoida;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
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Pred. No. 1.3e+03;
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Mismatches
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/db_xref="taxon:7668"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (2004)
Contact: Dr. James A. Coffman
WashU Sea urchin EST Project
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Strongylocentrotus purpuratus
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/lab_host="DH10B"
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100.0%; Pre
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                                  3 CCTGAATGCGGCTAAT
                                                          408 CCTGAATGCGGCTAAT
16; Conservative
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Best Local
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/note=_record to the provided by the property of full-length Site_2: Smal; Arrayed normalized library of full-length Site_2: Smal; Arrayed normalized library of full-length or Sons representing blastula stage transcriptome of the sea urchin Strongylocentrotus purpuratus, cloned into the vector pCMVSport6.1 (Invitrogen)"
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Coffman,J.A., Robertson,A.J., Clifton,S., Pape,D., Hillier,L.,
Martin,J., Wylie,T., Dante,M., Meyer,R., Theising,B., Bowers,Y.,
Gibbons,M., Ronko,I., Tsagareishvili,R., Ritter,E., Kennedy,S. and
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Strongylocentrotus purpuratus
Strongylocentrotus purpuratus
Sukaryota; Metazoa; Echinoca; Echinozoa;
Echinoidea; Buechinoidea; Echinacea; Echinoida;
Strongylocentrotidae; Strongylocentrotus;
1 (bases I to 632)
1 (bases I to 632)
Martin, J. A., Robertson, A. J., Clifton, S., Pape, D., Hillier, L.,
Martin, J., Wylie, T., Dante, M., Meyer, R., Theising, B., Bowers, Y.,
Gibbons, M., Ronko, I., Tsagareishvili, R., Ritter, E., Kennedy, S. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA sequencing by: Washington University Genome Sequencing Center Seq primer: -28RPpOT High quality sequence stop: 596. Location/Qualifiers
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Unpublished (2004)
Contact: Dr. James A. Coffman
WashU Sea urchin EST Project
WashIngton University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Fax: 314 286 1810
Email: est@watson.wustl.edu
DNA sequencing by: Washington University Genome Sequencing Center
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Bukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
Echinoidea; Euechinoidea; Echinacea; Echinoida;
Strongylocentrotidae; Strongylocentrotus.
                                                                                                                                                                                                                                                                                                     Unpublished (2004)
Contact: Dr. James A. Coffman
WashU Sea urchin EST Project
Washington University School of Medicine
4444 Porrest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Pax: 314 286 1810
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1.3e+03;
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100.0%; Pred. No.
:ive 0; Mismatch
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/db_xref="taxon:7668"
/clone="ydd56d01"
/lab_host="DH108"
                                                                                                                                                                                                                                                                         WashU Sea Urchin EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: est@watson.wustl.edu
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CX691884.1 GI:57953941
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EST 19-JAN-2005

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CX692600 676 bp mRNA linear EST 19-JAN-2005 yde83d07.y2 Sea urchin EST Libl Strongylocentrotus purpuratus cDNA clone yde83d07 5' similar to TR:Q9U2M4 Q9U2M4 Y38FIA.6 PROTEIN. [1]
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Eukaryota, Metazoa, Echinodermata, Eleutherozoa, Echinozoa,
Eukaryota, Metazoa, Echinodea, Echinodea,
Echinoidea, Euchinoidea, Etrongylocentrotus,
1 (baes 1 to 676)
1 (baes 1 to 676)
1 (offman,J.A., Robertson,A.J., Clifton,S., Pape,D., Hillier,L.,
Martin,J., Wyle,T., Dante,M., Meyer,R., Theising,B., Bowers,Y.,
Gibbons,M., Ronko,I., Tsagareishvili,R., Ritter,E., Kennedy,S. and
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (2004)
Contact: Dr. James A. Coffman
WashU Sea urchin EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Strongylocentrotus purpuratus"
                       Pred. No. 1.3e+03; Mismatches 0;
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/db_xref="taxon:7668"
/clone="yde83d07"
/lab_host="DH10B"
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Fax: 314 286 1810
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Matches 16; Conserv
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                                                                                                                                                                                                                                                                     /lab host="DH10B"
/clone_lib="Sea urchin EST Libl"
/clone_lib="Sea urchin EST Libl"
/note="Vector: pCWVSport6.1 (Invitrogen); Site_1: Not1;
Site_2: Snal; Arrayed normalized library of full-length
cDNAB representing blastula stage transcriptome of the sea
urchin Strongylocentrotus purpuratus, cloned into the
vector pCWVSport6.1 (Invitrogen)"
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/note="Vector: pCMVSport6.1 (Invitrogen); Site 1: Not1;
Site 2: Sna1; Arrayed normalized library of full-length
cDNAs representing blastula stage transcriptome of the sea
urchin Strongylocentrotus purpuratus, cloned into the
vector pCMVSport6.1 (Invitrogen)"
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Coffman,J.A., Robertson,A.J., Clifton,S., Pape,D., Hillier,L.,
Martin,J., Wylie,T., Dante,M., Meyer,R., Theising,B., Bowers,Y.,
Gibbons,M., Ronko,I., Tsagareishvili,R., Ritter,E., Kennedy,S. and
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DNA sequencing by: Washington University Genome Sequencing Center
Seq primer: -28RPpOT
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Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
Echinoidea; Euechinoidea; Echinacea; Echinoida;
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         84.2%; Score 16; DB 8; Length 632; 100.0%; Pred. No. 1.3e+03; ive 0; Mismatches 0; Indels

    632
/organism="Strongylocentrotus purpuratus"

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High quality sequence stop: 519.
Location/Qualifiers
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/db_xref="taxon:7668"
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/db xref="taxon:7668"
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Contact: Dr. James A. Coffman
WashU Sea urchin BST Project
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Strongylocentrotus purpuratus
                                               High quality sequence stop: E
Location/Qualifiers
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WashU Sea Urchin EST Project
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                Seq primer: -28RPpOT
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Best Local Similarity
Matches 16; Conserv
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COMMENT
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/note="Vector: pcMVSport6.1 (Invitrogen); Site 1: Not1; Site 2: Smal; Arrayed normalized library of full-length CDNB representing blastula stage transcriptome of the sea urchin Strongylocentrotus purpuratus, cloned into the vector pcMVSport6.1 (Invitrogen)"
                                                                                                                                                                                                                                                                                                                                                                                                                                           CC751823 1near GSS 25-JUN-2003 ZMMBBb0133A03.r ZMMBBb Zea mays genomic clone ZMMBBb0133A03 3',
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                                                                                                                                                                                      Length 676;
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                                                                                                                                                                                 84.2%; Score 16; DB 8; Le
100.0%; Pred. No. 1.3e+03;
iive 0; Mismatches 0;
/clone_lib="Sea urchin EST Lib1"
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Zea mays
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KEYWORDS
SOURCE
ORGANISM
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DB 8; Length 675;

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column: 07
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Unpublished (1997)
                                                                                                                                                                                                                                                                                                                     Best Local Similarity 100.
Matches 16; Conservative
                  row:
                               Seq primer: M13r
Class: BAC ends.
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ZMMBBb0137J07.r ZMMBBb Zea mays genomic clone ZMMBBb0137J07 3',
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (Bases 1 to 784)
Yu,Y., Kim, H.R., Hatfield,J., Soderlund,C., Bharti,A.K., Messing,J.
and Wing,R.
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1 (bases 1 to 787)
Yu,Y., Kim,H.R., Hatfield,J., Soderlund,C., Bharti,A.K., Messing,J. and Wing,R.
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/note="Vector: pBeloBAC11; Site_1: HindIII; Site_2:
HindIII; Zea mays L. ssp. mays"
                                                                                                                                                                       Arizona Genomics Institute
University of Arizona
Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ
85721-0089, USA
Tel: 520 626 3967
Fax: 520 621 9288
Email: rwing@genome.arizona.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Arizona Genomics Institute
University of Arizona
Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ
85721-0088, USA
Tel: 520 626 3967
Pax: 520 621 9288
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             /mol_type="genomic DNA"
/cultivar="B73"
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BACKWARD: MI31
Plate: 0133 row: A column: 03
Seg primer: MI31
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PCR PRimers
FORWARD: T7
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/lab_host="DH10B"
                                                                                                                    Sequencing of the maize genome Unpublished (2003)
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1. .784
/organism="Zea mays"
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CC753964.1 GI:32215638
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Best Local Similarity 100.
Matches 16; Conservative
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| 1...000
| Lype="mRNA"
| | Mol_type="mRNA"
| | Mole="mctamorphosis stage 62"
| | Mole="organ: Developing Tadpole; Vector: pDNR-LIB; |
| Site 1: Sfil; Site 2: Sfil; 5' and 3' adaptors were used in clouing as follows: 5' adaptor sequence: 5'-ATYCTAGAGGCCGAGGCGCAATG-dT(30) BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.7 kb |
| C, or G and N = A, C, G, or T). Average insert size 1.7 kb |
| Krange 0.8-3.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Drs. Danald Brown and Liquan Cai
Tissue Procurement: Drs. Donald Brown and Liquan Cai
CDNA Library Preparation: CLOWIECH
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LIML)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: NCI-GCAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LiML at:
http://image.llh.gov
Plate: LLCM3248 row: b column: 03
High quality sequence stop: 447.
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809 bp mRNA linear EST 29-APR-2003
AGENCOURT 13841963 NICHD XGC Tad2 Xenopus laevis cDNA clone
INAGE:6933220 5', mRNA sequence.
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1 (bases 1 to 809)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                          /clone lib="ZMMBBb"
/note="Vector: pBeloBAC11; Site_1: HindIII; Site_2:
HindIII; Zea mays L. ssp. mays"
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                                                                                                      /mol_type="genomic DNA"
/cultivar="B73"
/db_xref="taxon:4577"
/clone="ZMMBBb0137J07"
                                1. .787
/organism="Zea mays"
Location/Qualifiers
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us-10-829-474-1.rst

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sequence tags
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Best Local Similarity
Matches 17; Conserv
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                                     ö
                                                                                                                                                                               CG038424 10_KB 2ea mays genomic clone ZMMBTa0672P22,
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1 (bases 1 to 262)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                   Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xxefe="taxon:4577"
/dlone="XMMBTa672P22"
/clone="Ib="ZM-0.61.0 KB"
/note="Vector: pCK4-TOPO; Site 1: EcoRI; 0.6-1.0 kb high
CoT selected genomic DNA library"
                                                                                                                                                                                                                                                                                                                                 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD, clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 838)
Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T.,
Resnick, A., Fraser, C.M., Yuan, Y., San Miguel, P., Ma, J. and
Bennetzen, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                     Gaps
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MRO-BN0070-120500-021-a06_1 BN0070 Homo sapiens cDNA, mRNA
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llarity 100.0%; Pred. No. 1.3e+03;
Conservative 0; Mismatches 0; Indels
 DB 6; Length 809;
1.3e+03;
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                                Mismatches
84.2%; Score 16;
100.0%; Pred. No.
ive 0; Mismatch
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/mol_type="genomic DNA"
/strain="B73"
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Class: sheared ends.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
                                                                                                                                                                                                               genomic survey sequence.
CG038424
CG038424.1 GI:33910580
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (2003)
Other GSSs: PUFKT95TB
Contact: Cathy Whitelaw
                                                                                     454 CCCCTGAATGCGGCTA 469
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CG038424/c
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/mol_Lype="mrm" or properties of the following and conditions of the stranger of the following products of the from 1b="breast normal; Vector: puc18; Site_1: Smal; Site_2: Smal; A mini-library was made by cloning products of the stranger from Or RESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC18 vector. Reverse transcription of tissue mRNA and CDNA amplification were performed under low stringency conditions."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=MRO-BN0070-120 500-021-a06_1&t3=2000-05-12&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 262.
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Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Mateukuma, A., Bala, G.S., Sinpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
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Oryza sativa (japonica cultivar-group)
Bukaryota, Vizidiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 300)
Sasaki,T. and Yamamoto,K.
Ellowering stage (2001)
Unpublished (2001)
                                                                                                                                                                                                                                                                                           Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                Shotgun sequencing of the human transcriptome with ORF expressed
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PROJECT = 'RGP'.
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National Institute of Agrobiological Resources
Rice Genome Research Program, Kannondai 2-1-2,
305-8602, Japan
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llarity 89.5%; Pred. No. 1.5e+03;
Conservative 0; Mismatches 2;
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                                                                                                                                                                                                                             Proc. Natl. Acad. Sci.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tel: +55-11-2704922
Fax: +55-11-2707001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tel: 81-298-38-7441
Fax: 81-298-38-7468
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Hordeum vulgare subsp. vulgare

Hordeum vulgare subsp. vulgare

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Pooldeae; Triticeae; Hordeum.

El (bases 1 to 417)

Sato,K., Saisho,D. and Takeda,K.

Barley EST sequencing project in NIG and Okayama Univ

Unpublished (2002)

Contact: Tadasus Shin-i

Contect: Tadasus Shin-i

Contect: Tadasus Shin-i

Contect: Tadasus Shin-i

Tal: 81-559-81-6856

Fax: 81-559-81-6856

Fax: 81-559-81-6856

Fax: 81-559-81-6856

Fax: Brail: tshini@genes.nig.ac.jp.
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Hordeum vulgare subsp. vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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/tissue type="top three leaves"
/dev stage="adult, heading stage"
/clone_lib="K. Sato unpublished cDNA_library, cv. Haruna
were performed in the
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89.5%; Pred. No. 1.5e+03;
tive 0; Mismatches 2;
                                                                                                                                     83.2%; Score 15.8; DB 2;
89.5%; Pred. No. 1.5e+03;
iive 0; Mismatches 2;
             preparations and DNA sequencing
Anderson lab (all other authors)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /mol_type="mRNA"
/cultivar="Haruna Nijo"
/sub_species="vulgare"
/db_xref="taxon:112509"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tshini@genes.nig.ac.jp.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                     323 CCCTGAGTGCAGCTAATC 341
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BJ473149.1 GI:21151652
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Best Local Similarity
Matches 17; Conserv
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DEFINITION
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BJ468982
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//mol type="mRNA"
//mol type="mRNA"
//mol type="mRNA"
//mol type="mrna"
//do xere="weather fished for a stage="mrna"
//dow stage="relive day old etiolated seedling"
//dow stage="relive day old etiolated seedling"
//dow stage="relive day old etiolated seedling"
//dow stage="relive day old etiolated seedling root cDNA library"
//note="weather: Lambda Uni-Zap KR, excised phagemid;
//dome lib="wheat etiolated seedling root cDNA library"
//note="weather: Lambda Uni-Zap KR, excised phagemid;
//dome lib="wheat etiolated and grown aseptically in
the dark at room temperature on filter paper with water,
nystatin and cefotaxime in covered crystallization
nystatin and cefotaxime in covered crystallization
dishes. Roots were harvested. The tissue, total RNA, and
poly(A) RNA were prepared, a cDNA library was made, and
the cDNA clones were in vivo excised to give pBluescript
phagemids in the TJ Close lab (Choi, Close, Fenton) at the
University of California, Riverside. Plasmid DNA
                                                                                                                                                                                                                                         /dev_stage="flowering stage"
/clone_lib="Rice panicle at flowering stage"
/note="Organ: panicle, Rice cDNA from panicle at flowering
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Contact: Olin Anderson
Contact: Olin Anderson
West Area, Western Regional Research Center
800 Buchanan Street, Albany, CA 94710, USA
Fers: 5105595918
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The structure and function of the expressed portion of the wheat
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                                                                        /organism="Oryza sativa (japonica cultivar-group)"
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/cultivar="Nipponbare"
/db xref="taxon:39947"
/clone="E3017"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                             83.2%; Score 15.8; DB 1; Length 300; 89.5%; Pred. No. 1.5e+03; ive 0; Mismatches 2; Indels (
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             location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     261 CCCCTGAGTGCAGCTAATC 279
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Best Local Similarity 89.5.
Local 17; Conservative
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JOURNAL
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Hordeum vulgare subsp. vulgare
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Booidaae; Triticae; Hordeum.

( bases 1 to 431)
Radchuk, v., Zhang, H., Weschke, W., Potokina, B. and Wobus, U.
Barley ESTs from developing seeds
Unpublished (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                         cDNA library, cv. Haruna
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; Hordeum.
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Molecular Markers Group, Department Genbank
Institute of Plant Genetics and Crop Plant Research (IPK)
Correnstr. 3, 06466, Gatersleben, Germany
Tel: 039482-5522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 15.8; DB 3; Length 422;
Pred. No. 1.6e+03;
0; Mismatches 2; Indels (
                                                                       Okayama Univ
                                                                                                                                                                                                                                                                                                                                                             /clone="baal38103"
/tissue type="top three leaves"
/dev.stage="adult, heading stage"
/clone lib="K. Sato unpublished cDNA librar
Nijo adult, heading stage top three leaves"
                                                                                                                                                                                                                                                                          organism="Hordeum vulgare subsp. vulgare"
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                                                                                                                                                              1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
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/tissue_type="developing caryopsis"
                                Sato,K., Saisho,D. and Takeda,K.
Barley EST sequencing project in NIG and Unpublished (2002)
Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
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                                                                                                                                                                                                                                                                                       /mol type="mRNA"
/cultivar="Haruna Nijo"
/sub_species="vulgare"
/db_xref="taxon:112509"
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|db_xref="GABI:236006"
|db_xref="taxon:112509"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: stein@ipk-gatersleben.de
Insert Length: 431 Std Brror:
Plate: 16 row: N column: 7
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Location/Qualifiers
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/cultivar="Barke"
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Best Local Similarity 89.5%; Pr
Matches 17; Conservative 0;
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AZ233765
RPCI-23-99L13.TJ RPCI-23 Mus musculus genomic clone RPCI-23-99L13,
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Akinret, B., Levins, M., Mcgann, S., Tsegaye, G., Geer, K., Krol, M., de
Jong, P. and Fraser, C.M.
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Clones are derived from the mouse BAC library RPCI-23. For BAC

Clones are derived from the mouse BAC library availability, please contact Piecer de Jong

Iphrary availability, please contact Piecer de Jong

(piecer@dejong.med.buffalo.edu). Clones may be purchased from

BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm)

or from Resea ch Genetics (info@resgen.com). BAC end page:

http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html

Seq primer: SP6
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/note="Organ: Kidney/Brain; Vector: pBACe3.6; Site_1:
EcoRI; Site_2: EcoRI; Female C57BL/6J mouse kidney and/or
brain genomic DNA was isolated and partially digested
with a combination of EcoRI and EcoRI Methylase. Size
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Mammalia; Eutheria; Buarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     selection for recombinats is not 100% reliable.
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'dev_stage="8-15 DAP (days after pollination)"
'lab_host="XL10-Gold"
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Department of Eukaryotic Genomics
The Institute for Genomic Research
712 Medical Center Dr., Rockville, MD 20850, USA
712: 301 838 0208
Fax: 301 838 0208
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Unpublished (1999)
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/clone="RPCI-23-99L13"
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227 CCCTGAGTGCAGCTAATC 245
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CA657673
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Mukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Pooldeae, Triticeae, Hordeum.
I (bases I to 4556)
Zierold, U. and Schweizer, P.
Transcriptome analysis of mlo-mediated resistance in the epidermis
 selected DNA was cloned into the pBACe3.6 vector at the
                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mol. Plant Pathol. (2005) In press
Contact: Patrick Schweizer
Transcriptome Analysis, Cytogenetics Department
Institute of Plant Genetics and Crop Plant Research (IPK)
Correnser. 3, D-06466 Gatersleben, Germany
Tel: 0049 (0)39482-5660
Fax: 0049 (0)39482-5595
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                                                                              83.2%; Score 15.8; DB 9; Length 443; 89.5%; Pred. No. 1.6e+03; ive 0; Mismatches 2; Indels (
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/tissue type="leaf epidermis, 6 h an inoculation with Blumeria graminis"
/dev stage="7 d after germination"
/lab_host="XL10-Gold"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: schweiz@ipk-gatersleben.de
Insert Length: 456 Std Brror: 0.00
Plate: 16 row: I column: 14
Seg primer: SK.
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/cultivar="Ingrid BC mlo-5"
/db_xref="GABI:1094605"
/db_xref="taxon:4513"

    .456
    /organism="Hordeum vulgare"

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DN183928.1 GI:60279185
                                                                Query Match
Best Local Similarity 89.5-
Best Local 17; Conservative
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Gaps

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1 CCCCTGAATGCGGCTAATC 19

17; Conservative

Matches

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Hordeum vulgare subsp. vulgare
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; Hordeum.

El (bases 1 tro 463)
Sato,K., Saisho,D. and Takeda,K.
Barley EST sequencing project in NIG and Okayama Univ
Unpublished (2002)
Contact: Tadasu Shin-i
Contact:
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ISM Triticum aestivum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Bopermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Pooideae; Triticae; Triticum.

I (bases 1 to 472)

STINGEY,S.V., Powell,W., Wolters,P., Dolan,M., Hainey,C., Yuan,Z.,

Miao,G., Caraher,N. and Hanafey,M.K.

DuPont Wheat cDNA Sequence

U mpublished (2002)

Contact: Scott V. Tingey

Crop Genetics

E. I. DuPont de Nemours and Company
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AV932335 K. Sato unpublished cDNA library, cv. Haruna Nijo adult, heading stage top three leaves Hordeum vulgare subsp. vulgare cDNA clone baal3d09 5', mRNA sequence.
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/clone lib="K. Sato unpublished cDNA library, cv. Haruna
Nijo adult, heading stage top three leaves"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        organism="Hordeum vulgare subsp. vulgare"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /tissue_type="top three leaves"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /sub_species="vulgare"
/db_xref="taxon:112509"
/clone="baal3d09"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /mol_type="mRNA"
/cultivar="Haruna Nijo"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: tshini@genes.nig.ac.jp.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 CCCCTGAATGCGGCTAATC 19
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                                                                                                                                                                                                                                                              AV932335.1 GI:18228132
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Best Local Similarity
Matches 17; Conserv
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JOURNAL
COMMENT
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GSS 16-JUN-2003

to 398

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Email: rholt@bcgsc.ca

clones are derived from the bovine BAC library CHORI-240

(http://www.chori.org/bacpac/bovine240.htm). For BAC library

availability, please contact Pierer de Jong (pdejong@mail.cho.org).

Clones may be purchased from BACPAC Resources

(http://www.chori.org/bacpac/ordering_information.htm). This work

was undertaken as part of the International Bovine BAC Mapping

Consortium (IBBMC) by CSIRO Livestock Industries, Australia and the

British Columbia Genome Sciences Centre, Canada.

Seq primer: SP6

Gaprimer: SP6
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HO16J13S HO Hordeum vulgare cDNA clone HO16J13 5-PRIME, mRNA
sequence.
                                                                                                                                                                                                                                                                                                                                                                                                             Holt, R., Stott, J., Yang, G., Barber, S., Smailus, D., Prabhu, A.-L., Tsai, M., Cloutier, A., Lee, D., Girn, N., Olson, T., Mayo, M., Butterfield, Y., Kirkpatrick, R., Liu, J., Guin, R., Chan, A., Mathewson, C., Way, N., Masson, A., Brown-John, M., Jones, S., Schein, J., Marra, M., G. Jong, P., McMilliam, S., Barris, W., Dalrymple, B.P. and Tellam, R.

Bovine BAC End Sequences from Library CHORI-240, PLATES 294 to 398
                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
Pecora; Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone_ilb="CHORI-240"
/note="Vector: pTARBAC1.3; Site_1: MboI; Site_2: MboI;
Hereford bull L1 Domino 99375; CHORI-240 Bovine BAC
library (Male) produced by Pieter de Jong"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    600 W. 10th Ave, Vancouver, British Columbia, Canada V5Z 4E6
Tel: 604-877-6085
                                                                                                               CH240_296A12.TARBAC13P2 CHORI-240 BOB taurus genomic clone CH240_296A12, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 494;
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Pred. No. 1.6e+03;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /mol_type="genomic DNA"
/strain="breed: Hereford"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       organism="Bos taurus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone="CH240_296A12"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             db_xref="taxon:9913"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (2003)
Other GSSs: CH240 296A12.T7
Contact: Rob Holt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               type="Blood"
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                   448 CCCCTGAATGTGGCTAAAC 430
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                                                                                                                                                                                                                              CC472389.1 GI:31749506
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89.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /sex="Male"
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Bos taurus
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Best Local Similarity
Matches 17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequencing
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LOCUS
DEFINITION
                                                                                                             CC472389/c
LOCUS
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ORGANISM
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                                                                                                                                                                                                      ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                    AUTHORS
                                                                                         RESULT 44
                                                                                                                                                                                                                            VERSION
KEYWORDS
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Characteristics of the Lotus japonicus gene repertoire deduced from
large-scale expressed sequence tag (EST) analysis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: asamizu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lotus corniculatus var. japonicus (Lotus japonicus)
Lotus corniculatus var. japonicus
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Loteae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone="MPD061h04 f"
/tissue_type="Pods (20-30 mm in length)"
/clone_lib="Lotus japonicus Pods (20-30 mm in length)"
/note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2:
                                                                                                                                                                                                                                             /db xref="taxon.4565"
/clone="wlm0.pk038.i13"
/tissue type="leaf"
/clone_Tib="wlm0"
/note="Vector: pBluescript SK+; Site 1: EcoRI; Site 2:
/note="Weat (Triticum aestivum L.) seedlings 0 hr after inoculation with Erysiphe graminis f. sp tritici"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
1 Innovation Way, P.O. Box 6104, Newark, DE 19714-6104, USA Tel: 302-631-2602
Rax: 302-631-2607
Email: Scott.V.Tingey@USA.dupont.com
Seq primer: M13.
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AV774105 Lotus japonicus Pods (20-30 mm in length) Lotus corniculatus var. japonicus CDNA clone MPD061h04_£ 3', mRNA
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/mol_type="mRNA"
/molate="Miyakojima MG-20"
/db_xref="taxon:3430s"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  83.2%; Score 15.8; DB 1; Length 487;
89.5%; Pred. No. 1.6e+03;
ive 0; Mismatches 2; Indels C
                                                                                                                                                                                                                                                                                                                                                                                                                                                             83.2%; Score 15.8; DB 6; Length 472;
89.5%; Pred. No. 1.6e+03;
iive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
                                                                                                                                                                            organism="Triticum aestivum"
                                                                                                                                                                                                    'mol_type="mRNA"
'cultivar="Stephens"
                                                                                                                                Location/Qualifiers
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AV774105.1 GI:45397780
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 89.5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17; Conservative
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VERSION
KEYWORDS
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AUTHORS
TITLE
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COMMENT
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Best Local Similarity 89.5
Matches 17; Conservative
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JOURNAL
COMMENT
                       JOURNAL
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KEYWORDS
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                                           COMMENT
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/note="Vector: pBluescript SK+; Site_l: EcoRI (5'-end of CDNA); Site_2: Xhol (3'-end of CDNA); Approximately 5 % of the clones correspond to cDNA from the fungi B. graminis horder and tritici, respectively. Due to a cloning attefact caused by the kit, in most cases the EcoRI site is NOT present, as well as the EcoRIadapter used for cloning. To excise the insert, restriction sites upstream EcoRI should be used (e.g. BamHI, Sall, Pstl). NOTE: Also due to the cloning system used Blue/White selection for recombinate is not 100% reliable. Average insert size is 1.2 kb"
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                                                                               Hordeum vulgare
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; Hordeum.
1 (bases 1 to 511)
Zierold,U. and Schweizer,P.
                                                                                                                                                                                       Transcriptome analysis of mlo-mediated resistance in the epidermis of barley
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Harrison, M.J., Liu, J., Peng, H., Gonzales, M., Ellis, L., Town, C.D., Bowman, C.L., Craven, M.B., Hansen, T.S., Holt, I.E. and Fraser, C.M. ESTs from roots of Medicago truncatula after colonization with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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library CDNA clone MHAM-23C8, mRNA sequence.
                                                                                                                                                                                                                                                                  Contact: Patrick Schweizer
Transcriptome Analysis, Cytogenetics Department
Institute of Plant Genetics and Crop Plant Research (IPK)
Correnstr. 3, D-06466 Gatersleben, Germany
Tel: 0049 (0)39482-5660
Fax: 0049 (0)39482-5595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /tissue_type="leaf epidermis, 6 h and 24 h post
inoculation with Blumeria graminis"
dev stage="7 d after germination"
lab_host="XL10-Gold"
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1 (bases 1 to 513)
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Pred. No. 1.6e+03;
0; Mismatches 2; Indels (
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                                                                                                                                                                                                                                                                                                                                                                                             Email: schweiz@ipk-gatersleben.de
Insert Length: 511 Std Error: 0.00
Plate: 16 row: J column: 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /mol_type="mRNA"
/culTivar="Ingrid BC mlo-5"
/db_xref="GABI:1094623"
/db_xref="taxon:4513"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'organism="Hordeum vulgare"
                                                                                                                                                                                                                                                   Mol. Plant Pathol. (2005) In press
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 513 bp
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                   DN183756.1 GI:60279013
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89.5%;
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Best Local Similarity 89.5'
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                                                            Hordeum vulgare
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/tissue_type="roots colonized with Glomus versiforme"
/dev_stage="Roots harvested at 10, 17, 22, 31 and 38 days
post-inoculation with Glomus versiforme. The library was
made from a mixture of RNA from each of these stages."
/lab_hore="E. coli strain XLOLR"
/lab_hore="E. coli strain XLOLR"
/lab_hore="Tector: pBluescript SK-; Site_1: EcoRI; Site_2:
XhoI; cDNA was prepared from polyA+ enriched RNA from
roots harvested at 10, 17, 22, 31 and 38 days
post-inoculation with Glomus versiforme. The cDNA was
directionally ligated into the Unizap XR vector from
Stratagene and packaged using Gigapack III Gold packaging
extracts. Plasmids containing CDNA inserts were excised
Glomus versiforme
Unpublished (2000)
Contact: Harrison M.J.
Plant Biology Division
The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73401
Tel: 580-223-5810
Fax: 580-221-7380
Email: mjharrison@noble.org
Corper name: MHAM-23b-B04; Date: 3/14/00; Updated to the Database of Expressed Sequence Tags (dbEST) on 04/27/00; More information is available at "http://chrysie.tamu.edu/medicago'.
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/organism="Medicago truncatula/Glomus versiforme mixed EST
library"
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Entratroideae; Oryzae.

I (bases 1 to 525)

Cho, S.K., Jeung, J.U., Shim, K.S., Jung, K.W., Kang, K.H., Chung, Y.S., Ok, S.H., Choi, H.C. and Shin, J.S.

Oryza minuta 101144 subtracted cDNA library
Unpublished (2003)

Contact: Sung Ki Cho, Ji Ung Jeung, Kyu Suk Shim, Kwang Wook Jung, Kyung Hok Anng, Young Soo Chung, Sung Han Ok, Hae Chune Choi and Plant Molecular Genetics
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                from the recombinant lambda-Zap phage using Ex-assist helper phage and propagated in XLOLR cells."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /mol_type="mRNA"
/culfivar="medicago truncatula genotype A17"
/db xref="taxon:119092"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         83.2%; Score 15.8; DB 1; Length 513; 89.5%; Pred. No. 1.6e+03; ive 0; Mismatches 2; Indels (
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Length 525;

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83.2%;
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                                                                                                                                                                                            /dev_stage="Wound treatment & vegetative stage" / Cone_lib="Orgxa minte 101144 subtracted CDNA library" / Cone_lib="Orgxa minte 101144 subtracted CDNA library" / note="Vector: pCR2.1(Invitrogen); After the suppression subtractive hybridization and MOS (Nucleic Acids Research, Vol 28, No 20, e90), cDNA fragments induced by wound treatment were cloned by TA cloning method, and screened by microarray.
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Spermatoldeae; Oryzeae; Oryza.
1 (bases 1 to 525)
Cho,S.K., Jeung,J.U., Shim,K.S., Jung,K.W., Kang,K.H., Chung,Y.S.,
Ok,S.H., Choi,H.C. and Shin,J.S.
Oryza minuta 101144 subtracted cDNA library
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Kyung Ho Kang, Young Soo Chung, Sung Han Ok, Hae Chune Choi and
Jeong Sheop Shin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     School of Life Science and Biotechnology, Korea University 5 Ga, Anam-Dong, Sungbuk-Gu, Seoul, 136-701, Republic of Korea Tel: 82 2 3290 3430 Fax: 82 2 927 9028 Email: jsshin@korea.ac.kr
                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                         83.2%; Score 15.8; DB 6; Length 525;
.larity 89.5%; Pred. No. 1.6e+03;
Conservative 0; Mismatches 2; Indels
                                                                             'organism="Oryza minuta"
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|mol_type="mRNA"
|strain="101144"
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/clone="omii-855"
                                                                                                                                                                            tissue_type="leaf"
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Seq primer: M13R.
Location/Qualifiers
                                      Location/Qualifiers
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                                                                                           /mol_type="mRNA"
/strain="101144"
                                                                                                                                                          /clone="omwi-146"
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email: jsshin@korea.ac.kr
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                      Seg primer: M13R
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Hordeum vulgare subsp. vulgare

Hordeum vulgare subsp. vulgare

Hordeum vulgare subsp. vulgare

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Pooideae; Triticeae; Hordeum.

El (bases 1 to 544)

Sato,K., Saisho,D. and Takeda,K.

Barley EST sequencing project in NIG and Okayama Univ

Unpublished (2002)

Contact: Tadasu Shin-i

Contact: Tadasu Shin-i

Conter For Genetic Resource Information

National Institute of Genetics

1111 Yata, Winshima, Shizuoka 411-8540, Japan

Tel: 81-559-81-6855
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                                                                                                                                                                                                                                                                                             BJ469271 EST 23-MAY-2002 BJ465271 K. Sato unpublished cDNA library, cv. Haruna Nijo adult, heading stage top three leaves Hordeum vulgare subsp. vulgare cDNA clone baal13p10 5', mRNA sequence.
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                                                       Gaps
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/dev_stage="adult, heading stage"
/clone_lib="K. Sato unpublished cDNA library,
Nijo adult, heading stage top three leaves"
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Score 15.8; DB 6;
Pred. No. 1.6e+03;
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89.5%; Pred. No. 1.6e+03;
iive 0; Mismatches 2;
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SSS; genome survey sequence.
Takifugu rubripes (Fugu rubripes)
Takifugu rubripes
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/db_xref="taxon:112509"
/clone="baal13p10"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /mol_type="mRNA"
/cultivar="Haruna Nijo"
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clone 0
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Location/Qualifiers
                                                                                                                                         488 CCCCTGAGTGCAGCTAATC 470
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                                                                                                          1 CCCCTGAATGCGGCTAATC 19
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AL004093
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40442rsiceg 8967.yl Oryza sativa cv. 93.11 tillering whole plant CN37253
CK037253.1 G:58609220
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Oryza sativa (indica cultivar-group)
Oryza sativa (indica cultivar-group)
Eukaryota, Vizidplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryza.

1 (baes 1 to 564)
Yu,J., Wang,J., Lin,W., Li,S., Li,H., Zhou,J., Ni,P., Dong,W.,
Thu,S., Zeng,C., Zhang,J., Zhang,Y., Li,R., Xu,Z., Li,S., Li,S.,
Zheng,H., Cong,L., Lin,L., Yin,J., Geng,J., Li,G., Shi,J., Liu,J.,
Li,C., Ren,X., Wang,J., Wang,X., Li,D., Liu,D., Zhang,X., Wu,Q.,
Li,C., Ren,X., Wang,J., Wang,X., Li,D., Liu,D., Zhang,X., Ji,Z.,
Zhao,W., Sun,Y., Zhang,Z., Bao,J., Han,Y., Dong,L., Ji,J., Chen,P.,
Wu,S. and Liu,J.
                                                                                                                                                                                                                                                   EST 04-FEB-2005
                                                                                                                                                                                                                                     564 bp mRNA linear EST 04-FEB-2(a) 15350rsicee 11213.yl Oryza sativa cv. LYP9 tillering whole plant cDNA library Oryza sativa (indica cultivar-group) cDNA 5', mRNA sequence.
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/clone lib="oryza sativa cv. LYP9 tillering whole plant
cDNA library"
                                                Gaps
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/organism="Oryza sativa (indica cultivar-group)"
/mol_type="mrNa"
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/db_xref="taxon:39946"
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Score 15.8; DB 3; Length 546; Pred. No. 1.6e+03;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Yan Zhou
Bioinformatics Department
Hangzhou Genomics Institute
No.51 Zhijiang Road, Hangzhou 310008, China
Tel: 86-571-56805886
Pax: 86-571-56805884
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           83.2%; Score 15.8; DB 7;
89.5%; Pred. No. 1.6e+03;
ilve 0; Mismatches 2;
                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: zhouyan@genomics.org.cn
Seg primer: M13 Forward
High quality sequence stop: 564
PoLYA-No.
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83.2%;
  Query Match
Best Local Similarity 89.5'
Matches 17; Conservative
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Best Local Similarity 89.5
Matches 17; Conservative
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CF992378
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Hordeum vulgare subsp. spontaneum
Hordeum vulgare subsp. spontaneum
Bukaryota, Viridiplantae, Streptophyta, Embryophyta; Tracheophyta, Spermatophyta; Magnoliophyta, Liliopsida, Poales, Poaceae,
Pooddeae; Triticaee, Hordeum.
E 1 (bases I to 546)
Sato, K., Saisho, D. and Takeda, K.
Barley EST sequencing project in NIG and Okayama Univ
Unpublished (2002)
Contect: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
Illi Yata, Mishima, Shizuoka 411-8540, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              546 bp mRNA linear EST 23-MAY-2002 BJ47716 K. Sato unpublished cDNA library, strain H602 adult, heading stage top three leaves Hordeum vulgare subsp. spontaneum BJ47216 BJ47216.
  Generation and analysis of 25 Mb of genomic DNA from the pufferfish
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                                                                                   Elgar, G., Clark, M., Smith, S., Meek, S., Warner, S., Umrania, Y., Williams, G. and Brenner, S.
Milliams, G. and Brenner, S.
Submitted (09-SEP-1997) MRC Human Genome Mapping Project Resource Centre Hinxton, Cambridge, CB10 1SB. Email: biohelp@hgmp.mrc.ac.uk
V_type: phagemid
PRIMER: KS
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/tissue_type="top three leaves"
/dev_stage="adult, heading stage"
/clone lib="X. Sato unpublished cDNA library, strain H602 adult, heading stage top three leaves"
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/mol_type="mRNA"
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                                                                                                                                                                                                                                                                                                                                                                                  1. .545
/organism="Takifugu rubripes"
/mol_type="genomic DNA"
/db_xref="taxon:31033"
/clone="096E20aA7"
/clone_lib="cosmid 096E20"
                         Fugu rubripes by sequence scanning
Genome Res. 9 (10), 960-971 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sub_species="spontaneum"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp.
Location/Qualifiers
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Best Local Similarity 89.5'
Local 17; Conservative
                                                                                                                                                                                                                                                                                                                                           sequence.
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BJ479716
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SOURCE

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National Institute of Livestock and Grassland Science, Nishinasuno
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                                                     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Eukaryota; Viridiplantae; Streptophyta; Enhartochyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Enhartochaea; Oryzae; Oryza.

E Chases 1 to 564)

Yu,J., Wang,J., Lin,W., Li,S., Li,H., Zhou,J., Ni,P., Dong,W., Zhong,H., Cong,L., Lin,L., Yin,J., Geng,J., Li,S., Li,S., Li,S., Li,S., Li,S., Li,S., Li,S., Li,J., Li,J., Li,J., Wang,J., Deng,Y., Ran,L., Shi,Z., Wang,X., Wang,J., Li,D., Liu,D., Zhang,X., Wi,C., Zhao,W., Sun,X., Wang,J., Wang,X., Li,D., Liu,D., Zhang,X., Wi,S., Zhao,W., Sun,X., Zhang,Z., Bao,J., Han,Y., Dong,L., Ji,J., Chen,P., The Genomes of Oryza sativa: A History of Duplications
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AU249544 EST 14-MAR-2005
AU249544 LE Lolium multiflorum cDNA clone LE009H09-5, mRNA
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(basea; Poeae, Lolium.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Oryza sativa"
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/cultivar="93-11"
/du stref="texton:4530"
/tissue_type="whole plant"
/dev stage="tillering"
/clone_lib="doryza sativa cv. 93-11 tillering whole plant
cDNA library"
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Contact: Seiji Yazaki
Contact: Seiji Yazaki
Japan Grassland Agriculture and Forage Seed Association
Forage Crop Research Institute(FCRI)
Higasiakada 388-5, Nishinasuno, Tochigi 329-2742, Japan
Tel: 81-287-37-675
Fax: 81-287-37-675
Email: yazakis@jfsass.or.jp
contact:Tadashi Takamizo (takamizo@affrc.go.jp)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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Bioinformatics Department
Hangzhou Genomics Institute
No.51 Zhijiang Road, Hangzhou 310008, China
Tel: 86-571-56805886
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83.2%; Score 15.8; DB 7;
Best Local Similarity 89.5%; Pred. No. 1.6e+03;
Matches 17; Conservative 0; Mismatches 2;
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Seq primer: M13 Forward
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AU249544.1 GI:46506813
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                                             Oryza sativa
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KEYWORDS
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Kirkness BF
The Institute for Genomic Research
Department of Bukaryotic Genomics, TIGR, 9712 Medical Center Drive,
Rockville, MD 20850, USA
Tel: 301-838-0208
Fax: 301-838-0208
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                                                                                                                                                                                                                                                                                                                Gaps
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Kirkhaes, B.F., Bafna, V., Halpern, A.L., Levy, S., Remington, K.
Rusch, D.B., Delcher, A.L., Pop, M., Wang, W., Fraser, C.M. and
Venter, J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone_lib="Dog_Library"
/note="Site_l: BstXI; Libraries were prepared from
peripheral_blood"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The dog genome: survey sequencing and comparative analysis Science 301 (5641), 1898-1903 (2003)
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Best Local Similarity 89.5%; Pred. No. 1.6e+03;
Matches 17; Conservative '0; Mismatches 2;
                                                                                                                                                                                                                                                            Score 15.8; DB 1;
Pred. No. 1.6e+03;
0; Mismatches 2;
                                              1. .568
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/db_xref="taxon:4521"
/clone="LE009H09-5"
/tissue_type="Leaf"
/clone_lib="LL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                organism="Canis familiaris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /mol_type="genomic DNA"
/strain="Standard Poodle"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     db xref="taxon:9615"
Resistance gene analog.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                      533 ccccreacrecaecraarc 551
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: ekirknes@tigr.org
Class: shotgun.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               enomic survey sequence.
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CE815985.1 GI:37157005
                                                                                                                                                                                                                                                               83.2%;
89.5%;
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                                                                                                                                                                                                                                                                                                           17; Conservative
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Query Match 83.2%;
Best Local Similarity 89.5%;
Matches 17; Conservative (
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VERSION
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TITLE
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US Department of Agriculture, Agriculture Research Service, Pacific
West Area, Western Regional Research Center
Bob Duchanan Street, Albany, CA 94710, USA
Tel: 5105559773
Fax: 5105555818
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                                                                                                 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 570)
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; Triticum.
1 (bases 1 to 572)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Anderson, O.D., Chao, S., Choi, D.W., Close, T.J., Fenton, R.D.,
Han, P.S., Hsia, C.C., Kang, Y., Lazo, G.R., Miller, R., Rausch, C.J.,
Seaton, C.L. and Tong, J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The structure and function of the expressed portion of the wheat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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572 bp mRNA linear EST 21-UT
WHE0426_F08_K16ZS Wheat etiolated seedling root cDNA library
Triticum aestivum cDNA clone WHE0426_F08_K16, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence have been trimmed to remove vector sequence and low quality sequence with phred score less than 20 Seq primer: Strategene SK primer.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /dev stage="4-weeks after germination"
/clone lib="Oryza minuta HybriZAP-2.1 XR library"
/note="Organ: immature leaf"
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                                                                                                                                                                                                                                                                                              University of Korea
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89.5%; Pred. No. 1.6e+03;
ive 0; Mismatches 2; Indels
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                                                                                                                                                                                                           Oryza minuta HybriZAP-2.1 XR library
Unpublished (2003)
                                                                                                                                                                                                                                                     Contact: Jeong Sheop Shin
Plant Molecular Genetics
Graduate School of Biotechnology, U
136-701 Anam-dong 5/1 Seoul, Korea
Tel: 00 82 2 3290 3430
Fax: 00 82 2 927 9028
                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Oryza minuta"
/mol_type="mRNA"
/db_xref="taxon:63629"
                                                                                                                                                                                                                                                                                                                                                                       Email: jsshin@kuccnx.korea.ac.kr.
Location/Qualifiers
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Triticum aestivum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: oandersn@pw.usda.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                144 CCCCTGAGTGCAGCTAATC 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /mol_type="mRNA"
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                                    CB212741.1 GI:28258832
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Unpublished (2000)
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nRNA sequence.
                                                                           Oryza minuta
                                                                                               Oryza minuta
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KEYWORDS
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Triticum aestivum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatorphyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Pooideae; Triticeae; Triticum.

E 1 (bases 1 to 574)

S Cloutier; S., Dong, G. and Walsh, A.

Wheat functional genomics - Thatcher Lrl cDNA library

In Unpublished (2001)

Contact: Dr. Sylvie Cloutier

Cereal Research Centre, Agriculture and Agri-food Canada

195 Dafee Rd, Winnipeg, MB, Canada R3T 2M9

Tel: (204) 983-2340

Fax: (204) 983-24604
                                                                                                                                                                                                                                                                                                                                                                  the dark at room temperature on filter paper with water, nystatin and cefotaxime in covered crystallization dishes. Roots were harvested. The tissue, total RNA, and poly (A) RNA were prepared, a cDNA library was made, and the cDNA clones were in vivo excised to give pBluescript phagemids in the TJ Close lab (Choi, Close, Fenton) at the University of California, Riverside. Plasmid DNA
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was cloned directionally, not all sequences generated with reverse
primer were from the 5' end (same with forward primer and 3' end).
Average inset size is >2.2 kb
Plate: 163 row: H column: 10
Seq primer: M13 Reverse.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               preparations and DNA sequencing were performed in the OD Anderson lab (all other authors)."
                   /db xref="rexx.on:4565"
/clone="WHB0426_F08_K16"
/tismue_type="Root"
/dev stage="Five day old etiolated seedling"
/lab_host="B. coli SOLR"
/lab_host="Wector: Lambda Uni-ZAP XR, excised phagemid;
Site_1: EcoRI; Site_2: XhoI; Seeds were
surface=sterilized, germinated and grown aseptically in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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Pred. No. 1.6e+03;
0; Mismatches 2; Indels (
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/tissue_type="Leaf tissue"
/dev_stage="14 bays old"
/lab_host="E. coli XLOLR"
/clone_lib="Tairl"
cultivar="Chinese Spring"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /mol_type="mRNA"
/cultivar="Thatcher Lr1"
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CX625718/c LOCUS DEFINITION

ð g VERSION KEYWORDS SOURCE ORGANISM

ACCESSION

REFERENCE AUTHORS

TITLE JOURNAL COMMENT

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Oryza sativa (indica cultivar-group)
Oryza sativa (indica cultivar-group)
Oryza sativa (indica cultivar-group)
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta, Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhattoideae, Oryzae, C., Zhang, Y., Li, H., Zhou, J., Ni, P., Dong, W., Hu, S., Zeng, C., Zhang, Y., Li, R., Xu, Z., Li, S., Li, S., Zheng, H., Cong, L., Lin, L., Yin, J., Geng, J., Li, G., Shi, J., Liu, J., Liu, J., Wang, J., Mang, J., Wang, Y., Ran, L., Shi, X., Wang, X., Wu, Q., Li, C., Ren, X., Wang, J., Wang, X., Li, D., Liu, D., Zhang, X., Ji, Z., Zhao, W., Sun, Y., Zhang, Z., Bao, J., Han, Y., Dong, L., Ji, Ji, J., Chen, P., Wu, S., and Liu, J.
                                                                                                                     crys4381 581 bp mRNA linear EST 15-JAN-2004 5763reiceb 9633.yl Oryza sativa cv. PA648 leaf cDNA library Oryza estiva (indica cultivar-group) cDNA 5', mRNA sequence. CF954381
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /tisaue_type="leaf"
/dev_stage="trefoil"
/clone_lib="Oryza sativa cv. PA64s leaf cDNA library"

    581
/organism="Oryza sativa (indica cultivar-group)"
/mol_type="mRNA"
/cultivar="PA64s"

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        83.2%; Score 15.8; DB 7; Length 581;
89.5%; Pred. No. 1.6e+03;
ive 0; Mismatches 2; Indels (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bioinformatics Department
Hangzhou Genomics Institute
No.51 Zhijiang Road, Hangzhou 310008, China
TTE1: 86-571-56805886
Fax: 86-571-56805884
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: zhouyan@genomics.org.cn
Seq primer: M13 Forward
High quality sequence stop: 581
POLYA=No.
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     200 CCCCTGAATGCGGATTATC 182
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CA255155.1 GI:35939755
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Saccharum officinarum
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Best Local Similarity 89.54
Matches 17; Conservative
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CA255155
LOCUS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AUTHORS
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//note="Vector: pCR blunt (Invitrogen); Site_1: NotI;
Site_2: NotI; seedlings were grown at 18 deg_T. C, 60 $
Site_2: NotI; seedlings were grown at 18 deg_T. C, 60 $
rel. humidity, and a photoperiod of 16 h (100 microE * s-1
* m-2). A. 8 days, seedl. were treated with ASM (syn. BTH;
20 ppm soil drench). Leaf epid. was hav. 8, 44, 48, 72.
hpt). PolyA-RNA was isolated from leaf epidermis and used
to create a cDNA-library using the Time Saver
cDNA-Synthesis Kit (Amersham). Normalisation was performed
essentially as described by Ko (1990, Nucl. Acid Res. 16,
9877) with some modification of Kohchi et al. (1995, Plant
J. 8, 771-76). Normalised cDNAs were digested with NotI
and cloned into NortI digested pCRblunt vector.
(GABI-Agrotech Project)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hordeum vulgare
Hordeum vulgare
Bukaryota, Viridiplantae, Streptophyta, Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae, Triticaee, Hordeum.
1 (bases 1 to 579)
Biemelt,S., Jansen,C., Schaefer,P., Hueckelhoven,R., Felk,A.,
Schaefer,W., Scholz,U., Sonnewald,U. and Kogel,K.H.
Barley EST# from different tissues challenged with fungal pathogens
Unpublished (2004)
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                                                                                                                                                                                                                                                                                                                                                                                CX625718 579 bp mRNA linear EST 14-JAN-2005
GAN006111u GAN Hordeum vulgare cDNA clone GAN006111 3-PRIME, mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Sophia Biemelt
Molecular Developmental Physiology, Department Molecular Cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Biology
Institute of Plant Genetics and Crop Plant Research (IPK)
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race BBB carrying the avirulence gene Avrl."
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                                                                                  Length 574;
                                                                                                                                      2; Indels
                                                                          Query Match
83.2%; Score 15.8; DB 2;
Best Local Similarity 89.5%; Pred. No. 1.6e+03;
Matches 17; Conservative 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Corrensstr. 3, 06466 Gatersleben, Germany
Tel: +49 (0)39482-5476
Fax: +49 (0)39482-5515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         tissue type="leaf epidermis"
(lab_host="XL1-Blue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Hordeum vulgare"
mol type="mRNA"
culfivar="Ingrid WT"
db_xref="GABI:861142"
/db_xref="taxon:4513"
/clone="GAN006I11"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: biemelt@ipk-gatersleben.de
Insert Lenghh: 579 Std Brror: 0.00
Plate: 6 row: I column: 11
Seg primer: M13uni.
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CX625718.1 GI:57824505
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1 CCCCTGAATGCGGCTAATC 19
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1 Similarity 89.5%;
17; Conservative (
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Matches 17; Conserv
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//clone lib="FL4"
//clone lib="FL4"
//clone lib="FL4"
//clone lib="FL4"
//clone long); Vector: PSOPCHI, Site l: Sali, Site_2: Not!,
//clonelong); Vector: PSOPCHI, Site_1: Sali, Site_2: Not!,
An unidirectional CDNA library generated from [Developed inflorescence and rachis (20cm-long)]. CDNA was prepared from polyA+ mRNA using SuperScript Plasmid System Kit (Invitrogen). The double-strand cDNAs were fractionated in a sepharose CL-2B 40cm-columns and fragments sizing between 0.8 and 1.5 Kb were directionally cloned into the vector. Details of each source of RNA and library construction can be obtained at http://sucest.lad.ic.unicamp.br/public"
The libraries that made SUCEST
Genet. Mol. Biol. 24 (1-4), 1-7 (2001)
Contact: Arruda P.
Contract: Arruda Biologia Molecular e Engenharia Genetica
Universidade Estadual de Campinas
Caixa Postal 610, 13083-970, Campinas SP, Brazil
Tel: 55 19 3788 1137
Fax: 55 19 3788 1137
Fax: 55 19 3788 1137
Clone distribution: clone distribution information can be found
through the Brazilian Clone distribution information can be found
through the Brazilian Clone Collection Center (BCCC) at
http://www.boccenter.fcav.unesp.br
Plate: 176 row: B column: 07
Seq primer: T7 Promoter Primer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; Triticum.
1 (bases 1 to 597)
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
                                                                                                                                                                                                                                                                                                                                                                         /organism="Saccharum officinarum"
Mol_type="mRNA"
/db xref="taxon:4547"
/clone="SCEPFL4176B07"
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/mol_type="mRNA"
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                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /lab host="DH10B"
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AUTHORS
TITLE
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COMMENT
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JOURNAL
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Triticum assivum (Incompania) Triticum assivum (Incompania) Triticum assivum (Incompania) Triticum assivum (Incompania) Spermatorphyta, Magnollophyta; Liliopsida; Poales; Poaceae; Spermatorphyta, Magnollophyta; Liliopsida; Poales; Poaceae; Pooidaae; Triticaee; Triticum.

1 (bases 1 to 598)

1 (bases 1 to 598)

2 Anderson, O.D., Chao, S., Han, P.S., Heinen, S., Hsia, C.C., Kang, Y., Kruger, W.M., Lazo, G.R., Miller, S., Muehlbauer, G.J., Miller, R., Pritsch, C., Rausch, C.J., Seaton, C.L., Tong, J.C., Vance, C. and Wilson, C.F.

The structure and function of the expressed portion of the wheat genomes - Fusarium graminearum infected spike cDNA library Unpublished (2001)

Contact: Olin Anderson
US Department of Agriculture, Agriculture Research Service, Pacific West Area, Western Regional Research Center

800 Buchanan Street, Albany, CA 94710, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tel: 5105595773

Fax: 5105595818

Email: oandersn@pw.usda.gov

Sequences have been trimmed to remove vector sequence and low

quality sequence with phred score less than 20. No effort was taken

to identify ESTs of fungal origin from this library, thus this EST

could be of wheat or fungal origin.

Seq primer: Strategene SK primer.

Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone="WHE0454"H12"
/tissue type="Spike"
/tissue andlt plant
/lab_host="E. Coli Solm"
/clone_lib="Wheat Fusarium graminearum infected spike cDNA
                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EST 28-NOV-2001
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library Trificum aestivum cDNA clone WHE0454_H12_H12, mRNA
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                                                                                                                                                                                                                                                           Length 597;
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Pred. No. 1.6e+03;
0; Mismatches 2;
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/mol type="mRNA"
/cultivar="Sumai3"
/db_xref="taxon:4565"
/cultivar="recital"
/db xref="taxon:4565"
/clone="AZO3109F19"
/tissue type="leaf"
/clone_lib="AZO3"
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AV933787 K. Sato unpublished cDNA library, cv. Haruna Nijo adult, heading stage top three leaves Hordeum vulgare subsp. vulgare cDNA AV933787
  DN178545 602 bp mRNA linear EST 24-FBB-2005
HO33C05S HO Hordeum vulgare cDNA clone HO33C05 5-PRIME, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="Vector: pBluescript SK+; Site_1: EcoRI (5'-end of CDNA); Site_2: XhoI (3'-end of CDNA); Approximately 5 % of the clones correspond to cDNA from the fungi B. graminis horder and tritici, respectively. Due to a cloning artefact caused by the Kit, in most cases the EcoRI site is NOT present, as well as the EcoRIadapter used for cloning. To excise the insert, restriction sites upstream EcoRI should be used (e.g. BamHI, SalI, PBII). NOTE: Also due to the cloning system used Blue/white selection for recombinats is not 100% reliable. Average insert size is
                                                                                                                                                                Hordeum vulgare
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae;
Pooideae, Triticeae, Hordeum.
                                                                                                                                                                                                                                                           1 (bases 1 to 602)
Zierold, U. and Schweizer, P.
Transcriptome analysis of mlo-mediated resistance in the epidermis
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Hordeum vulgare subsp. vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                                                                                                                                                                                                                                                                                                                               of barley
Mol. Plant Pathol. (2005) In press
Contact: Patrick Schweizer
Transcriptome Analysis, Cytogenetics Department
Institute of Plant Genetics and Crop Plant Research (IPK)
Correnserr. 3, D-06466 Gatersleben, Germany
Tel: 0049 (0)39482-5560
Fax: 0049 (0)39482-5595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24 h post
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incoulation with Blumeria graminis"
'dev stage="7 d after germination"
'lab_host="XL10-Gold"
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Pred. No. 1.6e+03;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: schweiz@ipk-gatersleben.de
Insert Length: 602 Std Brror: 0.00
Plate: 33 row: C column: 5
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/cultivar="Ingrid BC mlo-5"
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                                                                                               DN178545.1 GI:60273802
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DNA preparations and DNA sequencing were performed in the OD Anderson lab (all other authors)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta; Liliopsida, Poales, Poaceae,
Ehrhartoldeae, Oryzeae, Oryza.

1 (bases 1 to 601)
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Large-scale identification of expressed sequence tags involved in
                                                                                                                                                                                                                                                                                                                                                                        OSJNEf06J19.f OSJNEf Oryza sativa (japonica cultivar-group) cDNA clone OSJNEf06J19.5', mNNA sequence.
                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Rod Wing
Arizona Genomics Institute
University of Arizona
Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              organism="Oryza sativa (japonica cultivar-group)"
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89.5%; Pred. No. 1.6e+03;
ive 0; Mismatches 2;
                                                                                          Score 15.8; DB 3;
Pred. No. 1.6e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ice and rice blast fungus interaction
lant Physiol. 138 (1), 105-115 (2005)
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BACKWARD: gga aac agc tat gac cat g
Plate: 06 row: J column: 19
Seq primer: gta aaa cga cgg cca gtg.
Location/Qualifiers
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/note="Vector: pBluescript
XhoI; Uninfected Control"
                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                  601 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: rwing@genome.arizona.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   db_xref="taxon:39947"
/clone="OSJNBf06J19"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /mol_type="mRNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /dev_stage="3 week"
/lab_host="DH10B"
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                                                                                          Query Match
Best Local Similarity 89.5%;
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tel: 520 626 3967
Fax: 520 621 9288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17; Conservative
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source

FEATURES

RESULT 65 DN178545

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ORIGIN

VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS

PUBMED JOURNAL

COMMENT

TITLE

LOCUS RESULT 64 CB680958

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Gaps

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Hordeum vulgare subsp. vulgare
ISM Hordeum vulgare subsp. vulgare
Brikaryord; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; Hordeum.

Is (bases 1 to 636)

Sato,K., Saisho, D. and Takeda, K.
Barley EST sequencing project in NIG and Okayama Univ
Contact: Tadamu Shin-i
Conter For Genetic Resource Information
National Institute of Genetics
National Institute of Genetics
Ill! Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6856
Email: tshini@qenes.nig.ac.jp.

Localion/Qualifiers

Localion/Qualifiers
                                                                                                                /note="Organ: leaf; Vector: pBCSK(-); Site 1: HincII; DNA prepared from purified nuclei was randomly sheared, end-repaired, size fractionated to enrich for the 0.5 to 5 kb fraction, ligated into HincII-digested pBCSK(-) vector and electroporated into B. coli cells. This is a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BJ469064 E. Sato unpublished cDNA library, cv. Haruna Nijo adult, heading stage top three leaves Hordeum vulgare subsp. vulgare cDNA clone baall2011 5', mRNA sequence.
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                               /db_xref="taxon:4558"
/clone="11470920"
/clone_lib="Sorghum methylation filtered library (LibID:
104)"
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/dev_stage="adult, heading stage"
/clome lib="K. Sato unpublished DNA library,
Nijo adult, heading stage top three leaves"
                                                                                                                                                                                                                                                                                                              Length 631;
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/mol type="mRNA"
/cultivar="Haruna Nijo"
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89.5%; Pred. No. 1.6e+03;
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/db_xref="taxon:112509"
/clone="baal12011"
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopaida; Poales; Poaceae; PACCAD

clade; Panicoideae; Andropogoneae; Sorghum.

1 (bases i to 631)

Bedell, J.A., Budiman, M.A., Nunberg, A., Citek, R.W., Robbins, D.,

McMones, J., Plick, E., Rohlfing, T., Fries, J., Bradford, K.,

McMonaw, J., Smith, M., Holman, H., Roe, B.A, Wiley, G., Korf, I.F.,

Martienssen, R.A.

Martienssen, R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone="baal8p11"
/tissue type="top three leaves"
/dev_stage="adult, heading stage"
/clone lib="K. Sato unpublished cDNA library, cv. Haruna
Nijo adult, heading stage top three leaves"
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; Hordeum.

S 1 (bases 1 to 627)
S Sato, K., Saisho, D. and Takeda, K.
Barley EST sequencing project in NIG and Okayama Univ
Unpublished (2002)
CONTEACT: Tadabau Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6855
Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp.
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89.5%; Pred. No. 1.6e+03;
ive 0; Mismatches 2; Indels (
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                                                                                                                                                                                                                                                                                                                                                         'organism="Hordeum vulgare subsp. vulgare"
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Orion Genomics, LLC
4041 Perest Park Ave, St. Louis, MO 63108, USA
4131 4615 6979
Fax: 314 615 5975
Email: jbedelledoriongenomics.com
Seq primer: SWfor Forward
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                                                                                                                                                                                                                                                                                                                                                                                 /mol_type="mRNA"
/cultivar="Haruna Nijo"
/sub_species="vulgare"
/db_xref="taxon:112509"
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High quality sequence stop: 631.
Location/Qualifiers
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CW312739.1 GI:55028927
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Best Local Similarity 89.5
Matches 17; Conservative
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/tissue_type="Leaf"
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/lab_host="DH108"
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XhoI; 6 hrs after innoculation with Rice_Blast (C9240-1)"
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                                                              Contact: Rod Wing
Arizona Genomics Institute
University of Arizona
Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ
85721-0088, USA
TE1: 520 626 3967
Pax: 520 621 9288
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/mol type="mRNA"
/cultivar="Nipponbare"
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Pred. No. 1.6e+03;
0; Mismatches 2;
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FORWARD: gta aaa cga cgg cca gtg
BACKWARD: gga aac agc tat gac cat g
Plate: 10 row: L column: 13
Seg primer: gta aac cga cgg cca gtg.
Location/Qualifiers
      rice and rice blast fungus interaction Plant Physiol. 138 (1), 105-115 (2005)
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/cultivar="Haruna Nijo"
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                                                                                                                                                                                                                                                                                                                                                                                                                                   /db xref="taxon:39947"
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                                                                                                                                                                                                           Email: rwing@genome.arizona.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bmail: tshini@genes.nig.ac.jp.
Location/Qualifiers
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Best Local Similarity 89.5%;
Matches 17; Conservative 0
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                                                                                 Oryza sativa (japonica cultivar-group)

Cryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatorophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzaae; Oryza.

I (bases 1 to 636)

S Jantasuriyarat.C., Gowda, M., Haller, K., Hatfield, J., Lu, G.,

Stahlberg, E., Zhou, B., Li, H., Kim, H., Yu, Y., Dean, R.A., Wing, R.A.,

Soderlund, C. and Wang, G.L.

Large-scale identification of expressed sequence tags involved in rice and rice blast fungus interaction

L Plant Physiol. 138 (1), 105-115 (2005)
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/note="Vector: pBluescript II KS +; Site_1: EcoRI; Site_2:
XhoI; 6 hrs after innoculation with Rice Blast (C9240-1)"
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Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Sukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Ehrhartoidese; Oryzase; Oryza,
I (bases 1 to 637)
Jantasuriyarat, C., Gowda, M., Haller, K., Hatfield, J., Lu, G.,
Stahlberg, E., Zhou, B., Li, H., Kim, H., Yu, Y., Dean, R.A., Wing, R.A.,
Soderlund, C. and Wang, G.L.
Large-scale identification of expressed sequence tags involved in
OSJNEC10P06.f OSJNEC Oryza sativa (japonica cultivar-group) cDNA clone OSJNEC10P06.5', mRNA sequence.
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Arizona Genomics Institute
University of Arizona
Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ
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/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nipponbare"
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89.5%; Pred. No. 1.6e+03;
ive 0; Mismatches 2; Indels
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BACKWARD: gga aac agc tat gac cat g
Plate: 10 row: P column: 06
Seq primer: gta aaa cga cgg cca gtg.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            clone="OSJNEc10P06"
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                                                              CB656521.1 GI:29660246
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Fax: 520 621 9288
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Best Local Similarity 89.5
Matches 17; Conservative
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Contact: Schulman AH
Institute of Biotechnology
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Hordeum vulgare subsp. vulgare

Hordeum vulgare subsp. vulgare

Hordeum vulgare subsp. vulgare

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnaliophyta; Liliopsida; Poales; Poaceae;

Pooideae; Triticeae; Hordeum.

E 1 (bases 1 to 654)

Sato,K., Saisho,D. and Tekeda,K.

Barley EST sequencing project in NIG and Okayama Univ

Unpublished (2002)

Contact: Tadasus Shin-i

Contact: Tadasus Shin-i

Contact: Tadasus Shin-i

Center For Genetic Resource Information

National Institute of Genetics

1111 Yata, Mishima, Shizuoka 411-8540, Japan

Tel: 81-559-81-6855

Fax: 81-559-81-6855
                                                                                                                                                                                                                                                                                                       BJ469669

BJ469669 K. Sato unpublished cDNA library, cv. Haruna Nijo adult, heading stage top three leaves Hordeum vulgare subsp. vulgare cDNA BJ469669

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Nijo adult, heading stage top three leaves"
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|cultivar="Haruna Nijo"
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Pred. No. 1.6e+03;
0; Mismatches 2;
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Location/Qualifiers
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89.5%;
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Best Local Similarity 89.5
Matches 17; Conservative
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Matches 17; Conservative
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Hordeum vulgare
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Eukaryotta; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticeae; Hordeum.

El (bases I to 662)
Sato, K., Saisho, D. and Takeda, K.
Barley EST sequencing project in NIG and Okayama Univ Unpublished (2002)
Contact: Tadasu Shin-i
Contact: Tadasu Shin-i
Contact: For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6855
Email: tshini@genee.nig.ac.jp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AV933115 K. Sato unpublished cDNA library, cv. Haruna Nijo adult, heading stage top three leaves Hordeum vulgare subsp. vulgare cDNA aV933115 K. Wato unpublished cDNA subsp. vulgare cDNA AV933115
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; Hordeum.
1 (bases 1 to 659)
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                                                                                                                                                                                                                                                                                                       University of Helsinki
P.O.Box 56 (Viikinkaari 6A), University of Helsinki FIN-00014,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                  Saren, A. M., Tanskanen, J., Paulin, L. and Schulman, A.H. Barley EST's
Unpublished (2002)
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89.5%; Pred. No. 1.6e+03;
tive 0; Mismatches 2; Indels
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/dev_tage="Shoot"
/clone lib="S00007"
/note="Z-,3-,4-days after germination"
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Hordeum vulgare subsp. vulgare
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us-10-829-474-1.rst

Matches

ઠે 셤 DEFINITION

ACCESSION

RESULT 75 CA744325

TITLE JOURNAL COMMENT

FEATURES

REFERENCE AUTHORS

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/notes welcor: pBluescript SK+; Site 1: EcoRI (5'-end of CDNA); Site 2: Xhol (3'-end of CDNA); Approximately 5 % of the clones Correspond to CDNA from the fungi B. graminis hordei and triltici, respectively. Due to a cloning artefact caused by the kit, in most cases the EcoRI site is NOT present, as well as the EcoRIadepter used for cloning. To excise the insert, restriction sites upstream EcoRI should be used (e.g. BamHI, SalI,PStI). NOTE: Also due to the cloning system used Blue/White selection for recombinats is not 100% reliable. Average insert size is
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Hordeum vulgare subsp. vulgare
Hordeum vulgare subsp. vulgare
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; Hordeum.
1 (base I to 695)
34to, K., Saisho, D. and Takeda K.
Barley EST sequencing project in NIG and Okayama Univ
of barley
Mol. Plant Pathol. (2005) In press
Contact: Patrick Schwalzer
Transcriptome Analysis, Cytogenetics Department
Institute of Plant Genetics and Crop Plant Research (IPK)
Correnserr. 3, D-06446 Gatersleben, Germany
Tel: 0049 (0)39482-5650
                                                                                                                                                                                                                                                                                                                                                /mol_type="mcNa" tragers
/mol_type="mcNa"
/cultivar="Ingrid BC mlo-5"
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/db_xref="taxon: 4513"
/clone="H001L09"
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/dev stage="7 d after germination"
/lab_host="Xilo-Gold"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 15.8; DB 6; Length 686;
Pred. No. 1.7e+03;
0; Mismatches 2; Indels (
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National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6856
Email: tshini@genes.nig.ac.jp.
Location/Qualifiers
                                                                                                                                                                                   Email: schweiz@ipk-gatersleben.de
Insert Length: 686 Std Error: 0.00
Plate: 1 row: L column: 9
                                                                                                                                                                                                                                                                                                                               'organism="Hordeum vulgare"
                                                                                                                                                                                                                                                                            Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   clone_lib="HO"
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Hordeum vulgare
Hordeum vulgare
Hordeum vulgare
Hordeum vulgare
Spermatogyta; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticaee; Hordeum.
I to 686;
Zierold, u. and Schweizer, P.
Transcriptome analysis of mlo-mediated resistance in the epidermis
                                                                                                                                                                                        Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; Triticum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone_lb="writh"
/clone="Vector: PGEM-T Basy; Site_l: Smal; Riband
/note="Vector: PGEM-T Basy; Site_l: Smal; Riband
(susceptible) wheat leaves infected with Septoria tritici
strain A, 24 bours after infection, subtracted w/
comparable uninfected leaves"
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Mado,G., Caraher,N. and Hanafey,M.K.
DuPont Wheat control Sequence
Unpublished (2002)
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       Gaps
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Crop Genetics
E. I. DuPont de Nemours and Company
1 Innovation Way, P.O. Box 6104, Newark, DE 19714-6104, USA
Far: 302-631-2607
Email: Scott.V.Tingey@USA.dupont.com
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89.5%; Pred. No. 1.7e+03;
ive 0; Mismatches 2; Indels
    Indels
  2;
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  Mismatches
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/tissue_type="leaf"
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                   Triticum aestivum (bread wheat)
Triticum aestivum
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/db_xref="taxon:4565"
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Location/Qualifiers
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                                                                                            256 CCCCTGAGTGCAGCTAATC 274
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                                                1 CCCCTGAATGCGGCTAATC 19
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CA744325.1 GI:25560148
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CD054348.1 GI:30595183
17; Conservative
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EST 23-MAY-2002

DEFINITION

CD054348 LOCUS

RESULT 76

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Matches

ORIGIN

AUTHORS TITLE

REPERENCE

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DN178149 700 bp mRNA linear EST 24-FEB-2005
HO34C21S HO Hordeum vulgare cDNA clone HO34C21 5-PRIME, mRNA
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BOHGR66TR BOHG Brassica oleracea genomic clone BOHGR66, genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note—"Information of County, Site 1: Ecori (5'-end of County); Site 2: Xhol (3'-end of County); Approximately 5 % of the clones Correspond to County, funding 1B. grammins horden and triltici, respectively. Due to a cloning artefact caused by the kit, in most cases the Ecori site is NOT present, as well as the Ecoriadapter used for cloning. To excise the insert, restriction sites upstream Ecori should be used (e.g. BamHi, Sali,Psti). NOTE: Also due to the cloning system used Blue/White selection for recombinats is not 100% reliable. Average insert size is 1.2 kb."
                                                                                                                                                                                                                              Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticeae; Hordeum.

1 (base; Lr 700)
Zierold,U. and Schweizer,P.
Transcriptome analysis of mlo-mediated resistance in the epidermis
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Contact: Patrick Schweizer
Contact: Patrick Schweizer
Transcriptome Analysis, Cytogenetics Department
Institute of Plant Genetics and Crop Plant Research (IPK)
Corrensstr. 3, D-06466 Gatersleben, Germany
Tel: 0049 (0)39482-5595
Fax: 0049 (0)39482-5595
Email: schweiz@ipk-gatersleben.de
Insert Length: 700 Std Error: 0.00
Plate: 34 row: C column: 21
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89.5%; Pred. No. 1.7e+03;
ive 0; Mismatches 2; Indels C
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inculation with Blumeria graminis"
/dev_stage="7 d after germination"
/lab_host="XL10-Gold"
/clone_lib="HO"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /mol_type="mRNA"
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/db_xref="taxon:4513"
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    .700
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Brassica oleracea
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BH516786
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Best Local Similarity
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                                                                                               sequence.
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RESULT 79
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/ organism="Brassica oleracea"

/mol_type="agnomic DNA"

/mol_type="agnomic DNA"

/db xref="taxon:3172"

/clone_lib="B.oleracea002"

/note="Vector: pOTW13; Whole genome shotgun library from flowering buds. DNA was purified from a crude nuclear prep using Brassica oleracea T01000DH3 buds provided by Thosmas Osborn at the University of Wisconsin. Genomic DNA was provided by Pablo Rabinowicz (CSHL) and the shotgun library prepared at Washington University Genome Sequencing Center."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BZ008560 698 bp DNA linear GSS 07-OCT-2002 oef04h07.b1 B.oleracea002 Brassica oleracea genomic, genomic survey
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnollophyta; endicotyledons; core eudicotyledons;

rosida; eurosida II; Brassicales; Brassicaceae; Brassica.

1 (bases 1 to 698)

Delehaunty,K., Fewell,G., Fulton,L., McCombie,W.R., Miner,T.,

Mash,W., Rabinowicz,P.D. and Wilson,R.K.

Whole genome shotgun reads from Brassica oleracea

Unpublished (2002)
                                                                                                                                                         /tissue type="top three leaves"
/dev_stage="adult, heading stage"
/clone_lib="K. Sato unpublished cDNA library, cv. Haruna
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                                                                                                                                                                                                                                                                                                  Nijo adult, heading stage top three leaves"
                       'organism="Hordeum vulgare subsp. vulgare"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genome Sequencing Center
Washington University School of Medicine
Manil: submissions@wateon.wustl.edu
Plate: oef@4 row: h column: 07
Seq primer: -21UPpOT forward
                                           /mol_type="mRNA"
/cultivar="Haruna Nijo"
/sub_specise="vulgare"
/db_xref="taxon:112509"
/clone="baal30j04"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              High quality sequence start: 17
High quality sequence stop: 543.
Location/Qualifiers
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BZ008560.1 GI:23556906
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Best Local Similarity 89.57
Pest Local 17; Conservative
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Best Local Similarity 89.5
Matches 17; Conservative
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organism="Saccharum officinarum"
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Bukaryota, Vizidiplantea, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Saccharum; Saccharum officinarum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CA240024 176 bp mRNA linear EST 25-SEP-2003 SCSBFL4063E11.9 FL4 Saccharum officinarum cDNA clone SCSBFL4063E11
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
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Plate: 05 row: E column: 11
Seg primer: 77 Promoter Primer.
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/note="Vector: pHOS1; Site_1: BstXI; 2-3 kb sheared
genomic DNA inserted into pHOS1 using BstXI linkers"
                                                             1 (bases 1 to 713)
Ayele,M., Haas,B.J., Kumar,N., Wu,H., Xiao,Y., Van Aken,S., Utterback,T.R., Wortman,J.R., White,O.R. and Town,C.D. Whole genome shotgun sequencing of Brassica oleracea and its application to gene discovery and annotation in Arabidopsis Genome Res. 15 (4), 487-495 (2005)
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The libraries that made SUCEST
Genet. Mol. Biol. 24 (1-4), 1-7 (2001)
Contact: Arruda P
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Pred. No. 1.7e+03;
0; Mismatches 2; Indels (
                                                                                                                                                                                                                                                                                                                                           Email: cdtcwn@tigr.org
DNA is from a doubled haploid provided by Tom Osborn.
Seg primer: TR
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Universidade Estadual de Campinas
Gaixa Postal 6010, 13083-970, Campinas SP, Brazil
Tel: 55 19 3788 1137
Fax: 55 19 3788 1089
                                                                                                                                                                                                                                                                                Medical Center Drive, Rockville, MD 20850,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            organism="Brassica oleracea"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mol_type="genomic DNA"
strain="TO1000DH3"
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89.5%;
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CA240024
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Other_GSS
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CA240024
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Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzae; Oryza.

El (bases 1 to 749)

S Jantasuriyarat, C., Gowda, M., Haller, K., Hatfield, J., Lu, G., Stahlberg, E., Zhou, B., Li, H., Kim, H., Yu, Y., Dean, R.A., Wing, R.A., Soderlund, C. and Wang, G.L.

Large-scale identification of expressed sequence tags involved in rice and rice blast fungus interaction

L plant Physiol. 138 (1), 105-115 (2005)
                                                                     /crom-long) vector: pSport1; Site_1: Sal1; Site_2: NotI; An unidirectional cDNA library generated from [Developed inflorescence and rachis (20cm-long)]. CDNA was prepared from polyA+ mRNA using SuperScript Plasmid System Kit (Invitrogen). The double-strand cDNAs were fractionated in a sepharose CL-2B 40cm-columns and fragments sizing between 0.8 and 1.5 Kb were directionally cloned into the vector. Details of each source of RNA and library construction can be obtained at http://sucest.lad.ic.unicamp.br/public"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EST 09-APR-2003
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University of Arizona
Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             83.2%; Score 15.8; DB 6; Length 716; 89.5%; Pred. No. 1.7e+03; ive 0; Mismatches 2; Indels (
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BACKWARD: gga aac agc tat gac cat g
Plate: 07 row: P column: 03
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Location/Qualifiers
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/clone="OSJNEG07F03"
/tissue_type="teaf"
/dev_stage="3 week"
/lab_host="DH108"
/clone_lib="OSJNEG"
/clone="SCSBFL4063E11"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: rwing@genome.arizona.edu
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/cultivar="Nipponbare"
                        /lab_host="DH10B"
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                                                      clone lib="FL4"
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Tel: 520 626 3967
Fax: 520 621 9288
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Best Local Similarity
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Email: rwing@genome.arizona.edu
PCR PRimers
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/clone="OSJNEc15M06"
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/dev_stage="3 week"
/lab_host="DH10B"
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nes 17; Conservative
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/note="Vector: pBluescript II KS +; Site 1: EcoRI; Site 2: XhoI; 24 hrs after innoculation with Rice Blast (C9240-1)"
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                                                                                                                                                                                                                                                                  EST 10-JUN-2004
                                                                                                                                                                                                                                                                                EST812164 Coccidioides posadasii spherule cDNA library, 0.5 to 5.3 kb Coccidioides posadasii cDNA clone CIFBP43 3' end, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="Vector: pExpress 1; Site_1: Not I; Site_2: Eco RV; Coccidioides posadasii spherule CDNA library, \overline{0}.5 to 5.3 kb "
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Oryza sativa (japonica cultivar-group)
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /dev_stage="spherules"
/lab_host="E. coli DH10B, T1 phage resistant"
/clone_lib="Coccidioides posadasii spherule cDNA library,
0.5 to 5.3 kb"
                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes; Onygenales; mitosporic Onygenales; Coccidioides.

1 (bases 1 to 777)
Gardner, M.J. and Cole, G.T.
Analysis of gene expression in Coccidioides posadasii mycelia and sphenules via expressed sequence tags
Unpublished (2003)
Other_ESTS: EST812165
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89.5%; Pred. No. 1.7e+03;
ive 0; Mismatches 2; Indels C
                                                                     83.2%; Score 15.8; DB 6; Length 749;
89.5%; Pred. No. 1.7e+03;
ive 0; Mismatches 2; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Gardner MJ
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850, USA
T=1: 301 838 3519
Fax: 301 838 0208
Email: gardner@tigr.org.
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                                                                                                                                                                                                                                                                  linear
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                                                                                                                                                                                                                                                                  mRNA
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/clone="CIFBP43"
                                                                                                                                                                                                                                                                  777 bp
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                                                                                                                                                              501 CCCCTGAGTGCAGCTAATC 519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /mol_type="mRNA"
/strain="C735"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             343 CCCCTGATTCCGGCTAATC 325
                                                                                                                                          1 CCCCTGAATGCGGCTAATC 19
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                                                                                                                                                                                                                                                                                                                                     C0033780.1 GI:48570202
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Coccidioides posadasii
                                                                                       Best Local Similarity 89.5
Matches 17; Conservative
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Best Local Similarity
Matches 17; Conserva
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CO033780/c
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AUTHORS
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CB659097
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OSIIEA12N18.r OSIIEA Oryza sativa (indica cultivar-group) cDNA
clone OSIIEA12N18 3', mRNA sequence.
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 778)
Jantasuriyarat, C., Gowda, M., Haller, K., Hatfield, J., Lu, G.,
Stahlberg, E., Zhou, B., Li, H., Kim, H., Yu, Y., Dean, R.A., Wing, R.A.,
Soderlund, C. and Mang, G.L.
Large-scale identification of expressed sequence tags involved in
rice and rice blast fungus interaction
Plant Physiol. 138 (1), 105-115 (2005)
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/note="Vector: pBluescript II KS +, Site_1: EcoRI; Site_2:
KhoI, 6 hrs after innoculation with Rice_Blast (C9240-1)"
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Oryza sativa (indica cultivar-group)
Oryza sativa (indica cultivar-group)
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Brematophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Spermatochyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
1 (bases 1 to 786)
Jantasuriyarat,C., Gowda,M., Haller,K., Hatfield,J., Lu,G.,
Stahlberg,E., Zhou,B., Li,H., Kim,H., Yu,Y., Dean,R.A., Wing,R.A.,
Soderlund,C. and Wang,G.L.
Large-scale identification of expressed sequence tags involved in
Plant and rice blast fungus interaction
Plant physiol. 138 (1), 105-115 (2005)
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Arizona Genomics Institute
Arizona Genomics Institute
University of Arizona
Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ
85721-0088, USA
TH: 520 626 3967
Fax: 520 621 9288
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University of Arizona
Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ
85721-0088, USA
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Corganism="Oryza sativa (japonica cultivar-group)"
/mol type="mkNa"
/cultivar="Nipponbare"
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89.5%; Pred. No. 1.7e+03;
cive 0; Mismatches 2;
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Plate: 15 row: M column: 06
Seq primer: gta aaa cga cgg cca gtg.
Location/Qualifiers
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PCR PRimers
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                                                                                                                                                                                                                                                                  셤
                                                                                                                                                                                                                                     /db_xref="taxon:39946"
/db_xref="taxon:39946"
/clone="toSIIBal2N18"
/dev_stage="last"
/lab_host="DH108"
/clone_lib="toSIIEa"
/note="Vector: pBluescript II KS +; Site_1: EcoRI; Site_2: XhoI; Lesion Mimic SPL 11"
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Oryza sativa (japonica cultivar-group)
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Ehrhartoideae, Oryzeae, Oryza.
1 (bases 1 to 790)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CB657398 790 bp mRNA linear EST 09-APR-20 OSJNEC12K24.f OSJNEC Oryza sativa (japonica cultivar-group) cDNA clone OSJNEC12K24 5', mRNA sequence.
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Arizona Genomics Institute
University of Arizona
Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Oryza sativa (japonica cultivar-group)"
mol_type="mRNA"
cultivar="Nipponbare"
                                                                                                                                                           1. 786
/organism="Oryza sativa (indica cultivar-group)"
/mol_type="mRNA"
/cultivar="IR36"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 786;
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89.5%; Pred. No. 1.7e+03;
ive 0; Mismatches 2;
Pax: 520 621 9288
Email: rwing@genome.arizona.edu
PCR PRimers
FORWARD: gta aaa cga cgg cca gtg
BACKWARD: gga aac agc tat gac cat g
Plate: 12 row: N column: 18
Seq primer: gga aac agc tat gac cat g
Location/Qualifiers
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BACKWARD: gga aac agc tat gac cat g
Plate: 12 row: K column: 24
Seq primer: gta aaa cga cgg cca gtg.
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/clone="OSJNEc12K24"
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Best Local Similarity 89.5
Matches 17; Conservative
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Tel: 520 626 3967
Fax: 520 621 9288
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SOURCE
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CB657398
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/tissue_type="Leaf"
/dev_stage="3 week"
/lab_host="DH10B"
/clone_lib="0SJNEC"
/note="Vector: pBluescript II KS +; Site_l: EcoRI; Site_2:
XhoI; 6 hrs after innoculation with Rice_Blast (C9240-1)"
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//note="Vector: pBluescript II KS +; Site_I: EcoRI; Site_2:
XhoI; 24 hrs after innoculation with Rice Blast (Che 86061)"
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Oryza sativa (japonica cultivar-group)
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Buraryota, Magnoliophyta; Liliopsida; Poales; Poaceae;
Brhartoideae; Oryzae, Oryza.

1 (bases 1 to 795)
Jantasuriyarat,C., Gowda,M., Haller,K., Hatfield,J., Lu,G.,
Stahlberg,E., Zhou,B., Li,H., Kim,H., Yu,Y., Dean,R.A., Wing,R.A.,
Soderlund,C. and Wang,G.L.
Large-scale identification of expressed sequence tags involved in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CB648104 795 bp mRNA linear EST 08-APR-20
OSJNEb11F13.f OSJNED Oryza sativa (japonica cultivar-group) cDNA
colone OSJNEb11F13 5', mRNA sequence.
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University of Arizona
Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'organism="Oryza sativa (japonica cultivar-group)"
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                                                                                                                                                                                                                      Length 790;
                                                                                                                                                                                                                                                                        2; Indels
                                                                                                                                                                                                                 Score 15.8; DB 6;
Pred. No. 1.7e+03;
0; Mismatches 2;
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BACKWARD: gga aac agc tat gac cat g
Plate: 11 row: F column: 13
Seq primer: gta aaa cga cgg cca gtg.
Location/Qualifiers
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                                                                                                                                                                                                                   83.2%;
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Fax: 520 621 9288
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Best Local Similarity
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요

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15888683
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OR_BBa0083P09.r OR_BBa Oryza nivara genomic clone OR_BBa0083P09 3',
genomic survey sequence.
CL746478.1 GI:50688734
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XhoI; Lesion Mimic SPL 11"
                                                                                            CB624345 1796 bp mRNA linear EST 08-APR-2003 OSIIEa12N18.f OSIIEa Oryza sativa (indica cultivar-group) cDNA clone OSIIEa12N18 5', mRNA sequence.
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Oryza sativa (indica cultivar-group)
Oryza sativa (indica cultivar-group)
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatcophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
I (Dasea; 1 to 796)
Jantasuriyarat, C., Gowda, M., Haller, K., Hatfield, J., Lu, G.,
Stahlberg, E., Zhou, B., Li, H., Kim, H., Yu, Y., Dean, R.A., Wing, R.A.,
Soderlund, C. and Wang, G.L.
Large-scale identification of expressed sequence tags involved in
rice and rice blast fungus interaction
Figure Physiol. 138 (1), 105-115 (2005)
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Oryza nivara
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
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Arizona Genomics Institute
University of Arizona
Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ
85721-0088, USA
TEL: 520 626 3967
Fax: 520 621 9288
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| Organism="Oryza sativa (indica cultivar-group)
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BACKWARD: gga aac agc tat gac cat g
Plate: 12 row: N column: 18
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497 CCCCTGAGTGCAGCTAATC 515
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Matches 17; Conserva
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CL746478/c
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CB624345
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Oryza sativa (japonica cultivar-group)
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Burhartoideae; Oryzeae; Oryza.
1 (bases I to 810)
Jantasuriyarat, C., Gowda, M., Haller, K., Hatfield, J., Lu, G., Stahlberg, E., Zhou, B., Li, H., Kim, H., Yu, Y., Dean, R.A., Wing, R.A., Soderlund, C. and Wang, G.L.
Large-scale identification of expressed sequence tags involved in Plant Physiol. 138 (1), 105-115 (2005)
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University of Arizona
Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ
                                                                                            Kim,H., Yu,Y., Stum,D., Yost,D., Rao,K., Luo,M., Jetty,R.,
Kudrna,D., Muller,C., Hatfield,J., Soderlund,C. and Wing,R.
                                                                                                                                                                                        OMAP Project (1004)
Contact: Rod A. Wing
Arizona Genomics Institute
University of Arizona
University of Arizon
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BACKWARD: gga aac agc tat gac cat
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PCR PRimers
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 800)
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Fax: 520 621 9288
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EST 09-APR-2003
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Oryza sativa (japonica cultivar-group)
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Burhartoideae; Oryzaa; Liliopsida; Poales; Poaceae;
I (bases I to 834)
Jahrattoideae; Oryzaa.
I (bases I to 834)
Stahlberg, E., Zhou, B., Li, H., Kim, H., Yu, Y., Dean, R.A., Wing, R.A., Soderlund, C. and Wang, G.L.
Large-scale identification of expressed sequence tags involved in Fice and rice blast fungus interaction
Plant Physiol. 138 (1), 105-115 (2005)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone lib="OSJNEC"
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XhoI; 6 hrs after innoculation with Rice_Blast (C9240-1)"
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                                                                                                                                                                                                                                            834 bp mRNA linear EST 09-APR-2(
OSJNEC12K24.r OSJNEC Oryza sativa (japonica cultivar-group) cDNA
CDGF OSJNEC12K24 3', mRNA sequence.
                                                                                       Gaps
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Arizona Genomics Institute
University of Arizona
Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ
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/organism="Oryza sativa (japonica cultivar-group)"
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89.5%; Pred. No. 1.7e+03;
tive 0; Mismatches 2; Indels (
                                              Length 825;
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                                            Score 15.8; DB 6;
Pred. No. 1.7e+03;
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BACKWARD: gga aac agc tat gac cat g
Plate: 12 row: K column: 24
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                                            83.2%;
89.5%;
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Tel: 520 626 3967
Fax: 520 621 9288
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Matches 17; Conserv
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Oryza sativa (japonica cultivar-group)
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Bukaryota; Windiplantae; Streptophyta; Embryophyta; Poales; Poaceae;
Ehrhartoideae; Oryzae, Dryza.
I (Dasea; 1 to 825)
Jantasuriyarat, C., Gowda, M., Haller, K., Hatfield, J., Lu, G., Stahlberg, E., Zhou, B., Li, H., Kim, H., Yu, Y., Dean, R.A., Wing, R.A., Soderlund, C. and Wang, G.L.
Large-scale identification of expressed sequence tags involved in rice and rice blast fungus interaction
Plant Physiol. 138 (1), 105-115 (2005)
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/note="Vector: pBluescript II KS +; Site 1: EcoRI; Site 2:
XhoI; 6 hrs after innoculation with Rice Blast (C9240-1)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CB656772 825 bp mRNA innear ESI USTARACOSUNECIH42.f OSUNEC ORVA (japonica cultivar-group) CDNAclone OSUNECIH42 5', mRNA sequence.
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    .810
/organism="Oryza sativa (japonica cultivar-group)"

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Arizona Genomics Institute
University of Arizona
Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Oryza sativa (japonica cultivar-group)"
mol type="mRNA"
cultivar="Nipponbare"
/db xref="taxon:39947"
/clone="OSJNEC11H22"
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                                                                                                                                                                                                                                                                                                                                        Length 810;
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                                                                                                                                                                                                                                                                                                                                    Score 15.8; DB 6;
Pred. No. 1.7e+03;
0; Mismatches 2;
                  Seq primer: gta aaa cga cgg cca gtg.
Location/Qualifiers
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Plate: 11 row: H column: 22
Seq primer: gta aaa cga cgg cca gtg.
Location/Qualifiers
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PCR PRimers
Plate: 09 row: M column: 13
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'dev_stage="3 week"
'lab_host="DH108"
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Best Local Similarity 89.5°
Matches 17; Conservative
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Fax: 520 621 9288
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Bioinformatics
University of Saskatchewan, Department of Computer Science
University of Saskatchewan, Department of Computer Science
10.101 Engineering Building, 57 Campus Drive, Saskatoon,
Saskatchewan, 57N 5A9, Canada
Tel: 306 966 1769
Fax: 306 966 2033
Email: fgas ests@cs.usask.ca
This sequence is the direct result of the Base calling software
Phred (default parameters). It is the raw base calls. To aid in the
identification of the high quality insert the software Lucy
(default parameters) has been run on this sequence. Lucy identified
the region [122,733].
Plate: Talc411 row: K column: 10.
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E. (bases it os 868)

E. (bases it to 868)

Gardner, M. J. and Cole, G.T.

Analysis of gene expression in Coccidioides posadasii mycelia and sphenules via expressed sequence tags

Dupublished (2003)

Other_ESTS: EST697234

Contact: Gardner MJ

The Institute for Genomic Research

712 Medical Center Drive, Rockville, MD 20850, USA

Tel: 301 838 9519

Fax: 301 838 9208

Email: gardner@etigr.org

Seq primer: M13 Reverse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db xref="taxon:4565"
/lab_host="DH5 alpha"
/clone lib="Triticum aestivum FGAS: TaLt4"
/note="Organ="Crown: Vector: pGBW-T; SSH (suppression subtractive hybridization) cDNA library from genotype PI178383 cold hardened at 2 C for 1 day (24 H) (tester) and subtracted against genotype Norstar cold hardened at 2 C for 1 day (24 H) (tester) and for all days and 49 days (equal amount of cDNA pooled together before subtraction, driver). Modified Smart cDNA (Clontech) priming and non-directional cloning."
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EST697235 Coccidioides posadasii saprobic phase cDNA library, 2 to 4 kb Coccidioides posadasii cDNA clone CIDA109 5' end, mRNA
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0
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/mol type="mRNA"
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/db_xref="taxon:199306"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /mol_type="mRNA"
/cultivar="Wheat line PI 178383"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Triticum aestivum"
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Coccidioides posadasii
     Unpublished (2003)
Contact: Wm L Crosby
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/note="Vector: pBluescript II KS +; Site 1: EcoRI; Site 2:
Khol; 24 hrs after innoculation with Rice Blast (C9240-I)"
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                                                                                                     Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Bhrhartoideae; Oryzaee; Oryza.
Ehrhartoideae; Oryzaee; Oryza.
I (basea; 1 to 83.1)
Jantasuriyarat, C., Gowda, M., Haller, K., Hatfield, J., Lu, G., Stahlberg, E., Zhou, B., Li, H., Kim, H., Yu, Y., Dean, R.A., Wing, R.A., Soderlund, C. and Wang, G.L.
Large-scale identification of expressed sequence tags involved in rice and rice blast fungus interaction
Plant Physiol. 138 (1), 105-115 (2005)
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1 (Dases 1 to 861)
Allard, F., Crosby, W.L., Danyluk, J., Eudes, F., Frick, M., Gaudet, D., Genswein, B., Graf, R., Gulick, P., Hrycan, L., D., Laroche, A., Links, M.G., McCarthy, E.L., Monroy, A., Muzak, I., Nilson, D., Penniket, C., Roach, J.L. and Sarhan, F.
Functional Genomics of Abiotic Stress In Wheat and Canola Crops
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Arizona Genomics Institute
University of Arizona
Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ
Tel: 520 626 3967
Fax: 520 621 9288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nipponbare"
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89.5%; Pred. No. 1.7e+03;
ive 0; Mismatches 2; Indels
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BACKWARD: gga aac agc tat gac cat g
Plate: 08 row: D column: 13
Seq primer: gga aac agc tat gac cat g
Location/Qualifiers
OSJNEd08D13 3', mRNA sequence.
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clone="OSJNEd08D13"
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Triticum aestivum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /dev_stage="3 week"
/lab_host="DH10B"
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CK156356.1 GI:38979376
                                                          CB663361.1 GI:29667086
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/note="Vector: pBluescript II KS +; Site_1: EcoRI; Site_2:
Kho1; Uninfected Control"
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Oryza sativa (japonica cultivar-group)
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Bhrhartoideae; Oryzae, Diliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzae, Dryza.
Jantasuriyarat, C., Gowda, M., Haller, K., Hatfield, J., Lu, G.,
Stahlberg, E., Zhou, B., Li, H., Kim, H., Yu, Y., Dean, R.A., Wing, R.A.,
Soderlund, C. and Wang, G.L.
Harge-scale identification of expressed sequence tags involved in
rice and rice blast fungus interaction
Plant Physiol. 138 (1), 105-115 (2005)
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                /dev_stage="saprobic phase (mycelia)"
/lab host="E. coli Dh10B, Tl phage resistant"
/clone lib="Coccidioides posadasii saprobic phase cDNA
library, 2 to 4 kb"
/note="Vector: pExpress 1, Site 1: Not I; Site 2: Eco RV;
Coccidioides posadasii saprobic phase cDNA library, aize
fractionated CDNA 2 to 4 kb"
                                                                                                                                                                                                                                                                                                                                                                                                         CB680959 876 bp mRNA linear EST 09-APR-20
OSJNEf06J19.r OSJNEf Oryza sativa (japonica cultivar-group) cDNA
clone OSJNEf06J19 3', mRNA sequence.
                                                                                                                                                                                                                                    Gaps
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Arizona Genomics Institute
University of Arizona
Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          organism="Oryza sativa (japonica cultivar-group)"
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                                                                                                                                                                                          Score 15.8; DB 6; Length 868;
Pred. No. 1.7e+03;
0; Mismatches 2; Indels
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Plate: 06 row: J column: 19
Seq primer: gga aac agc tat gac cat
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        mol type="mRNA"
cultivar="Nipponbare"
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clone="OSJNEf06J19"
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/lab_host="DH10B"
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clone="CIDA109"
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Best Local Similarity 89.5%;
Matches 17; Conservative
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Best Local Similarity 89.5
Matches 17; Conservative
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Fax: 520 621 9288
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VERSION
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CCCCTGAATGCGGCTAATC 19

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SM Coccidioides posadasii

Rukaryota; Fundi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Onygenales; mitosporic Onygenales; Coccidioides.

I (bases 1 to 529)
S Gardner,M.J. and Cole,G.T.

Analysis of gene expression in Coccidioides posadasii mycelia and spherules via expressed sequence tags
Unpublished (2003)
Other_ESTS: ESTS99219
Contact: Gardner MJ
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301 838 3519
Fax: 301 838 0208
  EST 01-APR-2004
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AGENCOURT 22410078 NIH_ZGC_9 Danio rerio cDNA clone IMAGE:7270525
5', mRNA Sequence.
CF821836

SST 01-APR-2004
EST699218 Coccidioides posadasii saprobic phase cDNA library, 2 to 4 kb Coccidioides posadasii cDNA clone CIDAC39 3' end, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="Vector: pExpress 1; Site_1: Not I; Site_2: Eco RV; Coccidioides posadasii saprobic_phase cDNA library, size fractionated cDNA 2 to 4 kb"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Cypriniformes, Cyprinidae, Danio.
(bases 1 to 941)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /dev stage="saprobic phase (mycelia)"
/lab_host="E. coli DH10B, T1 phage resistant"
/clone_lib="Coccidioides posadasii saprobic phase cDNA
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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Best Local Similarity 89.5%; Pred. No. 1.7e+03;
Matches 17; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            organism="Coccidioides posadasii"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="taxon:199306"
/clone="CIDAC39"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bmail: gardner@tigr.org.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /mol_type="mRNA"
/strain="C735"
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                                                                                                                                  GI:45927893
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Danio rerio
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AUTHORS
TITLE
JOURNAL
COMMENT
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Gaps

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Conteact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
Tissue Procurement: DCTD/DTP
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCMS15 row: p column: 20
High quality sequence start: 4
High quality sequence start: 4
High quality sequence start: 4
Location/Qualifiers
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/lab host="DH10B (phage-resistant)"
/clone_lib="NHH_MGS" (Perfor: pOTB7; Site_1: XhoI; Site_2: fnote="Organ: ovary; Vector: pOTB7; Site_1: XhoI; Site_2: Cloned into EcoRI/KhoI sites using the following 5' adaptor: GGCAGAGG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of Carlifornia, Berkeley) using 2AP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
                                                                                                                                                                                                                                                                                               /note="Vector: pExpress 1; Site_1: Not I; Site_2: Eco RV; Coccidioides posadasii spherule CDNA library, 0.4 to 2.3 kb".
                                                                                                                                                                             /dev_stage="spherules"
/lab_host="E. coli DH10B, Tl phage resistant"
/clome_lib="Coccidioides posadasii spherule cDNA library,
0.4 to 2.3 kD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 996)

NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                         'organism="Coccidioides posadasii"
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/organism="Homo sapiens"
                                                                                                                        /db_xref="taxon:199306"
/clone="CIEBH07"
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                                                                   /mol_type="mRNA"
/strain="C735"
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Best Local Similarity 89.59
Matches 17; Conservative
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BE743432
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LOCUS
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SOURCE
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Coccidioides posadasii

Coccidioides posadasii

Coccidioides posadasii

Coccidioides posadasii

Coccidioides posadasii

Divaryota; Pungi; Ascomycota; Pezizomycotina; Eurotiomycetes;

Onygenales; mitosporic Onygenales; Coccidioides.

E 1 (Dases I to 994)

S Gardner,M.J. and Cole,G.T.

Analyais of gene expression in Coccidioides posadasii mycelia and spherules via expressed sequence tags

L Unpublished (2003)

Other EST98682

Contact: Gardner MJ

The Institute for Genomic Research

712 Medical Center Drive, Rockville, MD 20850, USA

Tel: 301 838 9359

Fax: 301 838 0208

Email: gardner@tlgr.org.

Location/Qualifiers
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National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-r@mail.nih.gov
Tissue Prourement: Chi-Bin Chien
CDNA Library Preparation: Dr. Sumio Sugano
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at:
http://image.llnl.gov
Plate: LibrM15233 row: d column: 11
High quality sequence start: 28
High quality sequence stop: 313.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /tissue type="neural retina, retinal pigment epithelium, lens and overlying skin, pooled embryos"
/lab host="DH10B TonA"
/clone lib="NIH 500A"
/note="Organ: eye; Vector: pMB18S-FL3; Site 1: DraIII;
Site_2: DraIII; 1st strand cDNA was primed with an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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89.5%; Pred. No. 1.7e+03;
ive 0; Mismatches 2; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Danio rerio"
/mol_type="mRNA"
/db_xref="taxon:7955"
/clone="IMAGE:7270525"
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CO010346.1 GI:48517235
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Matches 17; Conserva
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Viruses; saRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
1 (bases 1 to 103)
Muir,P., Nicholson,F., Spencer,G.T., Ajetunmobi,J.F., Starkey,W.G.,
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Craig, M.E., Howard, N.J., Silink, M. and Rawlinson, W.D.
Subrect Submission
Submitted (03-DEC-2002) Virology Division, University of New South Wales, Prince of Wales Hospital, High Street, Randwick, NSW 2031, Australia
                                                                                                                                                                                                                                                                                                                                                                                                                         Viruses; SSRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
I (Dases 1 to 73)
Craig, M.E., Howard, N.J., Silink, M. and Rawlinson, W.D.
Reduced Frequency of HiA DRB1*03-DQB1*02 in Children with Type 1
Diabetes Associated with Enterovirus RNA
J. Infect. Dis. 187 (10), 1562-1570 (2003)
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Pred. No. 31;
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/isolate="NSW/51/97"
/db_xref="taxon:138949"
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 Location/Qualifiers
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                                                                                                                                  Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 20; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                               Human enterovirus 71
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ORIGIN
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AY189933/c
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ESU55869/c
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Khan, M., Archard, L.C., Cairns, N.J., Anderson, V.E.R., Leigh, P.N., Howard, R.S. and Banatvala, J.E.
Howard, R.S. and Banatvala, J.E.
Stretovirus infection of the central nervous system of humans: lack of association with chronic neurological disease
J. Gen. Virol. 77 (Pt 7), 1469-1476 (1996)
80757988
2 (bases 1 to 103)
Muir, P.

    (bases 1 to 109)
    Kawashima, H., Kashiwagi, Y. and Mori, T.
    Direct Submission
    Submitted (02-AUG-2001) Pediatrics, Tokyo Medical University, 6-7-1
    Nishishinjuku, Shinjuku-ku, Tokyo 160-0023, Japan
    Location/Qualifiers

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                                                                                                                                                                                     Direct Submission
Submitted (22-APR-1996) Peter Muir, Virology, UMDS, Lambeth Palace
Road, London SE1 7EH, UK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA stage;
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/organism="Enterovirus sp."
/mol_type="genomic RNA"
/mol_type="genomic RNA"
/olone="Entero-1"
/note="from cerebrospinal fluid"
                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 20; DB 13;
100.0%; Pred. No. 30;
trive 0; Mismatches 0;
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Viruses; ssRNA positive-strand viruses,
Picornaviridae; Enterovirus.
                                                                                                                                                                                                                                                                                1. .103
/organism="Enterovirus sp.
/nol_type="genomic RNA"
/db &ref="texon:47681"
/noTe="from patient A27"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Enterovirus sp. clone Entero-l
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Conservative
                                                                                      AY189177
AY189177.1
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                                                                           sequence.
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Best Local Simi
Matches 20;
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ORIGIN
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AY189178/c
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Viruses, BSRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
I (bases 1 to 109)
Zheng, Z.M., He, D.J., Caueffield, D., Neumann, M., Specter, S.,
Baker, C.C. and Bankowski, M.J.
Enterovirus 71 isolated from China is serologically similar to the prototype E71 Brcr strain but differs in the 5'-noncoding region
                                                                                               8830120
2 (Dases 1 to 109)
Bankowski,M.J.
Direct Submission
Submitted (17-AUG-1993) Bankowski M.J., Diagnostic Services, Inc.,
Clinical Virology & Molecular Medicine, 340 Goodlette Road South,
T. 33940, T. 11fiors
                                                                                                                                                                                                                                                                                                                        Gaps
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Human enterovirus B isolate NSW/47/97 5' untranslated region,
partical sequence.
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/strain="E 71 H"
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/isolate="NSW/47/97"
/db_xref="taxon:138949"
<1._.>112
                                                                                                                                                                                                                                                           db_xref="taxon:39054"
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Human enterovirus B
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Matches 20; Conserva
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Matches 20; Conserv
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                                                                                      J. Med.
8830120
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AY189177 115 bp RNA linear VRL 08-MAY-2003
Human poliovirus 1 strain Sabin isolate NSW/84/97 5' UTR, partial
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Human poliovirus 1 strain Sabin isolate NSW/96/97 5' UTR, partial
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Craig, M.B., Howard, N.J., Silink, M. and Rawlinson, W.D.
Direct Submission
Submitted (19-NOV-2002) Virology Division, South Eastern Area
Laboratory Services, University of New South Wales/Prince of Wales
Hospital, High Street, Randwick, NSW 2031, Australia
Location/Qualifiers
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Wiman poliovirus 1 strain Sabin
Viruses; sRRM, positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
I (bases 1 to 115)
Craig, M.E., Howard, N.J., Silink, M. and Rawlinson, W.D.
Reduced Frequency of HLA DRB1*03-DQB1*02 in Children with Type 1
Diabetes Associated with Enterovirus RNA
J. Infect. Dis. 187 (10), 1562-1570 (2003)
                                                                                                                                                                       Human poliovirus 1 strain Sabin
Miman poliovirus 1 strain Sabin
Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
1 (bases 1 to 115)
Craig, M.B., Howard, N.J., Silink, M. and Rawlinson, W.D.
Reduced Frequency of HLA DRB1*03-DOB1*02 in Children with Type 1
Diabetes Associated with Enterovirus RNA
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CraiglyM.B., Howard, N.J., Silink, M. and Rawlinson, W.D.
Direct Submission
Submitted (29-NOV-2002) Virology Division, South Eastern Area
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/mol type="genomic RNA"
/isolate="NSW/84/97"

    .115
/organism="Human poliovirus 1 strain Sabin"
/mol_type="genomic RNA"

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/note="Human poliovirus 1 strain Sabin"
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AY189178
AY189178.1 GI:28274401
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/virion
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Best Local Similarity
Matches 20; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished
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                                                                                                               source
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AY189158/c
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AY189213
AY189213.1 GI:28274436
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Craig, M. E., Howard, N. J., Silink, M. and Rawlinson, W. D.
Direct Submitssion
Submitted (129-NOV-2002) Virology Division, South Eastern Area
Laboratory Services, University of New South Wales/Prince of Wales
Hospital, High Street, Randwick, NSW 2031, Australia
Location/Qualifiers
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Human enterovirus A
Human enterovirus A
Yuruses; saRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
1 (bases 1 to 115)
Craig, M.E., Howard, N.J., Silink, M. and Rawlinson, W.D.
Craig, M.E., Howard, N.J., Silink, M. and Rawlinson, W.D.
Diabetes Associated with Enterovirus RNA
J. Infect. Dis. 187 (10), 1562-1570 (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                  Craig, M.E., Howard, N.J., Silink, M. and Rawlinson, W.D. Reduced Frequency of HLA DRB109120B1.02 in Children with Type 1 Diabetes Associated with Entercovirus RNA J. Infect. Abis. 187 (10), 1562-1570 (2003)
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Human enterovirus A isolate NSW/227/99 5' UTR, partial sequence.
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                                                                                            Length 115;
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Human enterovirus A
Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
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               /db_xref="taxon:12082"
/noce="Human poliovirus 1 strain Sabin"
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/organism="Human enterovirus A"
                                                                                          Score 20; DB
Pred. No. 30;
                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /mol type="genomic RNA"
/isolate="NSW/227/99"
/db_xref="taxon:138948"
<1._.>115
/isolate="NSW/96/97"
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                                                                                          100.0%;
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                                                                                       Query Match 100.
Best Local Similarity 100.
Matches 20; Conservative
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AY189213/c
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PEN295168 115 bp RNA linear VRL 15-MAY-2001
Porcine enterovirus 9 genomic RNA for partial 5'UTR, isolate
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2 (bases 1 to 115)
Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
Direct Submission
Direct Submission
Submitted (12-NOV-2002) Virology Division, South Eastern Area
Laboratory Services, University of New South Wales/Prince of Wales
Hospital, High Street, Randwick, NSW 2031, Australia
Location/Qualifiers
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Human enterovirus B isolate NSW/01/97 5' UTR, partial sequence.
AY189158.1 GI:28274381
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Submitted (03-NOV-2000) Muscillo M., Environmental Hygiene,
Istituto Superiore di Sanita', Viale Regina Elena 299, Rome,
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/isolate="ITA93-766BE93"
/specific_host="Sus scrofa"
/db_xref="taxon:64141"
/db="viral particles isolated from serum of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Porcine enterovirus 9
Porcine enterovirus 9
Porcine enterovirus 9
Viruses; saRNA postiive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
                                                                                                                                                                                                                                                                                                                      Length 115;
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/organle="Human enterovirus
/mol type="genomic RNA"
/isolate="NSW/255/99"
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Best Local Similarity 100.
Matches 20; Conservative
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Matches 20; Conservative
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Direct Submission
Submitted (29-NOV-2002) Virology Division, South Eastern Area
Laboratory Services, University of New South Wales/Prince of Wales
Hospital, High Street, Randwick, NSW 2031, Australia
Location/Qualifiers
                                                                                                                                                                                                         Submitted (29-NOV-2002) Virology Division, South Eastern Area Laboratory Services, University of New South Wales/Prince of Wales Hospital, High Street, Randwick, NSW 2031, Australia Location/Qualifiers
                     Viruses; SaRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
I (Dases I to 116)
Craig, M.E., Howard, N.J., Silink, M. and Rawlinson, W.D.
Reduced Frequency of HLA DRB1*03-DQB1*02 in Children with Type 1
Jiahetes Associated with Enterovirus RNA
J. Infect. Dis. 187 (10), 1562-1570 (2003)
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1 (Dases 1 to 116)
Craig, M.E., Howard, N.J., Silink, M. and Rawlinson, W.D.
Reduced Frequency of HLA DRB1*03-DQB1*02 in Children with Type 1 blabetes Associated with Enterovirus RNA
J. Infect. Dis. 187 (10), 1562-1570 (2003)
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Human enterovirus B isolate NSW/07/97 5' UTR, partial sequence.
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Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
Direct Submission
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/mol type="genomic RNA"
/isolate="NSW/01/97"
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/isolate="NSW/07/97"
/db_xref="taxon:138949"
<1. .>116
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Craig, M.E., Howard, N.J., Silink, M. and Rawlinson, W.D.
Direct Submission
Submitted (19-NOV-2002) Virology Division, South Eastern Area
Laboratory Services, University of New South Wales/Prince of Wales
Hospital, High Street, Randwick, NSW 2031, Australia
Location/Qualifiers
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Craig, M.E., Howard, N.J., Silink, M. and Rawlinson, W.D.
Direct Submission
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Submission, South Eastern Area
Laboratory Services, University of New South Wales/Prince of Wales
Hospital, High Street, Randwick, NSW 2031, Australia
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Human enterovirus B
Viruses; SERNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
1 (bases 1 to 116)
Craig, M.E., Howard, N.J., Sllink, M. and Rawlinson, W.D.
Reduced Frequency of HLA DRB1*03-DQB1*02 in Children with Type 1
Diabetes Associated with Enterovirus RNA
0. Infect. Dis. 187 (10), 1562-1570 (2003)
AY189161 116 bp RNA linear VRL 08-MAY-2
Human enterovirus 71 isolate NSW/08/97 5' UTR, partial sequence.
AY189161
                                                                                                                                      Human enterovirus 71
Human enterovirus 71
Viruses; ssRNA positive-strand viruses, no DNA stage;
Vicornaviridae; Enterovirus.
1 (bases 1 to 116)
Craig, M.E., Howard, N.J., Silink, M. and Rawlinson, W.D.
Reduced Frequency of HLA DRB1*03-DQB1*02 in Children with Type Diabetes Associated with Enterovirus RNA
J. Infect. Dis. 187 (10), 1562-1570 (2003)
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Human enterovirus B isolate NSW/14/97 5' UTR, partial sequence.
AY189162
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/mol type="genomic RNA"
/isolate="NSW/14/97"
/db_xref="taxon:138949"
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100.0%; Pred. No. 30,
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/isolate="NSW/08/97"
/db_xref="taxon:39054"
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Best Local Similarity
Matches 20; Conserv
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ORIGIN
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AY189165/c
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Craig, M.E., Howard, N.J., Silink, M. and Rawlinson, W.D.
Direct Submission
Submitted (129-NOV-2002) Virology Division, South Bastern Area
Laboratory Services, University of New South Wales/Prince of Wales
Hospital, High Street, Randwick, NSW 2031, Australia
                                                                                                                                                                                                                                                                                               Human enterovirus B
Viruses; sRNN positive-strand viruses, no DNA stage;
Virases; sRNN positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
1 (bases 1 to 116)
Craig, M. E., Howard, N. J., Sllink, M. and Rawlinson, W. D.
Reduced Frequency of HLA DRB1*03-DQB1*02 in Children with Type 1
Diabetes Associated with Enterovirus RNA
J. Infect. Dis. 187 (10), 1562-1570 (2003)
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Human enterovirus B
Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
1 (bases 1 to 116)
Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
Reduced Frequency of HLA DRB1*03-DOB1*02 in Children with Type
Diabetres Associated with Enterovirus RNA
J. Infect. Dis. 187 (10), 1562-1570 (2003)
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Human enterovirus B isolate NSW/17/97 5' UTR, partial sequence.
AY189164
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                                             Score 20; DB 13; Length 116; Pred. No. 30;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Human enterovirus B"
/mol_type="genomic RNA"
/isolate="NSW/16/97"
/db_tref="taxon:138949"
                                            Query Match 100.0%; Score 20; DB Best Local Similarity 100.0%; Pred. No. 30; Matches 20; Conservative 0; Mismatches
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                                                                                                                             104 AAGGAAACACGGACACCCAA 85
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Craig, M.E., Howard, N.J., Silink, M. and Rawlinson, W.D.
Direct Submission
Submitted (29-NOV-2002) Virology Division, South Eastern Area
Laboratory Services, University of New South Wales/Prince of Wales
Hospital, High Street, Randwick, NSW 2031, Australia
Location/Qualifiers
Submitted (29-NOV-2002) Virology Division, South Eastern Area Laboratory Services, University of New South Wales/Prince of Wales Hospital, High Street, Randwick, NSW 2031, Australia Location/Qualifiers
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Human enterovirus B
Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
I (Dases 1 to 116)
Craig, M.B., Howard, N.J., Silink, M. and Rawlinson, W.D.
Reduced Frequency of HIA DRB1*03-DQB1*02 in Children with Type
Diabetes Associated with Enterovirus RNA in Children with Type
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Human enterovirus B isolate NSW/19/97 5' UTR, partial sequence.
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Human enterovirus NSW/23/97 5' UTR, partial sequence.
AY189166
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100.0%; Score 20; DB 13; Length 116;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 20; Conservative 0; Mismatches 0; Indels
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Human enterovirus NSW/23/97
Viruses; sesta positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
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/organisma-"Human enterovirus B"
/mol_type="genomic RNA"
/isolate="NSW/17/97"
/db_xref="taxon:138949"
<1. .>116
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/mol type="genomic RNA"
/isoTate="NSW/19/97"
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<1._.>116
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AY189165.1 GI:28274388
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VRL 08-MAY-2003

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FEATURES

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Craig, M.E., Howard, N.J., Silink, M. and Rawlinson, W.D.
Craig, M.E., Howard, N.J., Silink, M. and Rawlinson, W.D.
Direct Submission
Submitted (29-NOV-2002) Virology Division, South Eastern Area
Laboratory Services, University of New South Wales/Prince of Wales
Hospital, High Street, Randwick, NSW 2031, Australia
Location/Qualifiers
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Cradig.M.B., Howard, N.J., Silink, M. and Rawlinson, W.D.
Direct Submission
Submitted (29-NOV-2002) Virology Division, South Eastern Area
Laboratory Services, University of New South Wales/Prince of Wales
Hospital, High Street, Randwick, NSW 2031, Australia
Location/Qualifiers
                                                                                                                                    Viruses; SSRNA positive-strand viruses, no DNA stage; Picornaviridae; Enterovirus.

1 (bases 1 to 116)
Craig, M.E., Howard, N.J., Silink, M. and Rawlinson, W.D.
Reduced Frequency of HIA DRB1*03-DDB1*02 in Children with Type 1 Diabetes Associated with Enterovirus RNA
J. Infect. Dis. 187 (10), 1562-1570 (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Viruses, ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
I (bases 1 to 116)
Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
Reduced Frequency of HiA DRB1*03-DDB1*02 in Children with Type 1
Diabetes Associated with Enterovirus RNA
J. Infect. Dis. 187 (10), 1562-1570 (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   116 bp RNA linear VRL 08-MAY-A1189172.1 GI:28274395
AY189171 116 bp RNA linear VRL 08-MAY.
Human enterovirus B isolate NSW/60/97 5' UTR, partial sequence.
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Pred. No. 30;
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/mol_type="genomic RNA"
/isolate="NSW/68/97"
/db_xref="taxon:138950"
                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Human enterovirus B"
/mol_type="genomic RNA"
/isolate="NSW/60/97"
/db_xref="taxon:138949"
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                                                            AY189171.1 GI:28274394
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Human enterovirus C
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Matches 20; Conservative
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Best Local Similarity
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AY189172/c
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Craig, M.E., Howard, N.J., Silink, M. and Rawlinson, W.D.
Direct Submission
Submitsed (29-NOV-2002) Virology Division, South Eastern Area
Laboratory Services, University of New South Wales/Prince of Wales
Hospital, High Street, Randwick, NSW 2031, Australia
Location/Qualifiers
                                                                                                                                      Craig, M.E., Howard, N.J., Silink, M. and Rawlinson, W.D.
Direct Submission
Direct Submission
Direct Submission
Laboratory Services, University of New South Wales/Prince of Wales Hospital, High Street, Randwick, NSW 2031, Australia
Location/Qualifiers
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Human enterovirus B
Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
I (bases 1 to 116)
Craig, M. E., Howard, N. J., Silink, M. and Rawlinson, W.D.
Reduced Frequency of HLA DRB1*03-DQB1*02 in Children with Type 1
Diabetes Associated with Enterovirus RNA
J. Infect. Dis. 187 (10), 1562-1570 (2003)
1 (bases 1 to 116)
Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.

Graig,M.E., Howard,N.J., Silink,M.
Diabetes Associated with Enterovirus RNA
J. Infect. Dis. 187 (10), 1562-1570 (2003)
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Best Local Similarity 100.0%; Pred. No. 30;
Matches 20; Conservative 0; Mismatches 0; Indels C
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                                                                                                                                                                                                                                                                     /organism="Human enterovirus NSW/23/97"
/mol_type="genomic RNA"
/isolate="NSW/23/97"
/bb_xref="taxon:220228"
<1. .>116
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/mol_type="genomic RNA"
/isolate="NSW/48/97"
/db_xref="teaxon:138949"
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Human enterovirus B isolate NSW/48/97 5
AY189170
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0; Mismatches
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AY189170/c
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AY189171/c
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VRL 08-MAY-2003

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organism="Human enterovirus B"
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Human enterovirus B
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Human enterovirus B
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Best Local Similarity 100.
Matches 20; Conservative
                                                                                                                                              Conservative
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AY189180/c
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Craig, M.E., Howard, N.J., Silink, M. and Rawlinson, W.D.
Direct Submission
Submitted (29-N0V-2002) Virology Division, South Eastern Area
Laboratory Services, University of New South Wales/Prince of Wales
Hospital, High Street, Randwick, NSW 2031, Australia
Location/Qualifiers
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Reduced Frequency of HLA DRB1*03-DQB1*02 in Children with Type 1
Diabetes Associated with Enterovirus RNA
J. Infect. Dis. 187 (10), 1562-1570 (2003)
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Picornaviridae; Enterovirus.

Carig, M.E., Howard, N.J., Silink, M. and Rawlinson, W.D.
Reduced Frequency of HLA DRB1*03-DQB1*02 in Children with Type 1
Diabetes Associated with Enterovirus RNA
J. Infect. Dis. 187 (10), 1562-1570 (2003)
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Human enterovirus B isolate NSW/82/97 5' UTR, partial sequence.
AY189175
                                                                                                                                           AY189173 116 bp RNA linear VRL 08-MAY.
Human enterovirus B isolate NSW/73/97 5' UTR, partial sequence.
   Gaps
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Submitted (29-NOV-2002) Virology Division, South Eastern Area
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Picornaviridae; Enterovirus.
1 (bases 1 to 116)
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/mol_type="genomic RNA"
/isolate="NSW/73/97"
/db_xref="taxon:138949"
 0; Mismatches
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Pred. No.
                               1 AAGGAAACACGGACACCCAA 20
                                                    104 AAGGAAACACGGACACCCAA 85
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AY189173.1 GI:28274396
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Human enterovirus B
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Human enterovirus B
20; Conservative
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Best Local Similarity 100.
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AY189175/c
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Picornaviridae; Enterovirus.
I (bases 1 to 116)
Craig, ME., Howard, N.J., Silink, M. and Rawlinson, W.D.
Reduced Frequency of HIA DRB1*03-DQB1*02 in Children with Type 1
Diabetes Associated with Enterovirus RNA
J. Infect. Dis. 187 (10), 1562-1570 (2003)
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Picornaviridae; Enterovirus.
1 (bases 1 to 116)
Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
Reduced Frequency of HLA DRB1*03-DQB1*02 in Children with Type 1
Diabetes Associated with Enterovirus RNA
J. Infect. Dis. 187 (10), 1562-1570 (2003)
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Human enterovirus B isolate NSW/111/98 5' UTR, partíal sequence.
AY189180
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Craig, M.E., Howard, N.J., Silink, M. and Rawlinson, W.D.
Direct Submission
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/mol_type="genomic RNA"
/isolate="NSW/83/97"
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/mol type="genomic RNA"
/isolate="NSW/82/97"
/db_xref="taxon:138949"
<1. .>116
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PUBMED REFERENCE AUTHORS

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Matches

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Submitted (29-NOV-2002) Virology Division, South Eastern Area Laboratory Services, University of New South Wales/Prince of Wales Hospital, High Street, Randwick, NSW 2031, Australia Location/Qualifiers
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Craig, M.E., Howard, N.J., Silink, M. and Rawlinson, W.D.
Direct Submission
Submitted (29-NOV-2002) Virology Division, South Eastern Area
Laboratory Services, University of New South Wales/Prince of Wales
Hospital, High Street, Randwick, NSW 2031, Australia
Location/Qualifiers
                                                               Picornaviridae, Enterovirus.

1 (bases 1 to 116)

Craig, M. E., Howard, N. J., Silink, M. and Rawlinson, W.D.
Reduced Frequency of HLA DRB1*03-DQB1*02 in Children with Type 1
Diabetes Associated with Enterovirus RNA
J. Infect. Dis. 187 (10), 1562-1570 (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Viruses; seRNA positive-strand viruses, no DNA stage; plocoraviridae; Enterovirus.

1 (Dases 1 to 116)
Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
Diabetes Associated with Enterovirus RNA
J. Infect. Dis. 187 (10), 1562-1570 (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AY189183 116 bp RNA linear VRL 08-MAY-2
Human enterovirus B isolate NSW/141/98 5' UTR, partial sequence.
AY189183
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 116;
                                                                                                                                                                                                              2 (bases 1 to 116)
Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
Direct Submission
Human enterovirus 70
Human enterovirus 70
Viruses; ssRNA positive-strand viruses, no DNA stage;
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ilarity 100.0%; Pred. No. 30;
Conservative 0; Mismatches 0:
                                                                                                                                                                                                                                                                                                                                                                               /organism="Human enterovirus 70"
/mol type="genomic RNA"
/isolate="NSW/140/98"
/db_xref="taxon:12090"
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/isolate="NSW/141/98"
/db_xref="taxon:138949"
<1. .>116
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Human enterovirus B
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les 20; Conserv
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                   Craig M.B., Howard, N.J., Silink, M. and Rawlinson, W.D.
Direct Submission
Submission
Submitted (29-NOV-2002) Virology Division, South Eastern Area
Laboratory Services, University of New South Wales/Prince of Wales
Hospital, High Street, Randwick, NSW 2031, Australia
Location/Qualiflers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (29-NOV-2002) Virology Division, South Eastern Area Laboratory Services, University of New South Wales/Prince of Wales Hospital, High Street, Randwick, NSW 2031, Australia Location/Qualifiers
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Picornaviridae; Enterovirus.
I (bases 1 to 116)
Craig, M.E., Howard, N.J., Silink, M. and Rawlinson, W.D.
Reduced Frequency of HLA DRB1*03-DQB1*02 in Children with Type 1
Dlabetes Associated with Enterovirus RNA
J. Infect. Dis. 187 (10), 1562-1570 (2003)
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Human enterovirus 70 NSW/140/98 5′ UTR, partial sequence.
AY189182
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0
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/mol type="genomic RNA"
/isolate="NSW/111/98"
/db_xref="taxon:138949"
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/mol_type="genomic RNA"
/isolate="NSW/135/98"
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0; Mismatches
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Human enterovirus B
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KEYWORDS SOURCE ORGANISM

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VERSION

AUTHORS TITLE

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AUTHORS

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FEATURES

RESULT 27 AY189181/c DEFINITION

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VRL 08-MAY-2003
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Human enterovirus B isolate NSW/151/98 5' UTR, partial sequence.
AY189188
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Human enterovirus B isolate N3W/149/98 5' UTR, partial sequence.
AY189187
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Picornaviridae; Enterovirus.

1 (bases 1 to 116)
Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
Reduced Frequency of HIA DRB1*03-DQB1*02 in Children with Type
Diabetes Associated with Enterovirus RNA
J. Infect. Dis. 187 (10), 1562-1570 (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Viruses; seRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
1 (Dasse 1 to 116)
Craig, M.E., Howard, N.J., Silink, M. and Rawlinson, W.D.
Reduced Frequency of HIA DRB1*03-DQB1*02 in Children with Type Diabetes Associated with Enterovirus RNA
J. Infect. Dis. 187 (10), 1562-1570 (2003)
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Direct Submission
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Craig, M.E., Howard, N.J., Silink, M. and Rawlinson, W.D.
Direct Submission
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/organism="Human enterovirus
/mol_type="genomic RNA"
/isolate="NSW/149/98"
   100.0%; Score 20; DB
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iive 0; Mismatches
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Human enterovirus B
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   Query Match
Best Local Similarity 100.0
Matches 20; Conservative
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Hospital, High Street, Randwick, NSW 2031, Australia
Location/Qualifiers
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Picornaviridae; Enterovirus.
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Craig.M.E., Howard, N.J., Silink, M. and Rawlinson, W.D.
Reduced Frequency of HLA DRB1*03-DQB1*02 in Children.with Type 1
Diabetes Associated with Enterovirus RNA
J. Infect. Dis. 187 (10), 1562-1570 (2003)
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1 (Dases 1 to 116)
Craig, M.E., Howard, N.J., Silink, M. and Rawlinson, W.D.
Craig, A.E., Howard, N.J., Silink, M. and Rawlinson, W.D.
Diabetes Associated with Enterovirus RNA
J. Infect. Dis. 187 (10), 1562-1570 (2003)
                           AX189184 116 bp RNA linear VRL 08-MAY-2
Human enterovirus B isolate NSW/143/98 5' UTR, partial sequence.
AX189184
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Human enterovirus B isolate NSW/147/98 5' UTR, partial sequence.
AY189186
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Pred. No. 30;
Mismatches 0; Indels (
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Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Human enterovirus B"
/mol_type="genomic RNA"
/isolate="NSW/143/98"
/db_xref="taxon:138949"
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/isolate="NSW/147/98"
/db xref="taxon:138949"
<1. .>116
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100.0%; Pre
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Human enterovirus B
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Human enterovirus B
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Best Local Similarity
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RESULT 30
AY189184/c
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Human enterovirus 71 isolate NSW/153/98 5' UTR, partial sequence.
AY189189.1 GI:28274412
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Direct Submission
Submitted (29-NOV-2002) Virology Division, South Eastern Area
Laboratory Services, University of New South Wales/Prince of Wales
Hospital, High Street, Randwick, NSW 2031, Australia
Location/Qualifiers
Laboratory Services, University of New South Wales/Prince of Wales Hospital, High Street, Randwick, NSW 2031, Australia Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                 Viruees; ssRNA positive-strand viruses, no DNA stage; Picornaviridae; Enterovirus.
I (bases 1 to 116)
Craig, M.E., Howard, N.J., Silink, M. and Rawlinson, W.D. Reduced Frequency of HLA DRB1*03-DQB1*02 in Children with Type 1 Jubetes Associated with Enterovirus RNA
J. Infect. Dis. 187 (10), 1562-1570 (2003)
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Human enterovirus NSW/154/98 5' UTR, partial sequence.
AY189190
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Human enterovirus NSW/154/98
Viruses; esRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
                                                                                                                                                                    13; Length 116;
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                                                         /organism="Human enterovirus
/mol_type="genomic RNA"
/isolate="NSW/151/98"
/db_xref="taxon:138949"
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/isolate="NSW/153/98"
/db_xref="taxon:39054"
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Human enterovirus 71
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AY189189/c
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Craig, M.B., Howard, N.J., Silink, M. and Rawlinson, W.D.
Direct Submission
Submitted (29-NOV-2002) Virology Division, South Eastern Area
Laboratory Services, University of New South Wales/Prince of Wales
Hospital, High Street, Randwick, NSW 2031, Australia
Location/Qualifiers
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Craig, M.E., Howard, N.J., Silink, M. and Rawlinson, W.D.
Direct Submission
Submitted (29-NOV-2002) Virology Division, South Eastern Area
Laboratory Services, University of New South Wales/Prince of Wales
Hospital, High Street, Randwick, NSW 2031, Australia
Location/Qualifiers
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Human enterovirus 71 isolate NSW/157/98 5' UTR, partial sequence.
AY189192
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Picornaviridae; Enterovirus.
1 (bases 1 to 116)
Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
Diabetes Prequency of HLA DRB1*03-DQB1*02 in Children with Type 1
Diabetes Associated with Enterovirus RNA
J. Infect. Dis. 187 (10), 1562-1570 (2003)
1 (bases 1 to 116)
Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
Reduced Frequency of HLA DRB1*03-DQB1*02 in Children with Type 1
Diabetes Associated with Entercovirus RNA
J. Infect. Dis. 187 (10), 1562-1570 (2003)
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/mol_type="genomic RNA"
/isolate="NSW/154/98"
/db_xref="taxon:220409"
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/mol type="genomic RNA"
/isolate="NSW/157/98"
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<1. .>116
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Human enterovirus 71
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Best Local Similarity 100.0
Matches 20; Conservative
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Length 116;

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100.0%; Score 20; DB 13;
100.0%; Pred. No. 30;
iive 0; Mismatches 0;
                                                                      1 AAGGAAACACGGACACCCAA 20
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hes 20; Conservative
                                       Conservative
   Query Match
Best Local Similarity
Matches 20; Conserv
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VERSION
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                    VRL 08-MAY-2003
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Submitted (29-NOV-2002) Virology Division, South Eastern Area
Laboratory Services, University of New South Wales/Prince of Wales
Hospital, High Street, Randwick, NSW 2031, Australia
Location/Qualifiers
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Laboratory Services, University of New South Wales/Prince of Wales
Hospital, High Street, Randwick, NSW 2031, Australia
                                                                                              Human enterovirus NSW/161/98
William enterovirus NSW/161/98
Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
I (Dases I to 116)
Craig M.E., Howard, N.J., Silink, M. and Rawlinson, W.D.
Reduced Frequency of HLA DRB1*03-DQB1*02 in Children with Type 1
Diabetes Associated with Enterovirus RNA
J. Infect. Dis. 187 (10), 1562-1570 (2003)
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                                    UTR, partial sequence.
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Picornaviridae; Enterovirus.
1 (bases 1 to 116)
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Craig, M.B., Howard, N.J., Silink, M. and Rawlinson, W.D.
Direct Submission
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                    linear
                                                                                                                                                                                                                                                                                                                                                                                                /organism="Human enterovirus NSW/161/98"
Mond_type="genomic RNA"
/isolate="NSW/161/98"
/db_xref="taxon:220410"
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Human enterovirus 71 isolate NSW/166/98 5'
AY189195
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|mol_type="genomic RNA"
/isolate="NSW/166/98"
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/note="Human enterovirus 71"
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100.0%; Score 20; DB
Best Local Similarity 100.0%; Pred. No. 30;
Matches 20; Conservative 0; Mismatches
                  AY189194 116 bp
Human enterovirus NSW/161/98 5'
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AY189194.1 GI:28274417
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Human enterovirus 71
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AY189195/c
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AY189194/C
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Human enterovirus 71 isolate NSW/169/98 5' UTR, partial sequence.
AX189196
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Craig, M.E., Howard, N.J., Silink, M. and Rawlinson, W.D.
Direct Submission
Submitted (29-NOV-2002) Virology Division, South Eastern Area
Laboratory Services, University of New South Wales/Prince of Wales
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (29-NOV-2002) Virology Division, South Eastern Area Laboratory Services, University of New South Wales/Prince of Wales Hospital, High Street, Radwick, NSW 2031, Australia Location/Qualifiers
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Human enterovirus 71
Viruses; saRNA positive-strand viruses, no DNA stage;
Viruses; saRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.

( bases 1 to 116)
Craig, M.E., Howard, N.J., Silink, M. and Rawlinson, W.D.
Reduced Frequency of HLA DRB1*03-DQB1*02 in Children with Type 1
Diabetes Associated with Enterovirus RNA
John Children with Type 1
Diabetes LDBS. 187 (10), 1562-1570 (2003)
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Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
Reduced Frequency of HLA DRB1*03-DQB1*02 in Children with Type 1
Diabetes Associated with Enterovirus RNA
J. Infect. Dis. 187 (10), 1562-1570 (2003)
Gaps
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Human enterovirus NSW/173/98 5' UTR, partial sequence.
AY189197
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Craig, M.E., Howard, N.J., Silink, M. and Rawlinson, W.D.
Direct Submission
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Human enterovirus NSW/173/98
Viruses; sestin positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
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/mol type="genomic RNA"
/isoTate="NSW/169/98"
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/note="Human enterovirus 71"
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Query Match
Best Local Similarity 100.
Matches 20; Conservative
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Matches 20;
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AY189202/c
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Human enterovirus 71 isolate NSW/180/98 5' UTR, partial sequence.
AX189198
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Direct Submission
Submitsed (29-NOV-2002) Virology Division, South Eastern Area
Laboratory Services, University of New South Wales/Prince of Wales
Hospital, High Street, Randwick, NSW 2031, Australia
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                  Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae; Enterovirus.

I (bases 1 to 116)

Craig, M.E., Howard, N.J., Silink, M. and Rawlinson, W.D. Reduced Frequency of HLA DRB1*03-DQB1*02 in Children with Type 1 Jubetes Associated with Enterovirus RNA
J. Infect. Dis. 187 (10), 1562-1570 (2003)
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Picornaviridae; Enterovirus.
1 (bases 1 to 116)
High Street, Randwick, NSW 2031, Australia
Location/Qualifiers
                           1. .116
/organism="Human enterovirus NSW/173/98"
/mol_type="genomic RNA"
/isolate="NSW/173/98"
/db_xref="taxon:220411"
<1. .>116
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/mol type="genomic RNA"
/isolate="NSW/180/98"
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Human enterovirus 71
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Human enterovirus 71
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AY189198/c
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Craig, M.B., Howard, N.J., Silink, M. and Rawlinson, W.D.
Direct Submission
Submitted (29-NOV-2002) Virology Division, South Eastern Area
Laboratory Services, University of New South Wales/Prince of Wales
Hospital, High Street, Randwick, NSW 2031, Australia
Location/Qualifiers
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Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
Direct Submission
Submitted (19-NOV-2002) Virology Division, South Eastern Area
Laboratory Services, University of New South Wales/Prince of Wales
Hospital, High Street, Randwick, NSW 2031, Australia
Location/Qualifiers
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Human enterovirus B
Viruses; saRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
I (bases 1 to 116)
Craig, M.E., Howard, N.J., Silink, M. and Rawlinson, W.D.
Reduced Frequency of HLA DRB1*03-DQB1*02 in Children with Type 1
Diabetes Associated with Enterovirus RNA
J. Infect. Dis. 187 (10), 1562-1570 (2003)
Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D. Reduced Frequency of HLA DRB1*03-DQB1*02 in Children with Type 1 Diabetes Associated with Enterovirus RNA
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Human enterovirus B isolate NSW/189/99 5' UTR, partial sequence.
AY189200
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Pred. No. 30;
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/isolate="NSW/182/98"
/db xref="taxon:39054"
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/isolate="NSW/189/99"
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Gaps

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KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS TITLE

JOURNAL

TITLE JOURNAL

FEATURES

AUTHORS

REFERENCE

DEFINITION ACCESSION

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VRL 08-MAY-2003
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Craig, M.E., Howard, N.J., Silink, M. and Rawlinson, W.D.
Direct Submission
Submitted (129-NOV-2002) Virology Division, South Eastern Area
Laboratory Services, University of New South Wales/Prince of Wales
Hospital, High Street, Randwick, NSW 2031, Australia
Location/Qualifiers
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Picornaviridae; Enterovirus.

1 (bases 1 to 116)
Craig, M.E., Howard, N.J., Silink, M. and Rawlinson, W.D.
Reduced Frequency of HLA DRB1*03-DOB1*02 in Children with Type 1
Diabetes Associated with Enterovirus RNA
J. Infect. Dis. 187 (10), 1562-1570 (2003)
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Picornaviridae; Enterovirus.
1 (bases 1 to 116)
Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
Reduced Frequency of HLA DREL*03.DOB1*02 in Children with Type 1
Diabetes Associated with Enterovirus RNA
J. Infect. Dis. 187 (10), 1562-1570 (2003)
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Human enterovirus B isolate NSW/198/99 5′ UTR, partial sequence.
AV189204 GI:28274427
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Human enterovirus B isolate NSW/208/99 5' UTR, partial sequence.
AY189206
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/mol_type="genomic RNA"
/isol_ate="NSW/198/99"
/db_xref="taxon:138949"
100.0%; Preα. ...
tive 0; Mismatches
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Best Local Similarity 100.0%;
Matches 20; Conservative (
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Human enterovirus B
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Matches 20; Conserv
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       AY189202 116 bp RNA linear VRL 08-MAY-2003
Human enterovirus 71 isolate NSW/196/99 5' UTR, partial sequence.
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Direct Submission
Submitted (29-NOV-2002) Virology Division, South Eastern Area
Laboratory Services, University of New South Wales/Prince of Wales
Hospital, High Street, Randwick, NSW 2031, Australia
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                      Craig, M.E., Howard, N.J., Silink, M. and Rawlinson, W.D.
Direct Submission
Submitted (29-NOV-2002) Virology Division, South Eastern Area
Laboratory Services, University of New South Wales/Prince of Wales
Hospital, High Street, Randwick, NSW 2031, Australia
Location/Qualifiers
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Human enterovirus B isolate NSW/197/99 5' UTR, partial sequence.
AY189203
                                                                                                                                 Human enterovirus 71
Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
1 (bases 1to 116)
Craig, M.E., Howard, N.J., Silink, M. and Rawlinson, W.D.
Reduced Frequency of HLA DRB1*03-DQB1*02 in Children with Type Diabetes Associated with Enterovirus RNA
J. Infect. Dis. 187 (10), 1562-1570 (2003)
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Picornaviridae; Enterovirus.
1 (bases 1 to 116)
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/note="Human enterovirus 71"
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/isolate="NSW/196/99"
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/isolate="NSW/197/99"
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Human enterovirus B
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5'UTR ORIGIN

ACCESSION VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS

TITLE

LOCUS DEFINITION AY189203/c

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PEATURES

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ACCESSION VERSION KEYWORDS SOURCE REFERENCE AUTHORS TITLE

JOURNAL PUBMED

REFERENCE AUTHORS TITLE

JOURNAL

FEATURES

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ллоэд14 116 bp RNA linear VRL 08-MAY-2003
Human enterovirus A isolate NSW/277/99 5' UTR, partial sequence.
AY189214
                                                          Craig M.E., Howard, N.J., Silink, M. and Rawlinson, W.D.
Direct Submission
Submitted (29-NOV-2002) Virology Division, South Eastern Area
Laboratory Services, University of New South Wales/Prince of Wales
Hospital, High Street, Randwick, NSW 2031, Australia
Location/Qualifiers
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Craig, M.E., Howard, N.J., Silink, M. and Rawlinson, W.D.
Craig, M.E., Howard, N.J., Silink, M. and Rawlinson, W.D.
Diabetes Associated with Bate rovirus RNA
J. Infect. Dis. 187 (10), 1562-1570 (2003)
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AY189215.1 GI:28274438
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Craig, M.E., Howard, N.J., Silink, M. and Rawlinson, W.D.
Direct Submission
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Picornaviridae; Enterovirus.
Infect. Dis. 187 (10), 1562-1570 (2003)
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/isolate="NSW/277/99"
/db_xref="taxon:138948"
<1. .>116
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/isolate="NSW/230/99"
/db_xref="taxon:138949"
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5' UTR, partial sequence.
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Submitted (129-NOV-2002) Virology Division, South Eastern Area Laboratory Services, University of New South Wales/Prince of Wales Hospital, High Street, Randwick, NSW 2031, Australia Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human enterovirus B
Human enterovirus B
Human enterovirus B
Yiusee; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
1 (bases 1 to 116)
Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
Craig,M.E., Howard, N.J., Silink,M. and Rawlinson,W.D.
Diabetes Associated with Enterovirus RNA
J. Infect. Dis. 187 (10), 1562-1570 (2003)
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1 (bases 1 to 116)
Craig, M.E., Howard, N.J., Silink, M. and Rawlinson, W.D.
Reduced Frequency of HLA DRB1*03-D0B1*02 in Children with Type 1 Diabetes Associated with Enterovirus RNA
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Human enterovirus B isolate NSW/214/99 5' UTR, partial sequence.
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Human enterovirus B isolate NSW/230/99
AY189211.1 GI:28274434
1. .116
/organism="Human enterovirus
/mol_type="genomic RNA"
/isolate="NSW/208/99"
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/isolate="NSW/214/99"
/db_xref="taxon:138949"
                                                                              /db_xref="taxon:138949"
<1. .>116
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AY189208.1 GI:28274431
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Human enterovirus B
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5'UTR ORIGIN

SOURCE ORGANISM

REFERENCE AUTHORS TITLE

ACCESSION VERSION KEYWORDS

RESULT 49 AY189211/c LOCUS DEFINITION

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Human enterovirus 71 isolate NSW/E71/99 5' UTR, partial sequence.
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                                                                                                                                                                                                         Craig M.E., Howard, N.J., Silink, M. and Rawlinson, W.D.
Direct Submission
Submitted (29-NOV-2002) Virology Division, South Eastern Area
Laboratory Services, University of New South Wales/Prince of Wales
Hospital, High Street, Randwick, NSW 2031, Australia
Location/Qualifiers
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Craig, M.E., Howard, N.J., Silink, M. and Rawlinson, W.D.
Reduced Frequency of HLA DRB1*03-DQB1*02 in Children with Type 1
Diabetes Associated with Enterovirus RNA
J. Infect. Dis. 187 (10), 1562-1570 (2003)
            Human enterovirus B
Human enterovirus B
Yūruses, saRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus
1 (Dases I to 116)
Craig, M.E., Howard, N.J., Silink, M. and Rawlinson, W.D.
Reduced Frequency of HIA DRB1*03-DQB1*02 in Children with Type Diabetes Associated with Enterovirus RNA
J. Infect. Dis. 187 (10), 1562-1570 (2003)
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Human enterovirus 71
Viruses; sesvirus positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
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/isolate="NSW/338/99"
/db_xref="taxon:138949"
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/isolate="NSW/E71/99"
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AY189216.1 GI:28274439
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Institute of Public Health and Environmental Sciences, Infectious Disease Research Division; 2-1-29, Arata-Cho, Hyogo-Ku, Kobe, Hyogo 652-0032, Japan (E-mail:Tsuguto_Fujimoto@pref.hyogo.jp, URL:http://www.iphes.pref.hyogo.jp/, Tel:81-78-511-6640(ex.236), Fax:81-78-531-7080)
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                                                                                                                                            VRL 02-JUL-2004
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southern Alberta isolate, Genomic RNA, 119 nt, segment 1 of 2].
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                                                                                                               Human enterovirus 71 genomic RNA, 5' UTR, partial sequence, isolate: 2279/EV71/Hyogo/2003.
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Picornaviridae; Enterovirus.
1 (bases 1 to 119)
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Genomic analysis of type 3 wild poliovirus isolates
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/isolate="2279/EV71/Hyogo/2003"
/isolation_source="cerebrospinal fluid"
/specific host="human"
/db_xref="taxon:39054"
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104 AAGGAACACGGACCCAA
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Human enterovirus 71
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Human poliovirus 3
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hes 20; Conservative
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VRL 02-JUL-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Molecular identification and typing of enteroviruses isolated from
                                 Molecular identification and typing of enteroviruses isolated from
Manzara, S., Muscillo, M., La Rosa, G., Marianelli, C., Cattani, P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /mol_trpe="genomic RNA"
/strain="1/ro/Roma98"
/isolate="1798-5102"
/db xref="taxon:82639"
/lab host="vero cell culture"
/note="throat swab from child with aseptic meningitis, identified by immunofluorescence assay"
<1. .>145
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                                                                                                                                                                                                                                                                                    /mol_type="genomic RNA"
/strain="/ra/Roma99"
/isolate="IT99-5108"
/db xref="taxon:82639"
/lab host="LLC-MK2 cell culture"
/note="throat swab from child with aseptic meningitis, identified by immunofluorescence assay"
                                                                                                                  Muscillo,M.
Direct Submission
Submitted (08-MAY-2001) Muscillo M., Environmental Hygiene,
Submitted (08-MAY-2001) Muscillo M., Environmental Hygiene,
Istituto Superiore di Santa', Viale Regina Blena 299, Rome,
00161, Italy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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Submitted (08-MAY-2001) Muscillo M., Environmental Hygiene,
Istituto Superiore di Sanita', Viale Regina Elena 299, Rome,
00161, Italy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          145 bp RNA linear VRL (
Human coxsackievirus B2 partial 5'UTR, strain /ro/Roma98.
AJ312091.1 G1:16555709
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Score 20; DB 13; Length 145;
; Pred. No. 30;
0; Mismatches 0; Indels C
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Picornaviridae; Enterovirus.
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J. Clin. Microbiol. 40 (12), 4554-4560 (2002)
12454151
                                                       clinical specimens
J. Clin. Microbiol. 40 (12), 4554-4560 (2002)

    145
/organism="Human coxsackievirus B2"

                                                                                                                                                                                                                                                organism="Human coxsackievirus B2"
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Human coxsackievirus B2
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Muscillo, M.
                                                                                                         2 (bases 1 to 145)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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                                                                                                                                                                                                                                     1. .145
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Best Local Similarity
                                                                                     12454151
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HEN312091/c
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ORIGIN
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                                                                                                                                                                                                                                                                                                                                       RNA linear VRL 12-AUG-2005 genomic RNA, isolate P20.
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Genomic mutations in oral poliovirus vaccine strains:Implications
for the eradication of poliovirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
Submitted (12-JUL-2004) Pavlov D.N., Medical Virology, University
of Pretoria, P.O.Box 2034, Pretoria, Gauteng, 0001, SOUTH AFRICA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       isolation_source="stool specimen from immunodeficient
                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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Human coxsackievirus B2
Viruses; seRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                           Human poliovirus 1
Viruees, ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
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                                                                                                                                         Length 119;
                                                                                                                                                                            0; Indels
                  1. .119
/organisma-Human poliovirus 3"
/mol_type="genomic RNA"
/db_xref="taxon:12086"
/country="Canada: southern Alberta"
                                                                                                                                          100.0%; Score 20; DB 13; 100.0%; Pred. No. 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /specific host="Homo sapiens"
/db xref="taxon:12080"
/country="South Africa:Gauteng"
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                                                                                                                                                                            0; Mismatches
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Human poliovirus 1, partial 5'UTR,
AJ783777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /mol_type="genomic RNA"
/isolate="P20"
Location/Qualifiers
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                                                                                                                                                                                                                 1 AAGGAAACACGGACACCCAA 20
                                                                                                                                                                                                                                     1 AAGGAAACACGGACACCCAA 20
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Matches 20; Conserv
                                                                                                                                                             Similarity
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Best Local
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ORIGIN
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HEN312090/c
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AJ783777/c
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<1. .>147
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Best Local Simi
Matches 20;
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ORIGIN
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AF314004/c
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                                                                                                                                                                                                                                                           Enterovirus 5506/SIN/001309
Enterovirus 5506/SIN/001309
Viruses; seRMA positive-strand viruses, no DNA stage;
Viruses: seRMA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.

1 (bases 1 to 147)
Singh,S., Chow,V.T.K., Phoon,M.C., Chan,K.P. and Poh,C.L.
Direct Detection of Enterovirus 71 (EV71) in Clinical Specimens from a Hand, Poot, and Mouth Disease Outbreak in Singapore by Reverse Transcription-PCR with Universal Enterovirus and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Viruses; seRNA positive-strand viruses, no DNA stage; plcornavirides; Enterovirus.

1 (Dases 1 to 147)
Singh,S., Chow,V.T.K., Phoon,M.C., Chan,K.P. and Poh,C.L.
Direct Detection of Enterovirus 71 (EVT) in Clinical Specimens from a Hand, Foot, and Mouth Disease Outbreak in Singapore by Reverse Transcription-PCR with Universal Enterovirus and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AF316322 147 bp mRNA linear VRL 31-JUL-
Enterovirus 71 isolate 5855/sin/000009 5'UTR, partial sequence
                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (18-OCT-2000) Microbiology, National University of Singapore, 5 Science Drive 2, Singapore 117597, Singapore Location/Qualifiers
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                                                                                                                                                                             AF314006 147 bp mRNA linear V
Enterovirus 5506/SIN/001309 5' UTR, partial sequence.
     Length 145;
                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1. .147
/organism="Enterovirus 5506/SIN/001309"
/mol type="mRNA"
/strain="5506/SIN/001309"
/db_xref="taxon:150715"
                                                                                                                                                                                                                                                                                                                                                                                                             EV71-Specific Primers
J. Clin. Microbiol. 40 (8), 2823-2827 (2002)
12149336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Clin. Microbiol. 40 (8), 2823-2827 (2002)
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ch 100.0%; Score 20; DB 13; Similarity 100.0%; Pred. No. 30; 20; Conservative 0; Mismatches 0;
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Singh,S., Chow,V.T.K. and Poh,C.L.
Direct Submission
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Singh,S., Chow,V.T.K. and Poh,C.L.
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                                                                   1 AAGGAAACACGGACACCCAA 20
                                                                                                                                                                                                                                AF314006.1 GI:12667229
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AF316322.1 GI:12744302
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Human enterovirus 71
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Best Local Similarity
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AF314006/c
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                                                                                                                                                                                                                                          /note="Human enterovirus 71 derived from human mouth swab, derived from isolates collected from human mouth swab, saliva, lung, heart, brain, rectal swab, tonsils, spleen, foot swab, throat swab, intestine, and oral mucosa."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 (bases 1 to 153)
Singh,S., Chow,V.T.K., Phoon,M.C., Chan,K.P. and Poh,C.L.
Bingth, B., Chow,V.T.K., Phoon,M.C., Chan,K.P. and Poh,C.L.
Direct Detection of Enterovirus 71 (EVT)1 in Clinical Specimens
from a Hand, Foot, and Mouth Disease Outbreak in Singapore by
Reverse Transcription-PCR with Universal Enterovirus and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
Submitted (24-OCT-2000) Department of Microbiology, National University of Singapore, 5, Science Drive 2, Singapore 117597, Singapore
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AF314004
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                                                                                                                                  organism="Human enterovirus 71"
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7ative 0; Mismatches 0;
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100.0%; Score 20; DB 13;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 20; Conservative 0; Mismatches 0;
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Mismatches
                                                                                                                                                              /mol_type="mRNA"
/isolate="5855/sin/000009"
/db_xref="taxon:39054"
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/strain="5589/SIN/001809"
/db_xref="taxon:150718"
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gh,S., Chow,V.T.K. and Poh,C.L.
                                                                                  Location/Qualifiers
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Enterovirus 5589/SIN/001809
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VRL 31-JUL-2002

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Enterovirus 5536/SIN/001409
Enterovirus 5536/SIN/001409
Viruses; seRMA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.

1 (bases 1 to 154)
Singh,S., Chow,V.T.K., Phoon,M.C., Chan,K.P. and Poh,C.L.
Direct Detection of Enterovirus 71 (EV71) in Clinical Specimens from a Hand, Foot, and Mouth Disease Outbreak in Singapore by Reverse Transcription-PCR with Universal Enterovirus and
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                                                                                                             Submitted (23-FEB-2001) Microbiology, National University o Singapore, 5 Science Drive 2, Singapore 117597, Singapore Sequence update by submitter on Feb 23, 2001 this sequence version replaced gi:12667228. Location/Qualifiers
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Singh,S., Chow,V.T.K. and Poh,C.L.
Submitted Source Submitted Corrections of Submitted Source Drive 2, Singapore 117597, Singapore Singh,S., Chow, Chow
Singapore, 5 Science Drive 2, Singapore 117597, Singapore 3 (bases 1 to 154)
Singh,S., Chow,V.T.K. and Poh,C.L.
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                                                                                                                                                                                                                                                                                  organism="Enterovirus 5656/SIN/002209"
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/strain="5536/SIN/001409"
/db_xref="taxon:150716"
<1...>154
                                                                                                                                                                                                                                                                                                               /mol_type="mRNA"
/strain="5656/SIN/002209"
/db_xref="taxon:150720"
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                                                                                                                                                                                                                                                                                Viruses, ssRNA positive-strand viruses, no DNA stage;
Plocoravitidae; Enterovirus.
1 (bases 1 to 154)
Singh,S., Chow,V.T.K., Phoon,M.C., Chan,K.P. and Poh,C.L.
Singh,S., Chow,V.T.K., Phoon,M.C., Chan,R.P. and Poh,C.L.
From a Hand, Foot, and Month Disease Outbreak in Singapore by
Reverse Transcription-PCR with Universal Enterovirus and
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1 (bases 1 to 154)
Singh,S., Chow,V.T.K., Phoon,M.C., Chan,K.P. and Poh,C.L.
Direct Detection of Enterovirus 71 (EV71) in Clinical Specimens from a Hand, Foot, and Mouth Disease Outbreak in Singapore by Reverse Transcription-PCR with Universal Enterovirus and
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Submitted (23-FEB-2001) Microbiology, National University of Singapore, 5 Science Drive 2, Singapore 117597, Singapore Sequence update by submitter
On Feb 23, 2001 this sequence version replaced gi:12667226.
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Singh,S., Chow,V.T.K. and Poh,C.L.
Direct Submission
Submitted (18-OCT-2000) Microbiology, National University of
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Singh,S., Chow,V.T.K. and Poh,C.L.
Direct Submission
Submitted (18-OCT-2000) Microbiology, National University of
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Singh,S., Chow,V.T.K. and Poh,C.L.
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Enterovirus 5656/SIN/002209 5′ UTR, partial sequence.
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UTR, partial sequence.
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J. Clin. Microbiol. 40 (8), 2823-2827 (2002)
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/strain="5627/SIN/002009"
/db_xref="taxon:150719"
                                                                                      154 bp
Enterovirus 5627/SIN/002009 5' t
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Enterovirus 5627/SIN/002009
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VRL 02-JUL-2003

Cattani, P. and

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Molecular identification and typing of enteroviruses isolated from clinical specimens
J. Clin. Microbiol. 40 (12), 4554-4560 (2002)
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/note="throat swab from child with aseptic meningitis.
identified by immunofluorescence assay"
cl. .>155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HUU295181 17-MAY-
Human coxsackievirus B5 genomic RNA for partial 5'UTR, isolate
IJA99-21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (08-MAY-2001) Muscillo M., Environmental Hygiene,
Istituto Superiore di Sanita', Viale Regina Elena 299, Rome,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Muscillo, M., La Rosa, G., Marianelli, C., Capobianchi, M.R.,
                                                                                                                                                                                                                                                        Score 20; DB 13; Length 154;
Pred. No. 30;
                                                                                                                                                                                                                                                                                                                                                                                         Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
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Human coxsackievirus B5
Viruses; sskievitive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
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/organism="Human coxsackievirus B2'
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0
                                                             Query Match
100.0%; Score 20; DB
Best Local Similarity 100.0%; Pred. No. 30;
Matches 20; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /mol_type="genomic RNA"
/strain="/ia/Roma99"
/isolate="IT99-5106"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               db_xref="taxon:82639"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                        103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        122 AAGGAAACACGGACACCCAA 103
                                                                                                                                      1 AAGGAAACACGGACACCCAA 20
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Human coxsackievirus B2
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                                                                                                                                                                    122 AAGGAAACACGGACACCCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (bases 1 to 155)
             <1. .>154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
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Best Local Similarity
Matches 20; Conserv
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5'UTR
ORIGIN
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TITLE
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HCO295181
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                                                                                                                                                               Enterovirus TS/SIN/001002
Enterovirus TS/SIN/001002
Enterovirus TS/SIN/001002
Viruses, seRNA positive-strand viruses, no DNA stage;
Picornaviridae: Enterovirus.
1 (bases 1 to 154)
Singh,S., Chow,V.T.K., Phoon,M.C., Chan,K.P. and Poh,C.L.
Direct Detection of Enterovirus 71 (EV71) in Clinical Specimens from a Hand, Foot, and Mouth Disease Outbreak in Singapore by Reverse Transcription-PCR with Universal Enterovirus and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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Unpublished
Unpublished
2 (bases 1 to 154)
Singh,S., Chow,V.T.K. and Poh,C.L.
Direct Submission
Submitted (122-FEB-2001) Microbiology, National University of
Singapore, 5 Science Drive 2, Singapore 117597, Singapore
Location/Qualifiers
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                Singh, S., Chow, V.T.K. and Poh, C.L.
Singh, S., Chow, V.T.K. and Poh, C.L.
Direct Submission
Submitted (12-FB2-2001) Microbiology, National University of
Singapore, 5 Science Drive 2, Singapore 117597, Singapore
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Singl,S., Chow,V.T.K. and Poh,C.L.
Enterovirus strains from an outbreak of Hand, Foot and Mouth
disease in Singapore (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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Enterovirus TF/SIN/000704
Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
                                                                       154 bp RNA linear
Enterovirus TS/SIN/001002 5'UTR, partial sequence.
AY027864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       154 bp RNA linear
Enterovirus TF/SIN/000704 5'UTR, partial sequence:
AY027865
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Enterovirus TS/SIN/001002"
|mol_type="genomic RNA"
/strain="TS/SIN/001002"
                                                                                                                                                                                                                                                                                                                                                    . Clin. Microbiol. 40 (8), 2823-2827 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="taxon:155429"
/note="isolated from tissue fluid"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="taxon:155431"
/note="isolated from throat swab"
<1. .>154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
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Pred. No.
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Best Local Similarity 100.0%;

Matches 20; Conservative 0;
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                                       RESULT 64
AY027864/c
                                                                                                              ACCESSION
VERSION
KEYWORDS
SOURCE
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Gaps

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Indels

VRL 15-MAY-2001

24

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Gaps

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Indels

VRL 15-MAY-2001

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Viruses; ssRNA positive-strand viruses, no DNA stage;
picornavitade; Enterovirus.
1 (Dases 1 to 184)
Thoelen,I., Lemey,P., Van Der Donck,I., Beuselinck,K.,
Lindbergy A.M. and Van Ranst,M.
Molecular typing and epidemiology of enteroviruses identified from an outbreak of aseptic meningitis in Belgium during the summer of
                                                                                                                                                                                                                                                                                                                                                                                                                                             A phylogenetic analysis of the two echovirus 30 isolated in Rome (Italy) in 1997 from an outbreak of aseptic meningitis associated with swimming pools Unpublished
2 (bases 1 to 177)
                                                                                                                                                                                  ESP295207 177 bp RNA linear VRL 15-MAY-200
Echovirus sp. genomic RNA for partial 5'UTR, isolate ATCC VR-322.
AJ295207
                                                                                                                                                                                                                                                                                                                                                                                           Muscillo, M., La Rosa, G., Marianelli, C., Capobianchi, M.R.,
Zaniratti, S., Cattani, P., Manzara, S., Fadda, G., Comparcola, D. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /isolate="ATCC VR:322"
/db_xref="taxon:145390"
/note="isolated from fecal specimen of 10-year-old boy with symptoms of headache, stiff neck, fever"
<1. .>177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
Submitted (03-NOV-2000) Muscillo M., Environmental Hygiene,
Istituto Superiore di Sanita', Viale Regina Elena 299, Rome,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          184 bp RNA linear VRL 17-u
Human echovirus 13 isolate BE00-82 5' UTR, partial sequence.
AF521491.1 GI:31790833
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 20; DB 13; Length 177; llarity 100.0%; Pred. No. 30; Conservative 0; Mismatches 0; Indels C
                                                                                                                                                                                                                                                                                                                                  Viruses; ssRNA positive-strand viruses, no DNA stage;
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J. Med. Virol. 70 (3), 420-429 (2003)
    red. No. 30;
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Echovirus sp."
      Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /mol_type="genomic RNA"
/strain="Bastianni"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                      Picornaviridae; Enterovirus.
                                                                                            120 AAGGAAACACGGACACCCAA 101
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                                                            1 AAGGAAACACGGACACCCAA 20
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0
Best Local Similarity 100.0%; Pr
Matches 20; Conservative 0;
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Human echovirus 13
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                                                                                                                                                                                                                                                                                        Echovirus sp.
Echovirus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           00161, Italy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 20; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Muscillo, M.
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ORIGIN
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LOCUS
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                                                                                                                                                        RESULT 69
ESP295207
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AUTHORS
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fadda,G.
Molecular identification and typing of enteroviruses isolated from
                            A phylogenetic analysis of the two echovirus 30 isolated in Rome (Italy) in 1997 from an outbreak of aseptic meningitis associated which swimming pools Unpublished

2 (bases 1 to 171)
  Zaniratti,S., Cattani,P., Manzara,S., Fadda,G., Comparcola,D. and
                                                                                                                        2 (bases 1 to 171)
Muscillo,M.
Direct Submission
Submitted (03-NOV-2000) Muscillo M., Environmental Hygiene,
Istituto Superiore di Sanita', Viale Regina Elena 299, Rome, RM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Muscillo,M.
Direct Submission
Submitted (08-MAX-2001) Muscillo M., Environmental Hygiene,
Istituto Superiore di Sanita', Viale Regina Elena 299, Rome, RM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /isolate="IT98-5114"
/db xref="taxon:39054"
/lab host="vero cell cultures"
/note="throat swab from child with aseptic meningitis,
identified by immunofluorescence assay"
                                                                                                                                                                                                                                                          /organism="Human coxsackievirus B5"
|mol_type="genomic RNA"
|strain="F4|Roma99"
|strain="F4|Roma99"|
|specific host="Homo sapiens"|
|db xref="taxon:12074"|
|nofe="sporadic case of aseptic menigitis; BGM cell
|culture of stools from a four years old child"
|culture of stools from a four years old child"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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Human enterovirus 71 partial 5'UTR, strain /di/Roma98.
AJ312088
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 20; DB 13; Length 171; 100.0%; Pred. No. 30; tive 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human enterovirus 71
Human enterovirus 71
Viruses; seRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
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J. Clin. Microbiol. 40 (12), 4554-4560 (2002)
12454151
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'virion
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strain="/di/Roma98"
                                                                                                                                                                                                                                  Location/Qualifiers
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VRL 17-JUN-2003

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Direct Submission
Submitted (12-UNN-2002) Laboratory of Clinical & Epidemiological
Virology, Department of Microbiology and Immunology, Rega Institute
for Medical Research, University of Leuven, Minderbroedersstraat
10, Leuven BE-3000, Belgium
Location/Qualifiers
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Human coxeackievirus B5 isolate BE00-1 5' UTR, partial sequence.
AF521435
                                                                                                                                                                                          Human coxsackievirus B5
Human coxsackievirus B5
Viruses; ssRNA positive-strand viruses, no DNA stage;
Viruses; ssRNA positive-strand viruses, no DNA stage;
Dicornaviridae; Enterovirus.

1 (bases 1 to 185)
Thoselen,I., Lemey,P., Van Der Donck,I., Beuselinck,K.,
Lindberg,A.M. and Van Ranst,M.
Molecular typing and epidemiology of enteroviruses identified from an outbreak of aseptic meningitis in Belgium during the summer of
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                                                                                   Arsz1434
Human coxeackievirus B5 isolate BE00-15 5' UTR, partial sequence.
AFS21434
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Human coxsackievirus B5
Human coxsackievirus B5
Human coxsackievirus B5
Picornaviridae, Enterovirus.
1 (Dases 1 to 185)
Thoelen, I., Lemey, P., Van Der Donck, I., Beuselinck, K., Lindberg, A.M. and Van Ranst, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                van der Donck, I., Beuselinck, K.,
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Thoelen,I., Lemey,P., van der Donck,I., Beuselinck,K.,
Lindberg,M.A. and Van Ranst,M.
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/db_xref="taxon:12074"
<1...>185
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Pred. No. 30;
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/isolate="BE00-15"
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Thoelen, I., Lemey, P., van der J
Lindberg, M.A. and Van Ranst, M.
     128 AAGGAAACACGGACACCCAA 109
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Best Local Similarity 100.00.
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                                                       RESULT 72
AF521434/c
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                                 Thoelen, I., Lemey, P., van der Donck, I., Beuselinck, K., Lindberg, M.A. and Van Ranst, M. Dindberg, M.A. and Van Ranst, M. Dindberg, M.A. and Van Ranst, M. Direct Submission Submitted (12-7UN-2002) Laboratory of Clinical & Epidemiological Virology, Department of Microbiology and Immunology, Rega Institute for Medical Research, University of Leuven, Minderbroedersstraat 10, Leuven BB-3000, Belgium
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Human echovirus 30
Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
1 (bases 1 to 185)
Thoelen, I., Lemey, P., Van Der Donck, I., Beuselinck, K.,
Lindberg, A.M. and Van Ranst, M.
Molecular typing and epidemiology of enteroviruses identified from
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/db_xref="taxon:41846"
                                                                                                                                                                                                                                                                                       82 - zipcode Belgium 8560"
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Human echovirus 30 isolate BEOO-14 5' UTR, partial sequence.
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Lindberg, M.A. and Van Ranst, M.
Direct Submission
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12767006
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/isolate="BE00-82"
/isolation_source="patient
/db_xref="taxon:47501"
                                                                                                                                                                                                      /organism="Human echovirus
/virion
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/isolate="BE00-14"
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12767006
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Direct Submission

Submitted (12-JN-2002) Laboratory of Clinical & Epidemiological Virology, Department of Microbiology and Immunology, Rega Institute for Medical Research, University of Leuven, Minderbroedersstraat 10, Leuven BE-3000, Belgium

Location/Qualifiers
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Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological
Virology, Department of Microbiology and Immunology, Rega Institute
for Medical Research, University of Leuven, Minderbroedersstraat
10, Leuven BE-3000, Belgium
Location/Qualifiers
                                                                                                                                                  Viruses; ssRNA positive-strand viruses, no DNA stage;
picornavitidae; Enterovirus.
1 (Dases 1 to 185)
Thoelen,I., Lemey,P., Van Der Donck,I., Beuselinck,K.,
Indobergy,A.M. and Van Ranst,M.
Molecular typing and epidemiology of enteroviruses identified from an outbreak of aseptic meningitis in Belgium during the summer of
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Human echovirus 30

Viruses; seRNA positive-strand viruses, no DNA stage;

Viruses; seRNA positive-strand viruses, no DNA stage;

Dicornaviridae; Enterovirus.

1 (bases 1 to 185)

Thoselen,I., Lemey,P., Van Der Donck,I., Beuselinck,K.,

Lindberg,A.M. and Van Ranst,M.

Molecular typing and epidemiology of enteroviruses identified from an outbreak of aseptic meningitis in Belgium during the summer of
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/db_xref="taxon:41846"
    AF521440 185 bp RNA linear VRL 17-
Human echovirus 30 isolate BE00-6 5' UTR, partial sequence
AF521440
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Thoelen,I., Lemey,P., van der Donck,I., Beuselinck,K.,
Lindberg,M.A. and Van Ranst,M.
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Pred. No. 30;
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Human echovirus 30 isolate BE00-11 5' L
AF521444
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/isolate="BE00-6"
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                                                                   AF521440.1 GI:31790782
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Matches 20; Conservative
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Human echovirus 30
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Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological Virology, Department of Microbiology and Immunology, Rega Institute for Medical Research, University of Leuven, Minderbroedersstraat 10, Leuven BE-3000, Belgium
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Lindberg, M.A. and Van Ranst, M.
Lindberg, M.A. and Van Ranst, M.
Direct Submission
Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological
Virology, Department of Microbiology and Immunology, Rega Institute
for Medical Research, University of Leuven, Minderbroedersstraat
10, Leuven BB-3000, Balgium
Location/Qualifiers
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/db_xref="taxon:12074"
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Human echovirus 30 isolate BE00-2 5' UTR, partial sequence.
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Human echovirus 30

Viruses; ssRNA positive-strand viruses, no DNA stage; picornaviridae; Enterovirus.
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Lindberg,A.M. and Van Ranst,M.
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/virion
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/isolate="BE00-2"
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/isolate="BE00-1"
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AF521445/c LOCUS

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ACCESSION VERSION KEYWORDS

ORGANISM

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REFERENCE AUTHORS

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Thoelen, I., Lemey, P., van der Donck, I., Beuselinck, K., Lindberg, M.A. and Van Ranst, M. Lindberg, M.A. and Van Ranst, M. Direct Submission Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological Virology, Department of Microbiology and Immunology, Rega Institute for Medical Research, University of Leuven, Minderbroedersstraat 10, Leuven BE-3000, Belgium
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Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological
Virology, Department of Microbiology and Immunology, Rega Institute
for Medical Research, University of Leuven, Minderbroedersstraat
10, Leuven BE-3000, Belgium
Human echovirus 16
Human echovirus 16
Viruses; seRNA positive-strand viruses, no DNA stage;
Viruses; seRNA positive-strand viruses, no DNA stage;
Dicornaviridae; Enterovirus.
1 (bases 1 to 185)
Thoselen, I., Lemey, P., Van Der Donck, I., Beuselinck, K.,
Lindberg, A.M. and Nanst, M.
Molecular typing and epidemiology of enteroviruses identified from an outbreak of aseptic meningitis in Belgium during the summer of
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Human echovirus 30
Viruses; saRNA positive-strand viruses, no DNA stage;
Viruses; saRNA positive-strand viruses, no DNA stage;
Dicornaviridae; Enterovirus.

1 (bases 1 to 185)
Thoelen,I., Lemey,P., Van Der Donck,I., Beuselinck,K.,
Inindberg,A.M. and Van Ranst,M.
Molecular typing and epidemiology of enteroviruses identified from an outbreak of aseptic meningitis in Belgium during the summer of
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Human echovirus 30 isolate BE00-30 5' UTR, partial sequence.
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Thoelen, I., Lemey, P., van der Donck, I., Beuselinck, K.,
Lindberg, M.A. and Van Ranst, M.
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Pred. No. 30;
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/organism="Human echovirus 16"
/virion
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/db_xref="taxon:47504"
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/organism="Human echovirus 30"
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/isolate="BE00-30"
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/isolate="BE00-13"
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                                                                                                        /isolation_source="patient 11 - zipcode Belgium 9400"
/db_xref="Taxon:41846"
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Human echovirus 30 isolate BE00-12 5' UTR, partial sequence.
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Muman echovirus 16 isolate BE00-13 5' UTR, partial sequence.
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AF521446.1 GI:31790788
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Picornaviridae; Enterovirus.
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Matches 20; Conservative 0; Mismatches
                                                          /mol_type="genomic RNA"
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ACCESSION VERSION KEYWORDS

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5' UTR

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FEATURES

PUBMED REFERENCE

JOURNAL

TITLE

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VRL 17-JUN-2003

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Submitted (12-70N-2002) Laboratory of Clinical & Epidemiological Virology, Department of Microbiology and Immunology, Rega Institute for Medical Research, University of Leuven, Minderbroedersstraat 10, Leven BE-3000, Belgium

Location/Qualifiers
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                                                                                                                                                                                                                                               AF521448 17-JUN-20
Human coxsackievirus B5 isolate BE00-31 5' UTR, partial sequence.
AF521448
/isolation source="patient 30 - zipcode Belgium 9310"
/db xref="taxon:41846"
<1. .>185
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/db_xref="taxon:12074"
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Human echovirus 30 isolate BE00-32 5' UTR, partial sequence.
AF521449.1 GI:31790791
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Human coxsackievirus B5
Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
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Picornaviridae; Enterovirus.
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                                                                               Length 185;
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12767006
                                                                           Query Match 100.0%; Score 20; DB Best Local Similarity 100.0%; Pred. No. 30; Matches 20; Conservative 0; Mismatches
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/isolate="BE00-31"
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(bases 1 to 185)

Thoelen, I., Lemey.P., van der Donck, I., Beuselinck, K.,
Lindberg, M.A. and Van Ranst, M.

Direct Submission
Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological
Virology, Department of Microbiology and Immunology, Rega Institute
for Medical Research, University of Leuven, Minderbroedersstraat
10, Leuven BB-3000, Belgium
Location/Qualifiers
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Lindberg, M.A. and Van Ranst, M.
Lindberg, M.A. and Van Ranst, M.
Direct Submission
Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological
Virology, Department of Microbiology and Immunology, Rega Institute
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10, Leuven BB-3000, Belgium
Location/Qualifiers
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/isolatie="BE00-33"
/isolation_source="patient 33 - zipcode Belgium 1745"
/db_xref="taxon:41846"
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Human echovirus 30 isolate BE00-33 5' UTR, partial sequence.
AF521450
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Human echovirus 30

Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.

1 (bases 1 to 185)

Thoelen,I., Lemey,P., Van Der Donck,I., Beuselinck,K.,
Thoelen, I., Lemey, P., Van Der Donck, I., Beuselinck, K.,
Lindberg, A.M. and Van Ranst, M.
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/organism="Human echovirus 30"
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/db_xref="taxon:41846"
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Pred. No. 30;
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/isolate="BE00-32"
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Similarity 100.0%;
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Human echovirus 30
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Direct Submission

Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological Virology, Department of Microbiology and Immunology, Rega Institute for Medical Research, University of Leuven, Minderbroedersstraat 10, Leuven BE-3000, Belgium

Location/Qualifiers
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Human echovirus 30

Viruses; ssRNA positive-strand viruses, no DNA stage;

Picornaviridae; Enterovirus.

1 (bases 1 to 185)

Thoselen, I., Emmey, P., Van Der Donck, I., Beuselinck, K.,

Lindberg, A.M. and Van Ranst, M.

Molecular typing and epidemiology of enteroviruses identified from an outbreak of aseptic meningitis in Belgium during the summer of
                                                                                                                                                                                                                                                                                  Viruees; BSRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
1 (bases 1 to 185)
Thoelen, I., Lemey, P., Van Der Donck, I., Beuselinck, K.,
Lindberg, A.M. and Van Ranst, M.
Molecular typing and epidemiology of enteroviruses identified from
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/db_xref="taxon:41846"
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Human echovirus 30 isolate BE00-34 5' UTR, partial sequence.
AF521451
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Human echovirus 30 isolate BE00-43 5' UTR, partial sequence
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 Score 20; DB 13;
Pred. No. 30;
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                                  Mismatches
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/isolate="BE00-34"
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AF521458.1 GI:31790800
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ch 100.0%;
1 Similarity 100.0%;
20; Conservative 0
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Human echovirus 30
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AF521451/c
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AF521458/c
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Thoelen, I., Lemey, P., van der Donck, I., Beuselinck, K.,
Lindberg, M. A. and Van Ranst, M.
Direct Submission
Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological
Virology, Department of Microbiology and Immunology, Rega Institute
for Medical Research, University of Leuven, Minderbroedersstraat
10, Leuven BB-3000, Belgium
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Direct Submitsed (12-JTM-2002) Laboratory of Clinical & Epidemiological Submitted (12-JTM-2002) Laboratory of Clinical & Epidemiological Virology, Department of Microbiology and Immunology, Rega Institute for Medical Research, University of Leuven, Minderbroedersstraat 10, Leuven BE-3000, Belgium

Location/Qualifiers
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Picornaviridae; Enterovirus.
1 (bases 1 to 185)
Thoelen,I., Lemey,P., Van Der Donck,I., Beuselinck,K.,
Lindberg,A.M. and Van Ranst,M.
Molecular typing and epidemiology of enteroviruses identified from an outbreak of aseptic meningitis in Belgium during the summer of
                                                                                                                                                                                                                                                                                                                                                        /isolation_source="patient 43 - zipcode Belgium 9402"
/db_xref="taxon:41846"
<1._.>185
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/db_xref="taxon:41846"
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Human echovirus 30 isolate BE00-48 5' UTR, partial seguence.
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100.0%; Pred. No. 30;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                   1. .185
/organism≃"Human echovirus 30"
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/organism="Human echovirus 30"
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                                                                                                                                                                                                                                                                                                                    /mol_type="genomic RNA"
/isolate="BE00-43"
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/isolate="BE00-48"
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[bases 1 to 185]
Thoselen, I., Lemey, P., van der Donck, I., Beuselinck, K.,
Thoselen, I., Lemey, P., van der Donck, I., Beuselinck, K.,
Lindberg, M.A. and Van Ranst, M.
Direct Submission
Submitted (12-UM-2002) Laboratory of Clinical & Epidemiological
Submitted (12-UM-2002) Laboratory of Clinical & Epidemiological
Virology, Department of Microbiology and Immunology, Rega Institute
for Medical Research, University of Leuven, Minderbroedersstraat
10, Leuven BE-3000, Belgium
Direct Submission
Submitted (I2-JUN-2002) Laboratory of Clinical & Epidemiological
Virology, Department of Microbiology and Immunology, Rega Institute
for Medical Research, University of Leuven, Minderbroedersstraat
10, Leuven BE-3000, Belgium
Location/Qualifiers
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Human coxsackievirus B5 isolate BE00-29 5' UTR, partial sequence.
AF521473
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locoravitidae; Briterovirus.
1 (bases 1 to 185)
Thoelen,I., Lemey,P., Van Der Donck,I., Beuselinck,K.,
Lindberg,A.M. and Van Ranst,M.
Molecular typing and epidemiology of enteroviruses identified from an outbreak of aseptic meningitis in Belgium during the summer of
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/db_xref="taxon:12074"
-.1. .>185
                                                                                                                                                                                                                             - zipcode Belgium 3545"
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Local Similarity 100.0%; Score 20; DB 13; Length 185;
Lecal Similarity 100.0%; Pred. No. 30;
les 20; Conservative O. Mix...
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/organism="Human coxsackievirus
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/db_xref="taxon:12074"
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Pred. No. 30;
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12767006
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/isolate="BE00-29"
                                                                                                                                                                                   /mol_type="genomic_RNA"
/isolate="BE00-25"
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Location/Qualifiers
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Human coxsackievirus B5
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Best Local Similarity 100.0%;
Matches 20; Conservative 0
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JOURNAL
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AF521471.1 GI:31790813
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Thoelen, I., Lemey, P., van der Donck, I., Beuselinck, K., Lindberg, M.A. and Van Ranst, M. Direct Submission Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological Virology, Department of Microbiology and Immunology, Rega Institute for Medical Research, University of Leuven, Minderbroedersstraat 10, Leuven BE-3000, Belgium
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Lindberg, A.M. and Van Ranst, M.
Molecular typing and epidemiology of enteroviruses identified from
an outbreak of aseptic meningitis in Belgium during the summer of
                                                                                                                                                                                                                                                                Viruses; SBRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
I (bases 1 to 185)
Thoelen, I., Lemey, P., Van Der Donck, I., Beuselinck, K.,
Lindberg, A.M. and Van Ranst, M.
Molecular typing and epidemiology of enteroviruses identified from an outbreak of aseptic meningitis in Belgium during the summer of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /isolation_source="patient 51 - zipcode Belgium 3583"
/db_xref="taxon:47501"
<1. .>185
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Muman echovirus 13 isolate BEOO-51 5' UTR, partial sequence
AF521464
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Thoelen,I., Lemey,P., van der Donck,I., Beuselinck,K.,
Lindberg,M.A. and Van Ranst,M.
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Human coxsackievirus B5
Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
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/organism="Human echovirus 13"
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12767006
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12767006
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100.0%; Pred. No. 30;
tive 0; Mismatches
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/isolate="BE00-51"
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    128 AAGGAAACACGGACACCCAA 109
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                                                                                                                                                                                                                             Human echovirus 13
Human echovirus 13
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Best Local Similarity 100.
Matches 20; Conservative
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Gaps

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Length 185; Indela VRL 17-JUN-2003

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Thoelen, I., Lemey, P., van der Donck, I., Beuselinck, K., Lindberg, M.A. and Van Ranst, M.

Direct Submission
Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological
Virology, Department of Microbiology and Immunology, Rega Institute for Medical Research, University of Leuven, Minderbroedersstraat
10, Leuven BE-3000, Belgium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Viruses; seRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.

1 (bases 1 to 185)
Thoelen, I., Lemey, P., Van Der Donck, I., Beuselinck, K.,
Lindberg, A.M. and Van Ranst, M.
Molecular typing and epidemiology of enteroviruses identified from
                                                                                                               /isolation_source="patient 17 - zipcode Belgium 3550"
/db_xref="taxon:41846"
<1._.>185
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/db_xref="taxon:41846"
<1._.>185
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Human echovirus 30 isolate BE00-18 5' UTR, partial sequence.
AF521476
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Human echovirus 30 isolate BE00-19 5' UTR, partial sequence.
AF521477.1 GI:31790819
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100.0%; Pred. No. 30;
ative 0; Mismatches 0;
                                              'organism="Human echovirus 30"
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/organism="Human echovirus 30"
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                                                                                     /mol type="genomic RNA"
/isolate="BE00-17"
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/isolate="BE00-18"
        location/Qualifiers
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                                                                                                                                                                                                                                                                   20; Conservative
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Human echovirus 30
                                                                     'virion
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Best Local Similarity
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Best Local Simi
Matches 20;
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AF521476/c
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Direct Submission

Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological Virology, Department of Microbiology and Immunology, Rega Institute for Medical Research, University of Leuven, Minderbroedersstraat 10, Leuven BE-3000, Belgium

Location/Qualifiers
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Lindberg, M.A. and Van Ranst, M.
Direct Submission
Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological
Virology, Department of Microbiology and Immunology, Rega Institute
for Medical Research, University of Leuven, Minderbroedersstraat
10, Leuven BE-3000, Belgium
                         VRL 17-JUN-2003
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                                                                                                                                                        Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
I (bases 1 to 185)
Thoelen, I., Lemey, P., Van Der Donck, I., Beuselinck, K.,
Lindberg, A.M. and Van Ranst, M.
Molecular typing and epidemiology of enteroviruses identified from
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Lindberg,A.M. and Van Ranst,M.
Molecular typing and epidemiology of enteroviruses identified from
an outbreak of aseptic meningitis in Belgium during the summer of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        - zipcode Belgium 3294"
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                       A linear VRL 17-J
UTR, partial sequence.
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Human echovirus 30 isolate BE00-17 5' UTR, partial sequence.
AF521475
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Human echovirus 30
Viruses; ssRND Extrand viruses, no DNA stage;
Picornaviridae; Enterovirus.
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                       AF521474
Human echovirus 30 isolate BE00-16 5'
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/isolate="BE00-16"
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                                                                               AF521474.1 GI:31790816
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Human echovirus 30
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nes 20; Conservative
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AF521475/c
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AUTHORS
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Thoelen, I., Lemey, P., van der Donck, I., Beuselinck, K., Lindberg, M.A. and Van Ranst, M. Direct Submission

Direct Submission

Submitted (12-7UN-2002) Laboratory of Clinical & Epidemiological Virology, Department of Microbiology and Immunology, Rega Institute for Medical Research, University of Leuven, Minderbroedersstraat 10, Leuven BB-3009, Balgium

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                      AF521480 17-JUN-2003 185 bp RNA linear VRL 17-JUN-2003 RNA coxsackievirus B5 isolate BE00-27 5' UTR, partial sequence. AF521480
                                                                                                                                                                                                                                                                                                                                                                                                                                Human coxsackievirus B5
Human coxsackievirus B5
Viruses; SaRNA positive-strand viruses, no DNA stage;
Viruses; SaRNA positive-strand viruses, no DNA stage;
Dicornaviridae; Enterovirus.

1 (bases 1 to 185)
Thoelen,I., Lemey,P., Van Der Donck,I., Beuselinck,K.,
Lindberg,A.M. and Van Ranst,M.
Molecular typing and epidemiology of enteroviruses identified from an outbreak of aseptic meningitis in Belgium during the summer of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /isolation_source="patient 27 - zipcode Belgium 9840"
/db_xref="taxon:12074"
<1. .>185
        /isolation source="patient 20 - zipcode Belgium 3294"
/db_xref="taxon:41846"
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5' UTR, partial sequence.
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Human echovirus 16
Viruses; ssRM positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
                                                                                                                    Score 20; DB 13; Length 185;
Pred. No. 30;
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    .185
    /organism="Human coxeackievirus B5"

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                                                                                                                                                           0; Mismatches
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/isolate="BE00-27"
    /isolate="BE00-20"
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                                                                                                                  100.0%;
ilarity 100.0%;
Conservative 0;
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Best Local Similarity
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Matches 20;
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AF521480/c
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Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological
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Virology, Department of Microbiology and Immunology, Rega Institute
for Medical Research, University of Leuven, Minderbroedersstraat
10, Leuven BB-3000, Belgium
Location/Qualifiers
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Lindberg,M.A. and Van Ranst,M.
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Virology, Department of Microbiology and Immunology, Rega Institute
for Medical Research, University of Leuven, Minderbroedersstraat
10, Leuven BB-3000, Belgium
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                                                     Viruses; BSRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.

1 (bases 1 to 185)
Thoelen, I., Lemey, P., Van Der Donck, I., Beuselinck, K.,
Lindberg, A.M. and Van Ranst, M.
Molecular typing and epidemiology of enteroviruses identified from an outbreak of aseptic meningitis in Belgium during the summer of
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Lindberg,A.M. and Van Ranset,M.
Molecular typing and epidemiology of enteroviruses identified from
an outbreak of aseptic meningitis in Belgium during the summer of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /isolation_source="patient 19 - zipcode Belgium 1830"
/db_xref="taxon:41846"
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Human echovirus 30
Viruses; sgRMA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
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12767006
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12767006
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/isolate="BE00-19"
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Length 185;

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Direct Submission
Submitted (12-UIN-2002) Laboratory of Clinical & Epidemiological
Virology, Department of Microbiology and Immunology, Rega Institute
for Medical Research, University of Leuven, Minderbroedersstraat
10, Leuven BE-3000, Belgium
                                                                                                                                                                                                                                                                                                                                                                                                   Viruees; BSRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.

( bases 1 to 185)
Thoelen, I., Lemey, P., Van Der Donck, I., Beuselinck, K.,
Lindberg, A.M. and Van Ranst, M.
Molecular typing and epidemiology of enteroviruses identified from an outbreak of aseptic meningitis in Belgium during the summer of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae, Enterovirus.
1 (bases 1 to 185)
Thoselen,I., Lemey,P., Van Der Donck,I., Beuselinck,K.,
Lindberg,A.M. and Van Ranst,M.
Molecular typing and epidemiology of enteroviruses identified from an outbreak of aseptic meningitis in Belgium during the summer of
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/db_xref="taxon:41846"
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Human echovirus 30 isolate BE00-74 5' UTR, partial sequence.
AF521483
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Human echovirus 16 isolate BE00-75 5' UTR, partial sequence.
AF521484
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/isolate="BE00-74"
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Lindberg, M.A. and Van Ranst, M.
Direct Submission
Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological
Virology, Department of Microbiology and Immunology, Rega Institute
for Medical Research, University of Leuven, Minderbroedersstraat
10, Leuven BB-3000, Belgium
Location/Qualifiers
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Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological
Virology, Department of Microbiology and Immunology, Rega Institute
for Medical Research, University of Leuven, Minderbroedersstraat
10, Leuven BE-3000, Belgium
Location/Qualifiers
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I (bases 1 to 185)
Thoelen,I., Lemey,P., Van Der Donck,I., Beuselinck,K.,
Lindberg,A.M. and Van Ranst,M.
Molecular typing and epidemiology of enteroviruses identified from an outbreak of aseptic meningitis in Belgium during the summer of
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Lindberg, A.M. and Van Ranst, M.
Molecular typing and epidemiology of enteroviruses identified from
an outbreak of aseptic meningitis in Belgium during the summer of
                                                                                                                                                                                                                                                                                                                                                                                                                                            /isolation_source="patient 72 - zipcode Belgium 3000"
/db_xref="taxon:47504"
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Lindberg, M.A. and Van Ranst, M.
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Picornaviridae; Enterovirus.
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/isolate="BE00-73"
/isolation_source="patient
/db_xref="taxon:47501"
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/isolate="BE00-72"
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                                                                                                       Direct Submission
Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological
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Virology, Department of Microbiology and Immunology, Rega Institute
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Location/Qualifiers
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Lindberg, M.A. and Van Ranst, M.
Lindberg, M.A. and Van Ranst, M.
Direct Submission
Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological
Virology, Department of Microbiology and Immunology, Rega Institute
for Medical Research, University of Leuven, Minderbroedersstraat
10, Leuven BE-3000, Belgium
Location/Qualifiers
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Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
1 (bases 1 to 185)
Thoelen,I., Lemey,P., Van Der Donck,I., Beuselinck,K.,
Lindberg,A.M. and Van Ranst,M.
Molecular typing and epidemiology of enteroviruses identified from an outbreak of aseptic meningitis in Belgium during the summer of
                                                                                                                                                                                                                                                                                                                   /isolation_source="patient 75 - zipcode Belgium 7700" /db_xref="taxon:47504" <1. .>185
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Thoelen, I., Lemey, P., van der Donck, I., Beuselinck, K., Lindberg, M.A. and Van Ranst, M. Direct Submission
Direct Submission
Submitted (12-70N-2002) Laboratory of Clinical & Epidemiological Virology, Department of Microbiology and Immunology, Rega Institute for Medical Research, University of Leuven, Minderbroedersstraat 10, Leuven BE-3000, Belgium
Location/Qualifiers
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Picornaviridae; Enterovirus.

1 (bases 1 to 185)
Thoelen, I., Lemey, P., Van Der Donck, I., Beuselinck, K.,
Lindberg, A.M. and Van Ranst, M.
Molecular typing and epidemiology of enteroviruses identified from an outbreak of aseptic meningitis in Belgium during the summer of
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Copyright (c) 1993 - 2006 Biocceleration Ltd.
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3 US-09-607-756- 3 US-09-027-449- 3 US-09-026-4444A, 3 US-09-121-952A, 3 US-09-121-952A, 3 US-09-23-170- 3 US-09-355-014- 2 US-08-683-007A, 2 US-08-92-314- 2 US-08-92-314- 2 US-08-92-314- 3 US-08-92-314- 2 US-08-92-312- 2 US-08-92-312- 3 US-08-92-312- 3 US-09-91-258- 3 US-09-072-967- 3 US-09-272-0178	08387845 paration of heteistronic vector staible arible BoS/MS-DOS lease #1.0, Vers S/08/387,845 5: 5: 6 7yp 1 (Mahoney 8' (M) (4708 bp),
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	SULT 1  -08-387-845-5/c  BAPLICANT: APPLICANT: TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION: NUMBER OF SEQUENCES: COMPUTER READABLE FOO COMPUTER: IBM PC OOPERATING SYSTEM: SOFTWARE: PARENTI CURRENT APPLICATION IAPPLICATION IAPPLICA
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18.08-809-326A-25 Sequence 25, 3 US-08-809-326A-25 Sequence 25, 3 US-09-689-913A-25 Sequence 25, 3 US-09-689-913A-25 Sequence 25, 3 US-09-689-913A-25 Sequence 25, 3 US-09-256-21 Sequence 1, 3 US-09-258-866-1 Sequence 785 Sequence 22, 2 US-08-450-25 Sequence 22, 2 US-08-450-25 Sequence 22, 2 US-08-450-25 Sequence 23, 2 US-08-450-25 Sequence 23, 2 US-08-690-33-2 Sequence 23, 2 US-08-690-33-2 Sequence 23, 2 US-08-690-33-2 Sequence 23, 2 US-08-913A-10 Sequen	US-08-908-469-99 US-09-469-99 US-09-482-273-47 US-09-492-002-735 US-08-807-352B-1 US-09-109-207C-1 US-09-109-207C-1 US-09-109-207C-1 US-09-705-005-1 US-09-705-005-1 US-09-705-005-1 US-09-705-701-1 US-09-701-1 US-09
US-08-809-326A-25 Sequence US-09-689-914A-25 Sequence US-09-689-914A-25 Sequence US-09-689-916A-25 Sequence US-09-32-96C-1 Sequence US-09-32-96C-1 Sequence US-09-702-705-785 Sequence US-09-614-124B-785 Sequence US-09-614-124B-785 Sequence US-09-614-124B-785 Sequence US-09-611-325-785 Sequence US-09-611-325-785 Sequence US-09-611-325-785 Sequence US-09-611-323-22 Sequence US-08-450-257-22 Sequence US-08-450-236-22 Sequence US-08-451-233-22 Sequence US-08-451-233-22 Sequence US-08-451-33-22 Sequence US-08-451-33-22 Sequence US-08-451-33-22 Sequence US-08-359-346-10 Sequence US-08-913A-10 Sequ	3 US-08-908-469-99 3 US-09-482-273-47 3 US-09-482-273-47 3 US-09-1949-002-735 5 Sequence 2 US-08-807-352B-1 5 Sequence 3 US-09-109-207C-1 3 US-09-206-005-1 3 US-09-206-005-1 3 US-09-207-171-1 5 Sequence 3 US-09-171-171-171-171-171-171-171-171-171-17
3 US-08-809-326A-25 Sequence 3 US-09-689-913A-25 Sequence 3 US-09-689-913A-25 Sequence 3 US-09-689-913A-25 Sequence 3 US-09-689-913A-25 Sequence 3 US-09-328-856C-1 Sequence 3 US-09-328-856C-1 Sequence 3 US-09-702-705-785 Sequence 3 US-09-614-124B-785 Sequence 3 US-09-614-124B-785 Sequence 3 US-09-614-124B-785 Sequence 3 US-09-619-642-785 Sequence 3 US-09-619-642-785 Sequence 3 US-09-619-642-785 Sequence 4 US-08-450-098-22 Sequence 5 US-08-450-257-22 Sequence 5 US-08-450-259-23 Sequence 6 US-08-451-233-22 Sequence 7 US-08-451-233-22 Sequence 7 US-08-451-233-22 Sequence 7 US-08-451-33-22 Sequence 7 US-08-959-967-3 Sequence 7 US-08-913A-10 Sequence 7 US-08-9144-916-3 Sequence 7 US-08-944-916-3 Sequence 9 US-08-944-91	0 6072 3 US-08-908-469-99 Sequence 0.115 3 US-09-482-273-47 Sequence 0.115 3 US-09-482-273-47 Sequence 0.115 3 US-09-482-273-47 Sequence 0.127 2 US-09-109-207C-1 Sequence 0.127 3 US-09-109-207C-1 Sequence 0.127 3 US-09-109-207C-1 Sequence 0.127 3 US-09-109-11 Sequence 0.127 3 US-09-109-109-1 Sequence 0.127 3 US-09-109-109-109-109-109-109-109-109-109-
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Gaps

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us-10-829-474-2.rni

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TITLE OF INVENTION: Multicistronic expression units and their use NUMBER OF SEQUENCES: 25 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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due to a base pair substitution from C to
at Location 610"
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628 nt of the 5' non-translated region of
poliovirus Typ 1 (Mahoney)"
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                                                                                    Score 20; DB 2; Length 628;
Pred. No. 2.7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (BPA)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/867,352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLONE: pGEM3-5'Polio (M) (4708 bp), (Sarnow, 1989)
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ORGANISM: Poliovirus Typ 1 (Mahoney strain)
IMMEDIATE SOURCE:
                                                                                                                            Mismatches
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/387,847
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                                                                                                                                                                                                                                              RESULT 3
US-08-867-352-5/c
; Sequence 5, Application US/08867352
; Patent No. 6060273
; GENERAL INFORMATION:
APPLICANT:
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                                                                                       100.08;
                                                                                                          100.0%;
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INFORMATION FOR SEQ ID NO: 5
SEQUENCE CHARACTERISTICS:
LENGTH: 628 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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LOCATION: 610
OTHER INFORMATION: due t
OTHER INFORMATION: at Lr
PUBLICATION INFORMATION:
ATTHORS: SARTOW, P.
                                                                                                                        20; Conservative
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Matches 20; Conservative
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LOCATION: 1..628
OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
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                                                                                                        Best Local Similarity
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NAME/KEY: -
; VOLUME: 63
; PAGES: 467-470
; DATE: 1989
US-08-778-275-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          63
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JOURNAL:
VOLUME: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-867-352-5
                                                                                       Query Match
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PREPLICANT:

TITLE OF INVENTION: bicistronic vector system in mammalian cells number of SEQUENCES: 16

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk COMPUTER: BW PC COMPUTIBLE OF OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PETENTINE RECENSION SYSTEM: PC-DOS/MS-DOS SOFTWARE: PETENTION DATA:

APPLICATION NUMBER: US/08/778,275

FILING DATE:

CLASSIFICATION:

RECENSION NUMBER: 08/387,845
                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "non-authentic sequence due to a base pair substitution from C to at position 610"
                /note= "shown are the first
628 nt of the 5' non-translated region of
poliovirus Typ 1 (Mahoney)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "shown are the first
628 nt of the 5' non-translated region of
poliovirus Typ 1 (Mahoney)"
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                                                                                                                     /note= "non-authentic sequence due to a base pair substitution from C at position 610"
                                                                                                                                                                                                                                                                                                                     Length 628
                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORIGINAL SOURCE:
ORGANISM: POLiovirus Typ 1 (Mahoney strain)
IMMEDIATE SOURCE:
CLONE: pGEM 3-5'Polio (M) (4708 bp), (Sarnow, 1989)
                                                                                                                                                                                                                                                                                                 100.0%; Scor.
100.0%; Pred. No. 2...
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                             1 AAGGAAACACGGACACCCAA 20
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Patent No. 5935819
GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 5
SEQUENCE CHARACTERISTICS:
LENGTH: 628 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                Query Match
Best Local Similarity 100.0
Matches 20; Conservative
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OTHER INPORMATION: /nc
OTHER INFORMATION: du
OTHER INFORMATION: at
HUBLICATION INFORMATION: A
JUHICATION INFORMATION:
AUTHORS: Sarnow, P.
JOURNAL: J. Virol.
            OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
FEATURE:
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NAME/KEY:
-1.628

CICATION:
-1.628

OTHER INFORMATION:
OTHER INFORMATION:
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VOLUME: 63
PAGES: 467-470
DATE: 1989
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NAMB/KEY:
COCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY:
                                                                                                                                                                                                                                                              , DATE: 19
US-08-387-845-5
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APPLICANT: LO, CHENG-KAIL
APPLICANT: LO, CHENG-KAIL
APPLICANT: JANG, YING-CHUAN
APPLICANT: JENG, KING-SONG
APPLICANT: JENG, KING-SONG
APPLICANT: CHANG, EDWARD L.
APPLICANT: CHANG, EDWARD L.
TITLE OF INVENTION: SWINE VESICULAR DISEASE VIRUS AND MUTANT STRAINS AND
TITLE OF INVENTION: PREPERATION PROCESS AND USE THEREOF
FILE REFERENCE: 9751.79US01
CURRENT APPLICATION NUMBER: US/09/116,032
CURRENT FILING DATE: 1998-07-15
EARLIER PILING DATE: 1997-05-01
NUMBER OF SEQ ID NOS: 39
SOFTWARE: PATENTIN VEY: 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Racaniello, Vincent
APPLICANT: Tatem, Joanne M.
APPLICANT: Carolyn L.
APPLICANT: Carolyn L.
APPLICANT: Carolyn L.
APPLICANT: Coper & Dunham
STREET: 30 Rockefeller Plaza
CITY: New York
STREET: Wew York
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 20; DB 3; Length 7400; 100.0%; Pred. No. 3.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/852,260
FILING DATE: 19920619
CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             36607-B-PCT-US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: SWINE VESICULAR DISEASE VIRUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  568 AAGGAAACACGGACACCCAA 549
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Patent No. 5525715
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NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 366
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 977-9550
TELEPRONE: (212) 664-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEX: 422523 COOP UI INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 7432 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20; Conservative
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STRANDEDNESS: single
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Best Local Similarity
Matches 20; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
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APPLICANT: Kang, Sung Key
APPLICANT: Hanh, Bunguk
TITLE OF INVENTION: Hepatitis C Surrogate Virus for Testing
TITLE OF INVENTION: Hepatitis C Virus Protease, a Recombinant
TITLE OF INVENTION: Gene and a Use Thereof
FILE REPERENCE: A32210-PCT-USA 072944.0104
CURRENT APPLICATION NUMBER: US/09/202,904A
CURRENT FILING DATE: 2001-01-22
PRIOR APPLICATION NUMBER: PCT/KR97/00120
PRIOR FILING DATE: 1997-06-25
NUMBER OF SEQ ID NOS: 14
SOOFTWARE: FastSEQ for Windows Version 3.0
                                                  GENERAL INFORMATION:
APPLICANT: HWONG, CHING LONG
APPLICANT: HWONG, CHING LONG
APPLICANT: HWONG, CAUGA
APPLICANT: YANG, YING-CHUAN
APPLICANT: JENG, XING-CHUAN
APPLICANT: JENG, XING-CHUAN
APPLICANT: JENG, KING-CHUAN
TITLE OF INVENTION: SWINE VESICULAR DISEASE VIRUS AND MUTANT STRAINS AND
TITLE OF INVENTION: SWINE VESICULAR DISEASE VIRUS AND MUTANT STRAINS AND
TITLE OF INVENTION: SWINE VESICULAR DISEASE VIRUS
TITLE OF INVENTION: SWINE VESICULAR DISEASE VIRUS
FILE REFERENCE: 9751.79US01
CURRENT APPLICATION NUMBER: US/09/116,032
CURRENT FILING DATE: 1998-07-15
EARLIER FILING DATE: 1997-05-01
NUMBER OF SEQ ID NOS: 39
SOFTWARE: PATENTIN VEY: 2.0
SEQ ID NO 2
SEQ ID NO 2
LENGTH: 1220
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TYPE: DNA
; ORGANISM: SWINE VESICULAR DISEASE VIRUS
US-09-116-032-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-202-904A-10/c
; Sequence 10, Application US/09202904A
; Patent No. 6395471
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US-09-116-032-1/c
; Sequence 1, Application US/09116032
Sequence 2, Application US/09116032 Patent No. 6200576
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Best Local Similarity 100.0
Matches 20; Conservative
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Best Local Similarity 100.
Matches 20; Conservative
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LENGTH: 2320
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; Sequence 1, Application US/08465250
; Patent No. 6136570
                                                                                                                                          GENERAL INFORMATION:
                                                                            US-08-465-250-1/c
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                                                                                                                                                                               Query Match
Best Local Similarity 100.0%; Score 20; DB 2; Length 7432;
Best Local Similarity 100.0%; Pred. No. 3.5;
Matches 20; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Racaniello, Vincent
APPLICANT: Tatem, Joanne M.
APPLICANT: Weeks-Levy, Carolyn L.
TITLE OF INVENTION: METHODS FOR PRODUCING RNA VIRUSES
TITLE OF INVENTION: FROM CDNA
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 10112
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.25
CURSTYARE: Patentin Release #1.0,
APPLICATION NUMBER: US/08/461,503
FILING DATE: 5-UUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 20; DB 2;
Pred. No. 3.5;
); Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 36.07-D-PCT-US
REFERENCE/DOCKET NUMBER: 36607-D-PCT-US
TELEFORMUNICATION INFORMATION:
TELEFAX: (212) 391-0525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Cooper & Dunham
STREET: 1185 Avenue of the Americas
                                                                                                                                                                                                                                                                                                    568 AAGGAAACACGGACACCCAA 549
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100.0%; Pre
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                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1, Application US/08461503
Patent No. 5834302
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
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Best Local Similarity 100.
Matches 20, Conservative
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STATE: New York
COUNTRY: U.S.A.
ZIP: 10112
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STRANDEDNESS
                                                                                     ; NAME/KEY:
; LOCATION:
US-07-852-260-1
                                                                                                                                                                                                                                                                                                                                                                                                     US-08-461-503-1/c
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US-08-461-503-1
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NAME/KEY:
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568 AAGGAAACACGGACACCCAA 549

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Pred. No. 3.5;
APPLICANT: Racaniello, Vincent
APPLICANT: Tatem, Joanne M.
APPLICANT: Tatem, Joanne M.
APPLICANT: Weeks-Levy, Carolyn L.
TITLE OF INVENTION: METHODS FOR PRODUCING RNA VIRUSES FROM
TITLE OF INVENTION: CDNA
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Yong Soo, Bae
APPLICANT: Yong Soo, Bae
APPLICANT: Jung, Hye Rhan
TITLE OF INVENTION: Replication-Competent Sabin Type 1 Strain
FILE REFERENCE: Docket No. 6696289: 4220-109 US
CURRENT APPLICATION NUMBER: US/09/284,349B
CURRENT FILING DATE: 1999-06-04
                                                                                                                                                                                                                                                                                                                                                                                                                               GOTWARE: PREENTIN Release 1.30
GOTWARE: PREENTIN Release 1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,250
FILING DATE: 6-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28.678
REFERENCE/DOCKET NUMBER: 36607-E-PCT-US
TELECHONE: (212) 278-0400
TELEPHONE: (212) 278-0400
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PRIOR FILING DATE: 1998-07-08
                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-284-349B-1/c; Sequence 1, Application US/09284349B; Patent No. 6696289; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               568 AAGGAAACACGGACACCCAA 549
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 7432 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 100.
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
                                                                                                                                                                                                                                                              STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
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Sequence 20, Application US/09129686A
Sequence 20, Application US/09129686A
Sequence 20, Application US/09129686A
Settle Canal No. 6264940
GENERAL INFORMATION:
APPLICANT: Gromeier PhD, Matthias
APPLICANT: Wimmer Prof, Eckard
TITLE OF INVENTION: Recombinant Poliovirus For The Treatment of Cancer;
FILE REFERENCE: Recomb Poliovirus for Cancer Treatment
CURRENT APPLICATION NUMBER: US/09/129,686A
CURRENT FILING DATE: 1998-08-05
NUMBER OF SEQ ID NOS: 28
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 20
                                                                                                                                         Gaps
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0
                                                                                     92.0%; Score 18.4; DB 3; Length 1560; illarity 95.0%; Pred. No. 17; Conservative 0; Mismatches 1; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 85.0%; Score 17; DB 3; Length 33; Best Local Similarity 100.0%; Pred. No. 54; Matches 17; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-566-581-20

Sequence 20, Application US/09566581

Patent No. 6464971

GENERAL INFORMATION:

APPLICANT: Matthias Gromeier and Eckard Wimmer TITLE OF INVENTION: RECOMBINANT POLIOVIRUS FOR TITLE OF INVENTION: THE TREATMENT OF CANCER NUMBER OF SEQUENCES: 28

CORRESPONDENCE ADDRESS:

ADDRESSEE: MORGAN & FINNEGAN, L.L.P.

STREET: 345 PARK AVENUE

CITY: NEW YORK

STATE: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MICROSOFT WORD 97
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/566,581
FILING DATE: May 8, 2000
CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 09/129,686
FILING DATE: August 5, 1998
                                                                                                                                                                                                                 570 AAAGAAACACGGACACCCAA 551
                                                                                                                                                                                    1 AAGGAAACACGGACACCCAA 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Maria C.H. Lin
REGISTRATION NUMBER: 29,323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 AAGGAAACACGGACACC 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17 AAGGAAACACGGACACC 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; ORGANISM: Human rhinovirus 2
US-09-129-686-20
  ; TYPE: DNA
; ORGANISM: Enterovirus 71
US-09-724-678D-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY
                                                                                          Query Match
Best Local Similarity
Matches 19; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10154
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 14
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US-09-724-678D-11/C

i Sequence 11, Application US/09724678D

i Patent No. 6818397

i GENERAL INFORMATION:

i APPLICANT: Beir, Chi-Horng

i APPLICANT: Beir, Chi-Horng

APPLICANT: Wang, Yih-Weng

APPLICANT: Wang, Yih-Weng

APPLICANT: Wang, Shing-Hwan

ITILE OF INVENTION: and Probes Therefor

FILE REPERENCE: TAI 316

CURRENT FILING DATE: 2000-11-28

NUMBER OF SEQ ID NOS: 16

SOFTWARE: PatentIn version 3.1

SEQ ID NO 11

LENGTH: 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Lee, Kang-Hung
APPLICANT: Lee, Kang-Hung
APPLICANT: Tseng, Yang-Yuan
APPLICANT: Tseng, Yang-Yuan
APPLICANT: Wang, Yih-Weng
APPLICANT: Wang, Yih-Weng
APPLICANT: Wang, Shing-Hwan
TITLE OF INVENTION: and Probes Therefor
TITLE OF INVENTION: and Probes Therefor
FILE REPERRNCE: TAI 316
CURRENT APPLICATION NUMBER: US/09/724,678D
CURRENT APPLICATION NUMBER: US/09/724,678D
NUMBER OF SEQ ID NOS: 16
SOFTWARE: Patentin version 3.1
SEQ ID NO 16
LENGTH: 1560
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 20; DB 3; Length 28; 95.0%; Pred. No. 4.7; tive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: Artificial Sequence is Synthesized Patent No. 6818397
PRIOR APPLICATION NUMBER: KR 97/37812
PRIOR FILING DATE: 1997-07-08
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
LENGTH: 7441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 16, Application US/09724678D Patent No. 6818397 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                    565 AAGGAAACACGGACACCCAA 546
                                                                                                                                                                                                                                                                                                                         1 AAGGAAACACGGACACCCAA 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                       TYPE: DNA
CRGANISM: Human poliovirus 1
US-09-284-349B-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 95.0
Matches 19; Conservative
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Best Local Similarity
Matches 20; Conserv
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US-09-724-678D-16/c
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                                                               Length 39;
                                                                                                    Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                           METHOD FOR SELECTIVE INACTIVATION OF VIRAL REPLICATION
                                                           Query Match 85.0%; Score 17; DB 3; Best Local Similarity 100.0%; Pred. No. 55; Matches 17; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/221,816B
FILING DATE: 01-ARR-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A
REGISTATION UNMBER: 30,742
REFERENCE/DOCKET NUMBER: 7960-030
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 1155 Avenue of the Americas CITY: New York
                                                                                                                                                                                                                                                                           Sequence 31, Application US/08221816B
Patent No. 5738985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 31, Application US/10112547; Patent No. 6579674; GENERAL INFORMATION:
APPLICANT: Miles, Vincent J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/221,
                                                                                                                                                                                                                                                                                                                                     APPLICANT: Miles, vincent J. APPLICANT: Mathews, Michael B. APPLICANT: Katze, Michael G. APPLICANT: Witherell, Gary APPLICANT: Watson, Julia C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      568 GAAACACGGACACCCAA 552
                                                                                                                                           4 GAAACACGGACACCCAA 20
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    ; MOLECULE TYPE: synthetic DNA
US-09-061-273-8
                                                                                                                                                                               1 GAAACACGGACACCCAA 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (212) 869-8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 10036/2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 3:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TOPOLOGY: linear; MOLECULE TYPE: RNA US-08-221-816B-31
                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  USA
                                                                                                                                                                                                                                                           US-08-221-816B-31/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-10-112-547-31/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                           RESULT 16
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                                                                                                                                                                                                                                                                                                                                                                              DB 3; Length 33;
54;
                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Glustein, Joseph Z.
APPLICANT: Entlich, Garth D.
APPLICANT: Entlich, Garth D.
APPLICANT: Anang, Vingze
TITLE OF INVENTION: PCR Assay For Bacterial and
TITLE OF INVENTION: Viral Meningitis
NUMBER OF SEQUENCES: 12
CORRESSENDENCE ADDRESS:
ADDRESSENS: University of Pittsburgh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: No. 6258570 applicable
PILING DATE: No. 6258570 applicable
ATTORNEY/AGENT INFORMATION:
NAME: Mary-Elizabeth Buckles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: 3-1/2" high density diskette
COMPUTER: IBM PC or compatibles
OPERATING SYSTEM: MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: Office of Technology Transfer STREET: 911 William Pitt Union
REFERENCE/DOCKET NUMBER: 3927-4135US1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REGISTRATION NUMBER: 31,907
REFERENCE/DOCKET NUMBER: 017917/20132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/09/061,273
FILING DATE: 17-APR-1998
CLASSIFICATION: 435
PRIOR APPLICATION:
                                                                                                                                                                                                                                                                                                                                                                              85.0%; Score 17;
                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 8, Application US/09061273
                  TELEFAX: (212) 758-4800
TELEFAX: (212) 751-6849
INFORMATION FOR SEQ ID NO: 20: SEQUENCE CHARACTERISTICS:
LENGTH: 33
TYDE
                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100.0%; Pow Matches 17; Conservative 0;
                                                                                                                                                                                                                                                       ORGANISM: Human Rhinovirus
STRAIN: Type 2
POSITION IN GENOME:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 AAGGAAACACGGACACC 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17 AAGGAAACACGGACACC 33
                                                                                                                                                                                                                                                                                                            ; CHROMOSOME/SEGMENT: IRES
US-09-566-581-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEX: 64711
FORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 39 nucleotides
                                                                                                                                  TYPE: nucleotides
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: No
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 202/414/9299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Pittsburgh
STATE: Pennsylvania
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS
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85.0%; Score 17; DB 3; Length 627; 100.0%; Pred. No. 74;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                               CLASSIFICATION: cultal.....
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/221,816B
APTICATION NUMBER: US/08/221,816B
ATTORNEY/AGENT INFORMATION:
NAME: COTUZEJ, Laura
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7960-030
TELECOMMUNICATION INFORMATION:
TELEPHAX: (212) 869-8864
TELEFAX: (212) 869-8864
TELEFAX: (512) 869-8864
TELEFAX: (512) NO: 31:
SEQUENCE CHARACTERISTICS:
LENTH: 627 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: PASTSEQ VERSION 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/112,241
FILING DATE: 28-MAR-2002
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/221,816B
FILING DATE: 01-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/104, 611
FILING DATE: 22-Mar-2002
CLASSIPICATION: «Unknown»
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: RNA
SEQUENCE DESCRIPTION: SEQ ID NO: 31:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: USA
ZIP: 10036/2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS.
SOPTWARE: FastSEQ Version 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Miles, Vincent J. Matchews, Michael B. Katze, Michael G. Witherell, Gary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 31, Application US/10104611; Patent No. 6667152; GENERAL INFORMATION:
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100.0%; Pre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            568 GAAACACGGACACCCAA 552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4 GAAACACGGACACCCAA 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 100.
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-10-104-611-31/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-10-112-241-31
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APPLICANT: Michael B.
Katze, Michael G.
Witherell, Gary
Watson, Julia C.
TITLE OF INVENTION: METHOD FOR SELECTIVE INACTIVATION
OF VIRAL REPLICATION
Mathews, Michael B.
Katze, Michael G.
Witherell, Gary
Watson, Julia C.
TITLE OF INVENTION: METHOD FOR SELECTIVE INACTIVATION
OF VIRAL REPLICATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   85.0%; Score 17; DB 3; Length 627;
100.0%; Pred. No. 74;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COPERATING SYSTEM: DOS
SOFTWARE: FESTENCE DOS
SOFTWARE: FESTENCE DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/112,547
FILING DATE: 28-Mar-2002
CLASSIFICATION ONTHER: US/08/221,816B
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION UNBER: US/08/221,816B
FILING DATE: 01-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: COPLIZE, LAURA A
REFERENCE/DOCKET NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 30,742
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFRONE: (212) 790-9090
                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
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ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036/2711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: RNA
SEQUENCE DESCRIPTION: SEQ ID NO: 31:
US-10-112-547-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 31, Application US/10112241
Patent No. 6623961
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          568 GAACACGGACACCCAA 552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4 GAAACACGGACACCCAA 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEX: 66141 PENNIE INFORMATION FOR SEQ ID NO: 31:
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Best Local Similarity 100.
Matches 17; Conservative
                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                 CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                              COUNTRY: USA
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US-10-112-241-31/c
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Pred. No. 74;
                                                                                                                                      Mismatches
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STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                UMBER: US/09/724,380
01-APR-1994
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                                                   85.0%; Scc...
100.0%; Pre
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; Patent No. 6824976
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/221,816
APPLICATION NUMBER: 01-APR-1994
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Miles, Vincent J.
APPLICANT: Mathews, Michael B.
APPLICANT: Katze, Michael G.
APPLICANT: Witherell, Gary
APPLICANT: Wateon, Julia C.
TITLE OF INVENTION: METHOD FOR S.
TITLE OF INVENTION: OF VIRAL REP.
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM: DOS
SOFTWARE: FABLISEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/724
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   85.001
100.08; 24.
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NAME: Coruzzi, Laura A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7960
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
                                                                                                                                                                                                                                                   568 GAAACACGGACACCCAA 552
                                                                                                                                                                                            4 GAAACACGGACACCCAA 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
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                                                                      Query Match
Best Local Similarity 100.8
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100.9
Matches 17, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: USA
ZIP: 10036/2711
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-949-016-78843
                                                                                                                                                                                                                                                                                                                                     RESULT 21
US-09-724-380-31/c
               US-10-109-368-31
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MEDIUM TYPE: Diskette
COMPUTER: IDE Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ VETSION 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/109,368
FILING DATE: 27-Mar-2002
CLASSIFICATION: <UNKNOWN>
PRIOR APPLICATION NUMBER: US/08/221,816
FILING DATE: 01-APR-1994
ATTORNEY/AGENT INFORMATION:
AMANDA COMMENT ON THE OFFICE OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 33
CORRESPONDENCE PUDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OF VIRAL REPLICATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              85.0%; Score 17; DB 100.0%; Pred. No. 74; Live 0; Mismatches
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REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7960-030
                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear

MOLECULE TYPE: RNA

SEQUENCE DESCRIPTION: SEQ ID NO: 31:
US-10-104-611-31
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MOLECULE TYPE: RNA
SEQUENCE DESCRIPTION: SEQ ID NO: 31:
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 794
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 31, Application US/10109368
Patent No. 6777179
GENERAL INFORMATION:
MATHEWS, Michael B.
Katze, Michael B.
Katze, Michael G.
Witherell, Gary,
Watson, Julia C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
                                                                                                                                                                                                                                    LENGTH: 627 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (212) 869-8864
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TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         568 GAAACACGGACACCCAA 552
                                                                                                                                                     TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4 GAAACACGGACACCCAA 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 100.0
Matches 17; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
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NAME/KEY: misc_feature
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ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-949-016-12777
                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
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Patent No. 6812339

GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
CURRENT PELING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 06/241,755
PRIOR APPLICATION NUMBER: 60/231,768
PRIOR PILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR PILING DATE: 2000-09-08
SPIOR APPLICATION NUMBER: 06/231,498
PRIOR FILING DATE: 2000-09-08
SPIOR APPLICATION NUMBER: 2000-09-08
SPIOR APPLICATION NUMBER: 06/231,498
PRIOR PILING DATE: 2000-09-08
SPIOR APPLICATION NUMBER: 2000-10-30
SPIOR APPLICATION NUMBER: 06/231,498
PRIOR PILING DATE: 2000-09-08
SPIOR APPLICATION NUMBER: 2000-10-30
SPIOR APPLICATION NUMBER: 06/231,498
PRIOR PILING DATE: 2000-10-30
SPIOR APPLICATION NUMBER: 2000-10-30
SPIOR APPLICATION NUMBER: 06/231,498
PRIOR PILING DATE: 2000-10-30
GENERAL INFORMATION:

GENERAL INFORMATION:

1 APPLICANT: VENTER.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REPERENCE: CLOOU307

CURRENT APPLICATION NUMBER: 06/241,755

PRIOR FILING DATE: 2000-04-14

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR PRILICATION NUMBER: 60/231,498

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FASELSEQ for Windows Version 4.0

SEQ ID NO 78843
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Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2; Indels
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90.0%; Pred. No. 92;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 16.8;
Pred. No. 92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      162 AAGGAAAGACGCACACCCAA 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 AAGGAAACACGGACACCCAA 20
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Best Local Similarity 90.0°
Matches 18; Conservative
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Best Local Similarity 90.0
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TYPE: DNA
; ORGANISM: Human
US-09-949-016-78843
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US-09-949-016-78844
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; ORGANISM: Human
US-09-949-016-78844
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US-09-949-016-14033
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GENERAL INFORMATION:
APPLICAMT: VENTER, J. Craig et al.
APPLICAMT: VENTER, J. Craig et al.
TILLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
TILLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
TILLE REPREBNCE: CLOOL307
CURRENT APPLICATION NUMBER: US/9/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR PILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: PRESEQ FOR Windows Version 4.0
SEQ ID NO 12777
LEAGTH: WASHS OF WINDOWS PRIOR PRICED.
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Pred. No. 1.9e+02;
0; Mismatches 2; Indels 0;
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CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-03
SPIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
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US-09-949-016-78842
; Sequence 78842, Application US/09949016
nreat No. 6812339
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COTHER INFORMATION: n = A,T,C or G
US-09-949-016-14033
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| LOCATION: (1)...(828152)

| OTHER INFORMATION: n = A,T,C or G

US-09-949-016-12777
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Best Local Similarity 90.0%;
Matches 18; Conservative
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Best Local Similarity 90.0
Matches 18; Conservative
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Gaps

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GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLOO1307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04.14
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APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT APPLICATION NUMBER: US/09/949,016
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Pred. No. 3.2e+02;
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PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SEQ ID NO 12196
SEQ ID NO 12196
                                     PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR PILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-110-03
PRIOR PLING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FREESEQ for Windows Version 4.0
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100.0%; Pre
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, OTHER INFORMATION: n = A,T,C or G
US-09-949-016-12196
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Best Local Similarity 100.
Matches 16; Conservative
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Best Local Similarity
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; ORGANISM: Human
US-09-949-016-16963
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                                                                                                                                                                                                                               SEQ ID NO 16963
LENGTH: 18568
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Sequence 194126, Application US/09949016

Sequence 194126, Application US/09949016

Patent No. 6812339

GENERAL INPORMATION:
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REPERENCE: CL001307

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR PLILNG DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOCTHARE: PSECSEQ for Windows Version 4.0

LENGTH: 601
APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
FILE REFERENCE: CLOOL307;
CURRENT PELICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
FRIOR APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR PILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 78842
LENGTH: 601
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APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OP INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OP INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REPERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
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100.0%; Pred. No. 2.2e+02;
iive 0; Mismatches 0; Indels
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Patent No. 6812339
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100.08; Li
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85.0%;
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Best Local Similarity 85.0
Matches 17; Conservative
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Matches 16; Conservative
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US-09-949-016-16963/c
                                                                                                                                                                                                                                                                                                                                                                                           ; TYPE: DNA
; ORGANISM: Human
US-09-949-016-78842
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ORGANISM: Human
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Length 137949;

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PRIOR FILING DATE: 1997-08-15
NUMBER OF SEQ ID NOS: 6812
SOFWARE: Patentin version 3.1
SEQ ID NO 1077
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STRANDEDNESS: double
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Matches 17; Conserv
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US-08-743-637B-1
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APELICANT: VENTER, J. Craig et al.
APELICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
TITLE REFERENCE: CLOO1307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FRAESEQ for Windows Version 4.0
LENGTH: 601
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Patent No. 6617156

GENERAL INFORMATION:
FOR TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS FILE REFERENCE: 032796-032

CURRENT APPLICATION NUMBER: US/09/134,000C

CURRENT APLICATION NUMBER: US/09/134,000C

CURRENT PILING DATE: 1998-08-18

PRIOR APPLICATION NUMBER: US/0055,778
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                  80.0%; Score 16; DB 3; Le
ilarity 100.0%; Pred. No. 3.9e+02;
Conservative 0; Mismatches 0;
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR PILING DATE: 2000-10-03
PRIOR PLILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FREESEG for Windows Version 4.0
LENGTH: 137956
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; Sequence 56995, Application US/09949016
; Patent No. 6812339
                                                                                                                                                                                                                                                                                                                        ; LOCATION: (1)...(137956)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-17260
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Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
"...r.hes 16; Conservat
                                                                                                                                                                                                                                                                                                        NAME/KEY: misc_feature
                                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 32
US-09-134-000C-1077
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-949-016-56995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                  FEATURE:
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SPECIES-SPECIFIC AND UNIVERSAL DNA PROBES AND AMPLIFICATION PRIMERS TO RAPIDLY DETECT AND IDENTIFY COMMON BACTERIAL PATHOGENS AND ASSOCIATED ANTIBIOTIC RESISTANCE GENES FROM CLINICAL SPECIMENS ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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                                                                                                                        79.0%; Score 15.8; DB 3; Length 1560; 89.5%; Pred. No. 3.1e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US 08/526,840
FILING DATE: US 08/526,840
FILING DATE: US 08/526,840
ATTORNEY/AGENT INFORMATION:
NAME: BAKEN Jean C
NAME: BAKEN Jean C
NEGISTRATION NUMBER: 35,433
REFERENCE/DOCKET NUMBER: 35,433
REFERENCE/DOCKET NUMBER: 35,630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
79.0%; Score 15.8; DB 2;
Best Local Similarity 89.5%; Pred. No. 3.1e+02;
Matches 17; Conservative 0; Mismatches 2;
                                                                                                                                                                                 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1, Application US/08743637B; Patent No. 5994066; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: BERGERON, Michel G.
APPLICANT: PICARD, Francois J.
APPLICANT: OUELLETTE, Marc
APPLICANT: ROY, Paul H.
TITLE OF INVENTION: PROBES AND A
TITLE OF INVENTION: PROBES AND A
TITLE OF INVENTION: ANTIBIOTIC RI
NUMBER OF SEQUENCES: 273
CORRESPONDENCE ADDRESS:
ADDRESSEE: QUARLES & BRADY
                                                                                                                                                                                                                                                                            1194 AAGTAAACACGAACAACCA 1212
                                                                                                                                                                                                                                 1 AAGGAAACACGGACACCCA 19
LENGTH: 1560
TYPE: DNA
ORGANISM: Enterococcus faecalis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (414) 277-5000
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                 Conservative
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GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CLOO1307

CURRENT APPLICATION NUMBER: 60/241, 755

PRIOR PILING DATE: 2000-10-20

PRIOR PLILOR APPLICATION NUMBER: 60/231, 768

PRIOR PLILOR DATE: 2000-10-03

PRIOR PLILOR DATE: 2000-00-08

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 16011
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Patent No. 6812339
GENERAL INFORMATION:
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLO01307
CURRENT APPLICATION NUMBER: US/09/949,016
FILE REPERSOF OF DISCARD APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
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79.0%; Score 15.8; DB 3; Length 16434;
Best Local Similarity 89.5%; Pred, No. 3.9e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0;
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89.5%; Pred. No. 4.3e+02;
ive 0; Mismatches 2;
               CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 2007012
SEQ ID NO 13235
LENGTH: 16434
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US-09-949-016-16011
; Sequence 16011, Application US/09949016
; Patent No. 6812339
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Best Local Similarity 89.5'
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                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Human
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US-09-949-016-16011
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Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF FILE REFERENCE: CL001307
                                                                                                                                                                                                                                                                                                                  SPECIFIC AND UNIVERSAL PROBES AND
AMPLIFICATION PRIMERS TO RAPIDLY DETECT AND IDENT
COMMON BACTERIAL PATHOGENS AND ANTIBIOTIC RESIST?
FROM CLINICAL SPECIMENS FOR ROUTINE DIAGNOSIS IN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Milwaukee
STATE: Wisconsin
COUNTRY: USA
ZIP: 53202-4497
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/526,840B
FILING DATE: 11-SEP-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER: 35,433
REFERENCE DOCKET NUMBER: 850586.90012
TELECOMUNICATION INFORMATION:
TELEPHONE: (414) 277-500
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/304,732
FILING DATE: 12-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: BAKER, Jean C.
REGISTRATION NUMBER: 35,433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E: QUARLES & BRADY
411 East Wisconsin Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Enterococcus faecalis
                         1426 AAGTAAACACGGACAACCA 1444
                                                                                                                                                                  Sequence 1, Application US/08526840B
Patent No. 6001564
                                                                                                                                                                                                              GENERAL INPORMATION:
APPLICANT: BERGERON, Michel G.
APPLICANT: OUELLETTE, Marc
APPLICANT: OUELLETTE, Marc
APPLICANT: OUTLIETTE, Marc
TITLE OF INVENTION: SPECIFIC AND
TITLE OF INVENTION: AMPLIFICATIO
TITLE OF INVENTION: FROM CLINICA
NUMBER OF SEQUENCES: 177
CORRESPONDENCE ADDRESS:
ADDRESSEE: QUARLES & BRADY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 AAGGAAACACGGACACCCA 19
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TYPE: nucleic acid
STRANDEDNESS: double
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ORIGINAL SOURCE:
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US-09-949-016-13235
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APPLICANT:
APPLICANT:
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US-09-270-767-15529/c
US-09-270-767-15529/c
Sequence 15529, Application US/09270767
Facett No. 6703491
GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFRENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT PILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFUTANCE PATENTIN Ver. 2.0
SEQ ID NO 15529
LENGTH: 2053
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INPORMATION:
APPLICANT: Homburger et al.
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: 18709/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 247
LENGTH: 2053
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Pred. No. 4.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     77.0%; Score 15.4; DB 3; Length 2053; ilarity 94.1%; Pred. No. 4.9e+02; Conservative 0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  77.0%; Score 15.4; DB 3; Length 2053; 94.1%; Pred. No. 4.9e+02; tive 0; Mismatches 1; Indels 0
                                                                                                                                                                                                                                                                                    2; Indels
                                                                                                                                                                                                                                                                                  0; Mismatches
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 13390
LENGTH: 46626
                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 38
US-09-270-767-247/c
Sequence 247, Application US/09270767
Patent No. 6703491
                                                                                                                                                                                                                                                                                                                                                                 32280 AAGGAAAGAGGGACACCCA 32262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
CRGANISM: Drosophila melanogaster
US-09-270-767-247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-15529
                                                                                                                                                                                                                                                                                                                         1 AAGGAAACACGGACACCCA 19
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89.5%;
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Best Local Similarity 89.5
Matches 17; Conservative
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Matches 16; Conservative
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Best Local Similarity
Matches 16; Conserv
                                                                                                                                                    ; TYPE: DNA
; ORGANISM: Human
US-09-949-016-13390
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APPLICANT: Tumes, P. Mickey
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, Williams, P. Mickey
APPLICANT: Wood, Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: ACIENT SECONDES
CURRENT APPLICATION NUMBER: US/09/999, 833A
CURRENT APPLICATION NUMBER: US/918585
PRIOR PILING DATE: 2001-10-30
PRIOR PILING DATE: 1997-10-30
PRIOR PILING DATE: 1997-11-03
PRIOR PILING DATE: 1997-11-03
PRIOR PILING DATE: 1997-11-13
PRIOR PILING DATE: 1997-11-13
PRIOR PILING DATE: 1997-11-21
PRIOR PILING DATE: 1998-03-10
PRIOR PILING DATE: 1998-03-10
PRIOR PILING DATE: 1998-03-10
PRIOR PILING DATE: 1998-03-10
PRIOR PILING DATE: 1998-03-11
PRIOR PILING DATE: 1998-03-12
PRIOR PILING DATE: 1998-03-13
PRIOR PILING DATE: 1998-03-20
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REIOR APPLICATION NUMBER: 60/078910
PRIOR APPLICATION NUMBER: 60/078910
PRIOR APPLICATION NUMBER: 60/078939
REIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/079294
PRIOR PILING DATE: 1998-03-25
REIOR APPLICATION NUMBER: 60/079656
PRIOR PILING DATE: 1998-03-26
PRIOR PILING DATE: 1998-03-26
PRIOR PILING DATE: 1998-03-26
US-09-999-833A-514/c
; Sequence 514, Application US/09999833A
; Patent No. 6916648
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Goddard, Audrey
Godowski, Paul J.
Grimaldi, J. Christopher
Gurney, Austin L.
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Paoni, Nicholas F.
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Ferrara, Napoleon
Filvaroff, Ellen
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Gerber, Hanspeter
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Kuo, Sophia S.
                                                                                      GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Bakerin, David
APPLICANT: Desnoyers, Luc
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PRIOR FILING DATE: 1998-03-27
PRIOR PLING DATE: 1998-03-37
PRIOR PLING DATE: 1998-03-31
PRIOR PLING DATE: 1998-04-08
PRIOR PLING DATE: 1998-04-15
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5e+02;
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PRIOR PILING DATE: 1998-05-15
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PRIOR APPLICATION NUMBER: 60/08559
PRIOR PILING DATE: 1998-05-15
PRIOR PILING DATE: 1998-05-15
PRIOR PILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085573
PRIOR PILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085573
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R FILING DATE: 1998-05-07
R APPLICATION NUMBER: 60/084640
R FILING DATE: 1998-05-07
R APPLICATION NUMBER: 60/084598
R APPLICATION NUMBER: 60/084600
R FILING DATE: 1998-05-07
R APPLICATION NUMBER: 60/084600
R APPLICATION NUMBER: 60/084617
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                                                                                                                                                                                                                 FILING DATE: 1998-04-29
APPLICATION NUMBER: 60/083500
FILING DATE: 1998-04-29
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APPLICATION NUMBER: 60/083742
FILING DATE: 1998-04-30
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FILING DATE: 1998-05-05
APPLICATION NUMBER: 60/084414
FILING DATE: 1998-05-06
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APPLICATION NUMBER: 60/083558
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APPLICATION NUMBER: 60/083559
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FILING DATE: 1998-05-06
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FILING DATE: 1998-05-07
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APPLICATION NUMBER: 60/085339
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APPLICATION NUMBER: 60/085338
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APPLICATION NUMBER: 60/085323
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Best Local Similarity
Matches 16; Conserv
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PRIOR
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PRIOR FILING DATE: 1986-04-01
PRIOR FILING DATE: 1986-04-01
PRIOR PELING DATE: 1986-04-01
PRIOR APPLICATION NUMBER: 60/080339
PRIOR PELING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/081039
PRIOR PILING DATE: 1998-04-08
PRIOR PILING DATE: 1998-04-09
PRIOR PILING DATE: 1998-04-15
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PRIOR PILING DATE: 1998-
                                                                                                        RICK AFFILING DATE: 1998-03-30
RICK APPLICATION NUMBER: 60/07923
RICK FILING DATE: 1998-03-30
RICK APPLICATION NUMBER: 60/080105
RICK APPLICATION NUMBER: 60/080105
RICK APPLICATION NUMBER: 60/080107
RICK APPLICATION NUMBER: 60/080107
RICK APPLICATION NUMBER: 60/080107
RICK APPLICATION NUMBER: 60/080107
RICK APPLICATION NUMBER: 60/080194
RICK APPLICATION NUMBER: 60/080197
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PRIOR APPLICATION NUMBER: 60/083495
PRIOR FILING DATE: 1998-04-29
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APPLICATION NUMBER: 60/083545
FILING DATE: 1998-04-29
APPLICATION NUMBER: 60/083554
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FILING DATE: 1998-03-30
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APPLICATION NUMBER: 60/083392
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APPLICANT: Wood, William I.
ITITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
ITILE OF INVENTION: Acids Encoding the Same
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CURRENT APPLICATION NUMBER: US/10/020,445A
CURRENT APPLICATION NUMBER: US/10/020,445A
CURRENT FILING DATE: 2001-07-30
PRIOR PILING DATE: 1997-11-01
PRIOR PILING DATE: 1997-11-01
PRIOR APPLICATION NUMBER: 60/064249
PRIOR PILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/064249
PRIOR PILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/065311
PRIOR APPLICATION NUMBER: 60/065364
PRIOR PILING DATE: 1997-11-01
PRIOR PILING DATE: 1999-11-01
PRIOR APPLICATION NUMBER: 60/077649
PRIOR PILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077649
PRIOR PILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077649
PRIOR PILING DATE: 1998-03-12
PRIOR APPLICATION NUMBER: 60/077649
PRIOR PILING DATE: 1998-03-12
PRIOR APPLICATION NUMBER: 60/077649
PRIOR PILING DATE: 1998-03-12
PRIOR APPLICATION NUMBER: 60/078936
PRIOR PILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/078936
PRIOR PILING DATE: 1998-03-20
PRIO
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Grimaldi, J. Christopher
Gurney, Austin L.
Hillan, Kenneth J
Kljavin, Ivar J.
Kuo, Sophia S.
Napier, Mary A.
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FILING DATE: 1998-03-27
APPLICATION NUMBER: 60/079728
FILING DATE: 1998-03-27
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Paoni, Nicholas F.
Roy, Margaret Ann
Shelton, David L.
Stewart, Timothy A.
Tumas, Daniel
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Filvaroff, Ellen
Fong, Sherman
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Gerber, Hanspeter
Baker Kevin P.
Botstein, David
Desnoyers, Luc
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FARCHAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLOOU3307
CURRENT APPLICATION NUMBER: 06/241,755
FRICH APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR PELING DATE: 2000-10-03
PRIOR PLING DATE: 2000-10-03
PRIOR PLING DATE: 2000-10-03
PRIOR PLING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SSOTHARE: PERCENG FOR WINDOWS VERSION 4.0
SEQ ID NO 14588
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APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
77.0%; Score 15.4; DB 3;
Best Local Similarity 94.1%; Pred. No. 7.7e+02;
Matches 16; Conservative 0; Mismatches 1;
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 11868
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Patent No. 6812339
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                                                                                                                                                                                                                                                                                                    PEATURE:

NAME/KEY: misc_feature

LOCATION: (1)...(300598)

OTHER INFORMATION: n = A,T,C or G
US-09-949-016-11868
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; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-14588
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US-09-949-016-14588/c
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                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Human
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                                                                                                                                                                                                                LENGTH: 300598
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APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF FILE REFERENCE: CLOUI307
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CURRENT FILING DATE: 2000-04-14
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Patent No. 6812339
                                                                                                                                                  60/083500
                                                                                                                                                                           FILING DATE: 1998-04-29
APPLICATION NUMBER: 60/083742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 1998-05-07
APPLICATION NUMBER: 60/084640
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PLICATION NUMBER: 60/084600
                                  60/083558
                                                                                                                                                                                                                                                                     LICATION NUMBER: 60/084366
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                                                                                                                                                                                                                                                                                                                             LICATION NUMBER: 60/084414
                                                                                                                                                                                                                                                                                                                                                                                        CATION NUMBER: 60/084441
                                                                                                                                                                                                                                                                                                                                                                                                                                                    LICATION NUMBER: 60/084637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ING DATE: 1998-05-07
LICATION NUMBER: 60/084639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: 60/084598
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LICATION NUMBER: 60/084627
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: 60/085697
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FILING DATE: 1998-04-29
                                                                                                                   ILING DATE: 1998-04-29
PPLICATION NUMBER: 60/
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                                                                                                                                                                                                                                                                                                                                                            NG DATE: 1998-05-06
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PLICATION NUMBER: 60/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 94.1
Matches 16; Conservative
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PRIOR FILING DATE: 2000-10
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; LOCATION: (B) LOCATION 1...507
; SEQUENCE DESCRIPTION: SEQ ID NO: 826:
US-09-107-532A-826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: GTC-012 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Enterococcus faecium
                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: PC
OPERATING SYSTEM: <Unknown>
SOFTWARE: ASCII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR SEQ ID NOS: 207012
                                                                                                     STREET: 100 Beaver Street
CITY: Waltham
STATE: Massachusetts
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (781)893-5007
TELEFAX: (781)893-8277
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: circular MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 507 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 820
SEQUENCE CHARACTERISTICS
                                                        CORRESPONDENCE ADDRESS
                              NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ANTI-SENSE: NO
ORIGINAL SOURCE:
                                                                                 ADDRESSEE:
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APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
ITILE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF TILE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: 60/241,755
CURRENT APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/231,768
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-010-03
PRIOR FILING DATE: 2000-00-08
NUMBER OF SEQ ID NOS: 2007-012
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 17119
LENGTH: 308362
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Patent No. 6583275
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ch 77.0%; Score 15.4; DB 3; Length 302604; al Similarity 94.1%; Pred. No. 7.7e+02; 16; Conservative 0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 77.0%; Score 15.4; DB 3; Length 308362; Best Local Similarity 94.1%; Pred. No. 7.8e+02; Matches 16; Conservative 0; Mismatches 1; Indels 0;
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR PILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: PABELEG for Windows Version 4.0
SEQ ID NO 44589
LENGTH: 302604
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US-09-949-016-17119/c
; Sequence 17119, Application US/09949016
; Patent No. 6812339
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; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-17119
                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc_feature
| LOCATION: (1)...(302664)
| CTHER INFORMATION: n = A,T,C or G
US-09-949-016-14589
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Best Local Similarity
                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Human
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ORGANISM: Human
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US-09-107-532A-826
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Sequence 26382, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: UNFORMATION:
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REPERENCE: CL0013N NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
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GENOME THERAPEUTICS CORPORATION
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76.0%; Score 15.2; DB 3;
Best Local Similarity 85.0%; Pred. No. 5.2e+02;
Matches 17; Conservative 0; Mismatches 3;
                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/081571
ATTORNEY AGENT INFORMATION:
NAME: Atiniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
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US-09-949-016-58448/c
       US-09-949-016-58446
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US-09-949-016-58447
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; ORGANISM: Human
US-09-949-016-58448
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Sequence 26383, Application US/09949016
Fatent No. 6812339
GENERAL INFORMATION:
FAPLICATT. VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLO01307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT PILING DATE: 2000-04-14
FRIOR APPLICATION NUMBER: 60/241,755
FRIOR APPLICATION NUMBER: 60/241,756
FRIOR PILING DATE: 2000-10-03
FRIOR FILING DATE: 2000-0-0-08
FRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SEQ ID NO 26383
LENGTH: 601
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Sequence 58446, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14
PRIOR PLIING DATE: 2000-10-20
PRIOR PELICATION NUMBER: 60/231,768
PRIOR PLIING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR PLIING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 54446

LENGTH: 601
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                                                                                                                                                                                                                 Indels
                                                                                                                                                                Score 15.2; DB 3;
Pred. No. 5.3e+02;
0; Mismatches 3;
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 26382
LENGTH: 601
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                                                                                                                                                              Query Match 76.0%;
Best Local Similarity 85.0%;
Matches 17; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                   US-09-949-016-26383/c
                                                                      ; TYPE: DNA
; ORGANISM: Human
US-09-949-016-26382
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US-09-949-016-26383
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ORGANISM: Human
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US-09-94-016-58447/c

i Sequence 58447, Application US/09949016

j Patenn No. 6812339

j Patenn No. 6812339

j GENERAL INFORMATION:

i TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT PRING DATE: 2000-04-14

PRIOR PILING DATE: 2000-10-20

PRIOR PELING DATE: 2000-10-20

PRIOR PELING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08
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Batent No. 6812339
GENERAL INFORMATION:
GENERAL INFORMATION:
JAPPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
ITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
ITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
ITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
ITLE OF INVENTION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR PILING DATE: 2000-10-30
PRIOR PILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FREESE FREESE FOR WINDOWS VERSION 4.0
SEQ ID NO 54448
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                                                     Gaps
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Pred. No. 5.3e+02;
0; Mismatches 3; Indels (
     Length 601;
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76.0%; Score 15.2; DB 3;
85.0%; Pred. No. 5.3e+02;
tive 0; Mismatches 3;
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Pred. No. 5.3e+02;
0; Mismatches 3;
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SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                              257 AAGGAGACACAGACAACCAA 238
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85.0%;
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85.0%;
Query Match
Best Local Similarity 85.0
Matches 17; Conservative
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Best Local Similarity 85.0.
The 17; Conservative
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Best Local Similarity
Matches 17; Conserv
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y Sequence 10.158, Application US/09949016

y Sequence 10.158, Application US/09949016

y Batent No. 6812339

general information:

y Application Volume Version of the Ver
                                                                                                           GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

CURRENT APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-03

SRIOR PLING DATE: 2000-10-03

SOFTWARE: FASTESED FOR WINGOWS VEFSION 4.0

SEQ ID NOS: 207012
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Pred. No. 5.3e+02;
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85.0%; Pred. No. 5.3e+02;
iive 0; Mismatches 3;
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                                                       Sequence 110157, Application US/09949016 Patent No. 6812339
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Best Local Similarity 85.0%;
Matches 17; Conservative
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Best Local Similarity 85.0°
....hes 17; Conservative
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US-09-949-016-110158
                             IS-09-949-016-110157
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US-09-949-016-110158
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GENERAL INFORMATION:

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;

FILE REFERENCE: CL001307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR PILING DATE: 2000-10-20

PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTHARE: FREESE OF WINDOWS VETRION 4.0

SEQ ID NO 58449
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85.0%; Pred. No. 5.3e+02;
iive 0; Mismatches 3; Indels
                                                                                                                                                     RESULT 52
10S-09-94-016-58449/c
; Sequence 58449, Application US/09949016
; Patent No. 6812339
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                                                          412 AAGGAGACACAGACAACCAA 393
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1 AAGGAAACACGGACACCCAA 20
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Best Local Similarity 85.0
Matches 17; Conservative
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Matches 17; Conserv
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US-09-949-016-58450/c
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; ORGANISM: Human
US-09-949-016-58450
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US-09-949-016-58449
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Gaps

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Indels

Length 601;

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Best Local Similarity 85.0 Matches 17; Conservative
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US-09-949-016-138288
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SEQ ID NO 149759
LENGTH: 601
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Fatent No. 681239

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;

FILLE REPERENCE: CL001307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

FRIOR PILING DATE: 2000-10-20

FRIOR PILING DATE: 2000-10-03

FRIOR FILING DATE: 2000-10-03

FRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SEQ ID NO 138287

LENGTH: 601

LENGTH: 601
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REPERENCE: CLOODING
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT PILING DATE: 2000-04-14
PRIOR PELING DATE: 2000-10-13
PRIOR PELING DATE: 2000-10-03
PRIOR PELING DATE: 2000-10-03
PRIOR PELING DATE: 2000-10-03
PRIOR PELING DATE: 2000-10-03
PRIOR PELING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: PRACES ELECT OF WINDOWS VERSION 4.0
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Patent No. 6812339
GENERAL INFORMATION:
GENERAL THORDATION:
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
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Pred. No. 5.3e+02;
0; Mismatches 3;
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Best Local Similarity 85.0%;
Matches 17; Conservative
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; ORGANISM: Human
US-09-949-016-138287
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ORGANISM: Human
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GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: POLYMORHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT PILING DATE: 2000-04-14
PRIOR PILING DATE: 2000-10-20
PRIOR PILING DATE: 2000-10-20
PRIOR PILING DATE: 2000-10-30
PRIOR FILING DATE: 2000-10-31
PRIOR PILING DATE: 2000-09-08
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APPLICANT: Michael W. Rey
APPLICANT: Jeffrey R. Shuster
APPLICANT: Jeffrey R. Shuster
APPLICANT: Ib Groth Clausen
APPLICANT: Peter Bjarke Olsen
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Pred. No. 5.3e+02;
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Best Local Similarity 85.0%; Pred. No. 5.3e
Matches 17; Conservative 0; Mismatches
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PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR PILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FBSESEQ for Windows Version 4.0
SEQ ID NO 139288
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SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-949-016-149759
; Sequence 149759, Application US/09949016
; Patent No. 6812339
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6902887
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85.0%;
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Sequence 13, Application US/08829553

Sequence 13, Application US/08829553

Patent No. 5817762

GENERAL INFORMATION:
APPLICANT: Kleyn, Patrick W.
APPLICANT: Moore, Karen J.
TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND
TITLE OF INVENTION: DIAGNOSIS OF BODY WEIGHT DISORDERS, INCLUDING OBESITY
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESSE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: Now York
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Pred. No. 5.9e+02;
0; Mismatches 3; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: 1 Elpopy disk
COMPUTER: 1 EM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/829,553
FILING DATE: 28-MAR-1997
CLASSIFICATION NUMBER: US 08/631,200
PRIOR APPLICATION NUMBER: US 08/631,200
FILING DATE: 12-APR-1996
ATTORNEY/AGENT INPORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 38,742
REFERENCE/DOCKET NUMBER: 30,742
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/631,200
FILING DATE: 12-APR-1996
                                                                                         CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Coruzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7853-057
TELECOMMUNICATION INFORMATION:
TELEFAN: (212) 790-9090
TELEFAN: (212) 8659-741/8864
TELERA: 66141 PENNIE
INFORMATION FOR SED ID NO: 13: SEQUENCE CHARACTERISTICS:
LENGTH: 1622 base pairs
TYPE: nucleic acid
STRATORNENBENSES: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1180 AAGGATAGACAGACACCCAA 1161
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   , MOLECULE TYPE: DNA (genomic) US-08-631-200-13
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Best Local Similarity 85.0%;
Matches 17; Conservative
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INPORMATION POR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 1622 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   unknown
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STRANDEDNESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-829-553-13/c
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APPLICANT: Keith Weinstock et al
APPLICANT: Keith Weinstock et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.132
CURRENT PILING DATE: 1999-02-12
PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR FILING DATE: 1998-02-13
PRIOR FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 13, Application US/08631200
Patent No. 5646040
GENERAL INFORMATION:
APPLICANT: Kleyn, Patrick W.
APPLICANT: Moore, Karen J.
TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND
TITLE OF INVENTION: DIAGNOSIS OF BODY WEIGHT DISORDERS, INCLUDING OBESITY
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
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Pred. No. 5.9e+02;
0; Mismatches 3; Indels 0
                                                                                                                                                                                                                                                                                                          76.0%; Score 15.2; DB 3; Length 675; 85.0%; Pred. No. 5.4e+02; tive 0; Mismatches 3; Indels
                       CURRENT FILING DATE: 2000-03-22
EARLIER APPLICATION NUMBER: 09/273,623
EARLIER FILING DATE: 1999-03-22
NUMBER OF SEQ ID NOS: 7860
SOFTWARE: FaetSEQ for Windows Version 4.0
SEQ ID NO 6526
LENGTH: 675
  CURRENT APPLICATION NUMBER: US/09/533,559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        E: Pennie & Edmonds
1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 4726, Application US/09248796A Patent No. 6747137
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STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Flappy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                         370 ACGGAAAAAGGACACCCAA 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            287 AACGAAATATGGACACCCAA 268
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Best Local Similarity 85.0%;
Matches 17; Conservative (
                                                                                                                                                                                                        ; TYPE: DNA; ORGANISM: Aspergillus oryzae
US-09-533-559-6526
                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 85.0%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TYPE: DNA; Candida albicans
; ORGANISM: Candida albicans
US-09-248-796A-4726
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STREET: 1152
TTTY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-248-796A-4726/c
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LENGTH: 1455
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LENGTH: 1622 base pairs
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Best Local Similarity 85.0%
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STRANDEDNESS: single
                                                                                                                                                                                                                                                               New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TOPOLOGY: linear; MOLECULE TYPE: DNA US-08-936-707A-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-936-706A-13/c
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                                                                                    Length 1622;
                                                                                                                       3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRAL.
STREET: 1.2.
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-ZIP:
TOGORDIUR RADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PALENTION DATA:
APPLICATION NUMBER: US/08/922,267A
FILING DATE: 2-SEP-1997
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/829,553
FILING DATE: 12-MAR-1997
CLASSIFICATION NUMBER: US 08/631,200
FILING DATE: 12-APR-1996
CLASSIFICATION NUMBER: US 08/631,200
FILING DATE: 12-APR-1996
CLASSIFICATION: 530
PRIOR APPLICATION NUMBER: TO 08/631,200
FILING DATE: 12-APR-1996
CLASSIFICATION NUMBER: 30,742
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7853-085
"COMMUNICATION INFORMATION:
"UNME: COLUZZI, LAURA A.
REGISTRATION NUMBER: 7853-085
"COMMUNICATION INFORMATION:
"UNME: (212) 790-9090
(212) 865-9741/8864
PENNIE
TO NOW: (212) 790-9090
TO NOW: (212) 790-9090
                                                                                  Score 15.2; DB 2;
Pred. No. 5.9e+02;
0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                       1180 AAGGATAGACAGACACCCAA 1161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELERAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 1622 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                        1 AAGGAAACACGGACACCCAA 20
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, MOLECULE TYPE: DNA (genomic)
US-08-829-553-13
                                                                                Query Match 76.0%;
Best Local Similarity 85.0%;
Matches 17; Conservative
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear;
MOLECULE TYPE: DNA
US-08-922-267A-13
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Best Local Similarity
Matches 17; Conserva
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1180 AAGGATAGACAGACACCCAA 1161

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Seguence 11, Application US/08935707A

PREMENAL INFORMATION:
GENERAL INF
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Gaps

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Length 1622; Indels

us-10-829-474-2.rni

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76.0%; Score 15.2; DB 3;
illarity 85.0%; Pred. No. 5.9e+02;
Conservative 0; Mismatches 3;
                                                         ; MOLECULE TYPE: DNA
US-09-248-203-13
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                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 17; Conserv
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Sequence 13, Application US/09248203
Sequence 13, Application US/09248203
Sequence 13, Application US/09248203
SERBEAL INFORMATION:
APPLICANT: Kleyn, Patrick W.
APPLICANT: Moore, Karen J.
TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND
TITLE OF INVENTION: DIAGNOSIS OF BODY WEIGHT DISORDERS, INCLUDING OBESITY
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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Pred. No. 5.9e+02;
0; Mismatches 3; Indels 0
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/936,706A
FILING DATE: 24-SEP-1997
CLASSIFICATION: 530
ATTONREY/AGENT INPORMATION:
NAME: COLUZZI, LAULA B.
REGISTRATION NUMBER: 30,742
REGISTRATION NUMBER: 30,742
REGISTRATION NUMBER: 30,742
REGISTRATION NUMBER: 30,742
RELERAX: (212) 790-9090
TELEFAX: (212) 790-9010
TELEFAX: (212) 790-9010
TELEFAX: (212) 790-9010
TELEFAX: (212) 869-9741/8864
TELERAX: 66141 PERNIE
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 1622 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
PILING DATE: US/09/248,203
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COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATER: PCOMPUTER: DCOMPUTER: DC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/936,707
FILING DATE: 24-SEP-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1180 AAGGATAGACAGACACCCAA 1161
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REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 13: SEQUENCE CHARACTERISTICS: LENGTH: 1622 base pairs TYPE: nucleac acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         76.0%;
85.0%;
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Best Local Similarity 85.0
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear MOLECULE TYPE: DNA
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US-09-248-203-13/c
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Karen J.
: COMPOSITIONS FOR THE TREATMENT AND
: DIAGNOSIS OF BODY WEIGHT DISORDERS, INCLUDING OBESITY
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85.0%; Pred. No. 5.9e+02;
tive 0; Mismatches 3; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/406,071
                                                                         US-09-406-071-13/c

Sequence 13, Application US/09406071

Sequence 13, Application US/09406071

Setent No. 6207386

GENERAL INFORMATION:
APPLICANT: Kleyn, Parrick W.
APPLICANT: Kleyn, Saren J.
TITLE OF INVENTION: COMPOSITIONS FOR TE.
TITLE OF INVENTION: DIAGNOSIS OF BODY W.
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
COUNTY.
                                                                                                                                                                                                                                                                                                                                                                                                            CITY: New York
CUTY: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Ploppy disk
"WEDIUM TYPE: Ploppy disk
"WEDIUM TYPE: Ploppy is NEW PROBOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Cortzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERRNCE/DOCKET NUMBER: 7853-100
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFRX: (212) 869-9741/8864
                                            1180 AAGGATAGACAGACACCCAA 1161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1180 AAGGATAGACAGACACCCAA 1161
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; Sequence 13, Application US/09814986
; Patent No. 6605437
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
CLASSIFICATION:
PRICE APPLICATION DATA:
APPLICATION NUMBER: 08/936,707
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1 AAGGAAACACGGACACCCAA 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 1622 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 85.0 Matches 17; Conservative
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STRANDEDNESS: single
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Gaps

us-10-829-474-2.rni

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APPLICANT: Burgess, Diane
TITLE OF INVENTION: A Starchless Variety of Pisum Sativum Having Elevated Levels of S
TITLE OF INVENTION: A Starchless Variety of Pisum Sativum Having Elevated Levels of S
TITLE SEPERACE: SVG3010903020S
CURRENT APPLICATION NUMBER: U5/09/555,820A
NUMBER OF SEQ ID NOS: 21
SOFTWARE: Patentin version 3.1
SEQ ID NO 1
LENGTH: 2391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Stork, Philip J
APPLICANT: Stork, Philip J
APPLICANT: Stork, Philip J
APPLICANT: Misra-Press, Anita
TITLE OF INVENTION: Mitogen Activated Protein Kinase Phosphatase CDNAs and
TITLE OF INVENTION: Their Biologically Active Expression Products
FILE REFERENCE: 4104-0003220SA
CURRENT APPLICATION NUMBER: US/08/990,379
CURRENT FILING DATE: 1997-12-12
EARLIER APPLICATION NUMBER: PCT/US96/10402
EARLIER FILING DATE: 1996-06-14
EARLIER FILING DATE: 1995-06-16
NUMBER OF SEQ ID NOS: 19
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                                                                                  Length 1987;
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                                                                   Score 15.2; DB 2;
Pred. No. 6.1e+02;
0; Mismatches 3;
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85.0%; Pred. No. 6.2e+02;
tive 0; Mismatches 3;
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NAME/KEY: misc_feature

LOCATION: (1274)..(1350)

SOTHER INFORMATION: N=A or C or G or T/U
US-09-555-820A-1
                                                                                                                                                                                                                                                                                       1826 AAGGAAAAACGGACACAAAA 1807
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Patent No. 680423
GENERAL INFORMATION:
APPLICANT: Webster, David
                                                                                                                                                                                                                               1 AAGGAAACACGGACACCCAA 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2, Application US/08990379
Patent No. 5998188
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                                                                          Query Match 76.0%;
Best Local Similarity 85.0%;
Matches 17; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: Rattus norvegicus
US-08-990-379-2
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Best Local Similarity 85.04
Matches 17; Conservative
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SEQ ID NO 2
LENGTH: 1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 17; Conserv
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           US-08-990-379-1
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              AFFILCENT: NOTE, KATEN J.

MOOTE, KATEN J.

TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND
DIAGNOSIS OF BODY WEIGHT DISORDERS, INCLUDING OBESITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:

APPLICANT: Stork, Philip J

APPLICANT: Stork, Philip J

APPLICANT: Stork, Philip J

APPLICANT: Stork, Philip J

APPLICANT: Misra-Press, Anita

APPLICANT: Misra-Press, Anita

TITLE OF INVENTION: Their Biologically Active Expression Products

TITLE OF INVENTION: Their Biologically Active Expression Products

FILE REFERENCE: 4104-000322USA

CURRENT APPLICATION NUMBER: US/08/990,379

CURRENT FILING DATE: 1997-12-15

EARLIER APPLICATION NUMBER: 60/000,263

EARLIER APPLICATION NUMBER: 60/000,263

EARLIER APPLICATION NOWER: 1995-06-16

NUMBER OF SEQ ID NOS: 19

SOFTWARE: PATENTIN Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          76.0%; Score 15.2; DB 3; Length 1622; ilarity 85.0%; Pred. No. 5.9e+02; Conservative 0; Mismatches 3; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/814,986
FILING DATE: 22-Mar-2001
CLASSIFICATION: <understand the control of the control
                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                              STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OMPUTER: IBM PC compatible
OMPUTER: SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 08/936,707
FILING DATE: 24-SEP-1997
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Coruzzi, Laura A. REGISTRATION NUMBER: 30,742 REFERENCE/DOCKET NUMBER: 7853-100 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: DNA
SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-09-814-986-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1180 AAGGATAGACAGACACCCAA 1161
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Patent No. 5998188
APPLICANT: Kleyn, Patrick W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEX: 66141 PENNIE
MATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
                                                                                                                                                                                                                                                                                           CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX:
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Gaps

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Sequence 12838, Application US/09949016

Sequence 12838, Application US/09949016

Patent No. 6812339

GENERAL INPORMATION:

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR PILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/231,768

PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-09-08

NUMBER: OF SEQ ID NOS: 207012

SEQ ID NO 12838
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-949-016-14781/c

Sequence 14781, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:

APPLICANT: VERYER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISRASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISRASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISRASE, METHODS OF DETECTION AND USES THEREOF

CURRENT FILING DATE: 2000-04-14

PRIOR FILING DATE: 2000-10-20

PRIOR PELING DATE: 2000-10-20

PRIOR PELING DATE: 2000-10-03

PRIOR PELING DATE: 2000-10-03

PRIOR PELING DATE: 2000-10-03

PRIOR PELING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTHARE: PESESEE for Windows Version 4.0

SEQ ID NO 14781
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PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 14437
LENGTH: 17353
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                                                                                                                                                                                               ORGANISM: Human
US-09-949-016-13437
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                                                                                                                                                                     TYPE: DNA
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Matches
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                                                                                                                      Sequence 2, Application US/09555820A
Pacent No. 6680429
GENERAL INFORMATION:
APPLICANT: Webster, David
APPLICANT: Webster, David
TITLE OF INVENTION: A Starchless Variety of Pisum Sativum Having Elevated Levels of
FILE REFERENCE: SVS380100303US
CURRENT APPLICATION NUMBER: US/09/555,820A
CURRENT PILING DATE: 2000-08-29
NUMBER OF SEQ ID NOS: 21
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
LENGTH: 2391
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Patent No. 681239
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION:
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
TITLE OF INVENTION:
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
TITLE OF INVENTION:
TITLE OF INVENTION:
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
CURRENT APPLICATION NUMBER: 60/294,016
CURRENT FILING DATE: 2000-04-14
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
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Patent No. 6703491

PERENT INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucledac acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT PILING DATE: 1990-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: PatentIN Ver. 2.0
SEQ ID NO 12587
LIENGTH: 4983
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     1947 ACGGAGACACGGACACCAAA 1966
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-12587
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TYPE: DNA; ORGANISM: Pisum sativum
US-09-555-820A-2
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US-09-270-767-12587
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                                                                                    RESULT 73
US-09-555-820A-2
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Query Match
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Sequence 17458, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR PLING DATE: 2000-10-03

PRIOR PLING DATE: 2000-10-03

PRIOR PLING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOUTHARE: FESTSEQ for Windows Version 4.0

SEQ ID NO 17458
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Fatent No. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;

FILLE REFERENCE: CLOR01307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

FRIOR APPLICATION NUMBER: 60/241,755

FRIOR APPLICATION NUMBER: 60/241,755

FRIOR FILING DATE: 2000-10-03

FRIOR FILING DATE: 2000-10-03

FRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

NUMBER OF SEQ ID NOS: 207012
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                                                                                                                   Query Match 76.0%; Score 15.2; DB 3; Length 57178; Best Local Similarity 85.0%; Pred. No. 8.6e+02; Matches 17; Conservative 0; Mismatches 3; Indels 0;
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Pred. No. 8.6e+02;
0; Mismatches 3;
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Best Local Similarity 85.0%;
Matches 17; Conservative (
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LENGTH: 57178
TYPE: DNA
ORGANISM: Human
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; ORGANISM: Human
US-09-949-016-17458
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                                                                          US-09-949-016-12838
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GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CL001307

CURRENT APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR PLILNG DATE: 2000-10-03

PRIOR PLILNG DATE: 2000-10-03

PRIOR PLILNG DATE: 2000-10-03

PRIOR PLILNG DATE: 2000-09-08

NUMBER: OF SEQ ID NOS: 207012

SOPTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 15544
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Fatent No. 6812339
GENERAL INFORMATION:
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
FILE REFERENCE: CLO01307
CURRENT PELLING DATE: 2000-04-14
CURRENT PELLING DATE: 2000-04-14
FRIOR PELLOATION NUMBER: 60/241,755
PRIOR PELLOATION NUMBER: 60/241,755
PRIOR PELLOATION NUMBER: 60/231,498
PRIOR PELLON DATE: 2000-10-03
NUMBER OF SEQ ID NOS: 207012
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85.0%; Pred. No. 8.8e+02;
tive 0; Mismatches 3; Indels 0;
                                                                                                        Length 75929;
                                                                                                                                                           3; Indels
                                                                                                   Score 15.2; DB 3;
Pred. No. 8.8e+02;
0; Mismatches 3;
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; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-15544
; LOCATION: (1)...(75929)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-15543
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                                                                                                     Query Match
Best Local Similarity 85.0%;
Matches 17; Conservative
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US-09-949-016-13597/c
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ORGANISM: Human
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SEQ ID NO 13597
LENGTH: 98439
TYPE: DNA
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TYPE: DNA
ORGANISM: Human
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US-09-949-016-15952
    US-09-949-016-12080
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                                                                                   Query Match
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Patent No. 681239

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CL001307

CURRENT APPLICATION NUMBER: US/09/949,016

PRIOR PRILING DATE: 2000-04-14

PRIOR PELING DATE: 2000-10-20

PRIOR PILING DATE: 2000-10-20

PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-09-08

PRIOR PILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: PRACE FRACE FRACE

SOFTWARE: PRACE 
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APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
TITLE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: 06/241,755
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR PELING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOUTHARD FASTESEQ for Windows Version 4.0
SEQ ID NO 12080
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85.0%; Pred. No. 9e+02;
tive 0; Mismatches 3; Indels 0;
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76.0%; Score 15.2; DB 3; Length 98439;
Best Local Similarity 85.0%; Pred. No. 9e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0;
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2-09-99-10-12080/c
; Sequence 12080, Application US/09949016
; Patent No. 6812339
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                                                                           | NAME/KEY: misc_feature
| LOCATION: (1)...(98439)
| OTHER INFORMATION: n = A,T,C or G
| US-09-949-016-13597
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Best Local Similarity 85.0
Matches 17; Conservative
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US-09-949-016-15953
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US-09-949-016-15953
ORGANISM: Human
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ORGANISM: Human
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Sequence 15952, Application US/09949016

Sequence 15952, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:

PAPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REPERENCE: CL001307

CURRENT APPLICATION NUMBER: US/09/949,016

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR PLING DATE: 2000-10-20

PRIOR PLING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FRESEEQ for Windows Version 4.0

SEQ ID NO 15952

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76.0%; Score 15.2; DB 3; Length 119594; 85.0%; Pred. No. 9.1e+02;
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Pred. No. 9.1e+02;
0; Mismatches 3; Indels 0;
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0
                                  0; Mismatches
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| LOCATION: (1)...(153642)

| OTHER INFORMATION: n = A,T,C or G

US-09-949-016-12114
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85.0%;
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Best Local Similarity 85.04
Matches 17; Conservative
                 Best Local Similarity 85.03
Matches 17; Conservative
                                                                                                                                                   RESULT 84
US-09-949-016-15952/c
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TYPE: DNA
ORGANISM: Human
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APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: WITH HUMAN DISRASE, METHODS OF DETECTION AND USES THEREOF
TITLE OF INVENTION: WITH HUMAN DISRASE, METHODS OF DETECTION AND USES THEREOF
TITLE OF INVENTION: WITH HUMAN DISRASE, METHODS OF DETECTION AND USES THEREOF
TITLE OF INVENTION: UNDER: USOO-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-03
PRIOR PELING DATE: 2000-10-03
PRIOR PELING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SEQ ID NO 15635
LENGTH: 153643
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Patent No. 6812339

GENERAL INFORMATION:

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;

TITLE OF INVENTION NUMBER: 0000-04-14

CURRENT APPLICATION NUMBER: 60/241,755

PRIOR PILING DATE: 2000-10-03

PRIOR PLILING DATE: 2000-10-03

PRIOR PLILING DATE: 2000-10-03

PRIOR PLILING DATE: 2000-10-03

PRIOR PLILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012
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                                                                Gaps
                 Length 153642;
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               Score 15.2; DB 3;
Pred. No. 9.2e+02;
0; Mismatches 3;
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76.0%; Score 15.2; DB 3;
Best Local Similarity 85.0%; Pred. No. 9.2e+02;
Matches 17; Conservative 0; Mismatches 3;
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Patent No. 6812339
                                                                                                                              121010 AAGGAAACACACACACAA 121029
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; OTHER INFORMATION: n = A,T,C or
US-09-949-016-15635
                   76.0%;
Query Match
Best Local Similarity 85.0*
...hes 17; Conservative
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                                                                                                                                                                                                     RESULT 86
US-09-949-016-15635
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Human
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LENGTH: 455726
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| CERERAL INFORMATION:
| APPLICANT: VENTER, J. Craig et al.
| APPLICANT: VENTER, J. Craig et al.
| TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
| TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
| TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
| CURRENT APPLICATION NUMBER: 06/241,755
| PRIOR PLING DATE: 2000-10-20
| PRIOR PLING DATE: 2000-10-03
| PRIOR PLING DATE: 2000-10-03
| PRIOR PLING DATE: 2000-09-08
| NUMBER OF SEQ ID NOS: 207012
| SOFTWARE: FastSEQ for Windows Version 4.0
| SEQ ID NO 11940
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                                                                                                                                                          Gaps
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                                                                                                        Length 455726;
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85.0%; Pred. No. 9.4e+02;
tive 0; Mismatches 3; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 12, Application US/08361337
; Patent No. 5728519
; GENERAL INFORMATION:
APPLICANT: Levenbook, Inessa S.
APPLICANT: Chumakov, Konstantin M.
APPLICANT: Chumakov, Konstantin M.
APPLICANT: No. 5728519wood, Laurie P.
APPLICANT: Roninson, Igor
ITTLE OF INVENTION: ASSAY FOR VIRULENT REVERTANTS OF
ITTLE OF INVENTION: ATTENUATED LIVE VACCINES
NUMBER OF SEQUENCES: 77
CORRESPONDENCE ADDRESS:
                                                                                                                                                       Indels
                                                                                                   Score 15.2; DB 3;
Pred. No. 9.4e+02;
0; Mismatches 3;
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                                                                                                                                                                                                                                                                                                                                                       US-09-949-016-11940/c
; Sequence 11940, Application US/09949016
; Patent No. 6812339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 127 Peachtree Street, N.E. CITY: Atlanta
                                                                                                                                                                                                                                                      416568 AAGGAAACACACACACAAA 416549
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; LOCATION: (1)...(455726)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-14157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: (1). ... (481115)
OTHER INFORMATION: n = A,T,C or G
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                                                                                                      76.0%;
85.0%;
                                                                                                Query Match
Best Local Similarity 85.01
Matches 17; Conservative
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Matches 17; Conservative
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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Sequence 17361, Application US/09949016

Sequence 17361, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:

APPLICANT: WENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CLOO1307

CURRENT APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/231,768

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 17361
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REPERENCE: CLOO1307
CURRENT APPLICATION NUMBER: 05/241,755
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR PLING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR PLING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR PLING DATE: 2000-10-03
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US-09-621-976-1696/c
; Sequence 1696, Application US/09621976
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; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-17361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION: (1)...(767677)

OTHER INFORMATION: n = A,T,C or G
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Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
NAME/KEY: misc_feature
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LOCATION: (1)...(76767
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Human
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ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-949-016-12147
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OTHER INFORMATION: Coding sequence for the Maize RPA Large Subunit
OTHER INFORMATION: Homologue-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1, Application US/09396149
; Patent No. 6538176
; Fatent No. 6538176
; GENERAL INFORMATION:
    TITLE OF INVERTION: Maize Replication Protein A and Use
; TITLE REFERENCE: 5718-59
; CURRENT APPLICATION NUMBER: US/09/396,149
; CURRENT APPLICATION NUMBER: US/09/396,149
; CURRENT APPLICATION NUMBER: 1999-09-15
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 2497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            75.0%; Score 15; DB 2; Length 34; 100.0%; Pred. No. 4.9e+02; tive 0; Mismatches 0; Indels
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NAME/KEY: misc_feature
LOCATION: (0)...(0)
CTHER INFORMATION: Maize RPA Large subunit Homologue-1
US-09-396-149-1
                                       CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/361,337

FILING DATE:

CLASSIFICATION: 435

ATTONEY/AGENT INFORMATION:

NAME: PETYRATION NUMBER: 33,438

REGISTRATION NUMBER: 34,438

REGISTRATION NUMBER: 34,438

REFERENCE/DOCKET NUMBER: 34,438

TELEPOMMUNICATION INFORMATION:

TELEPOMMUNICATION INFORMATION:

TELEPAK: (404) 688-0770

INFORMATION FOR SEQ ID NO: 12:

SEQUENCE CHARACTERISTICS:

LENGTH: 34 base pairs

TYPE: nucleic acid

STRANDENESS: single
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US-09-949-016-12147
; Sequence 12147, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
                        OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: Other nucleic acid
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Best Local Similarity 100."
Matches 15; Conservative
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Matches 15; Conserva
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US-09-396-149-1/c
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Gaps

; 0

Score 14.8; DB 3; Length 751; Pred. No. 8.5e+02;

74.0%; 88.9%;

0; Mismatches

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TYPE: DNA CRGANISM: Drosophila melanogaster US-09-270-767-24010
                                                                                                                                                                                                            2 AGGAACACGGACACCCA 19
                                                                                                                                             Query Match 74.0
Best Local Similarity 88.9
Matches 16; Conservative
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Matches 16; Conserv
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US-09-023-655-195
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                                                                                                                                                                                                                                                                                        RESULT 96
US-09-023-655-195
                                                SEQ ID NO 24010
LENGTH: 751
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TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster FILLE REFERENCE: FILE REFERENCE: FILE REFERENCE: Tale Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: PatentIn Ver. 2.0
SEG ID NO 9728
LENGTH: 751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 24010, Application US/09270767

Patent No. 6703491

GENERAL INFORMATION:

APPLICANT: Homburger et al.

TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster FILE REPERENCE: File Reference: 7326-094

CURRENT APPLICATION NUMBER: US/09/270,767

CURRENT PILING DATE: 1999-03-17

NUMBER OF SEQ ID NOS: 62517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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Score 14.8; DB 3;
Pred. No. 8.3e+02;
0; Mismatches 2;
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Pred. No. 8.5e+02;
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                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: Von Heijne matrix
OTHER INFORMATION: score 5
OTHER INFORMATION: seq HLLAGFCVWVULG/WV
US-09-621-976-1656
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-270-767-8728/c
; Sequence 8728, Application US/09270767
; Patent No. 6703491
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; ORGANISM: Drosophila melanogaster
US-09-270-767-8728
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88.9%;
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Best Local Similarity 88.9%;
Matches 16; Conservative
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Best Local Similarity 88.9
Matches 16; Conservative
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                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                    LOCATION: 139..378
NAME/KEY: 8ig_peptide
LOCATION: 139..198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 95
US-09-270-767-24010/c
                                                                                                                                                                                                                                                                                                       NAME/KEY: CDS
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APPLICANT: Cocks, Benjamin G.
APPLICANT: Susan G. Stuart
APPLICANT: Susan G. Stuart
APPLICANT: Jeffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
TITLE OF INVENTION: EXPRESSION
NUMBER OF SEQUENCES: 1508
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,655
                                                                                                                                                                                                                                                                                                                                                                               E: INCYTE PHARMACEUTICALS, INC
3174 PORTER DRIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0001 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
                                                                                                                   Sequence 195, Application US/09023655
Patent No. 6607879
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTY.

ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
383 AGGAAACACCGCCACCCA 366
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (650) 855-0555
TELEPAX: (650) 845-4166
INPORMATION FOR SEQ ID NO: 195:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic acid
STRANDEDNESS: sing
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STATE: CALIFORNIA
COUNTRY: USA
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US-09-360B-38/C

US-09-599-360B-38/C

Sequence 38, Application US/0959360B

Patent No. 6548633

GENERAL INFORMATION:

APPLICANT: Dunas Milne Edwards, J.B.

APPLICANT: Dunas Milne Edwards, J.B.

APPLICANT: Bougueleret, L.

APPLICANT: Complementary DNA's Encoding Proteins with Signal Peptides

TITLE OF INVENTION: Complementary DNA's Encoding Proteins with Signal Peptides

TITLE OF INVENTION: Complementary DNA's Encoding Proteins with Signal Peptides

FILE REPERENCE: GENSET.050CP3

CURRENT APPLICATION NUMBER: US/09/599,360B

PRIOR PILING DATE: 1999-12-22

PRIOR PILING DATE: 1999-12-22

PRIOR FILING DATE: 1999-12-21

NUMBER OF SEQ ID NOS: 123

SOFTWARE: Patent.pm

SEQ ID NO 38

LENCHTH: 1888
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                                                                                                                                                                                                                                                                                                                                                                                                                      Length 1635;
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Pred. No. 9.2e+02;
0; Mismatches 2;
                                  PRIOR PELING DATE: 20011123
PRIOR PELING DATE: 1997-07-29
PRIOR PELING DATE: 1997-07-29
PRIOR APPLICATION NUMBER: GB 9615879.5
PRIOR PELING DATE: 1996-07-29
PRIOR PELING DATE: 1996-07-29
PRIOR PELING DATE: 1996-10-30
PRIOR PELING DATE: 1996-10-30
PRIOR PELING DATE: 1997-03-07
NUMBER OF SEQ ID NOS: 79
SEQ ID NO 12
LENGTH: 1635
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCATION: 139..1389
NAME/KEY: sig_peptide
LOCATION: 139..198
OTHER INFORMATION: Von Heijne matrix
OTHER INFORMATION: score 5.00
OTHER INFORMATION: seq HLLAGFCVWVUG/WV
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ilarity 88.9%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Homo Sapiens
FEATURE:
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Best Local Similarity
Matches 16; Conserval
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; NAME/KEY: polyA_site
; LOCATION: 1873...1888
US-09-599-360B-38
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Best Local Similarity
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                                       Sequence 3518, Application US/09107532A
Patent No. 6583275
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 12, Application US/09722377

Sequence 12, Application US/09722377

Patent No. 6791007

GENERAL INFORMATION:
APPLICANT: Schulze-Lefert, Paul MJ
APPLICANT: Schulze-Lefert, Paul MJ
APPLICANT: Buschges, Rainer
TITLE OF INVENTION: Polynucleotide and its use for modulating a defence TITLE OF INVENTION: response in plants
FILE REFERENCE: 620-58
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                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESSE:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
CITY: Waltham
                                                                                                                                                                                                                                                                                                                                                                                              CURRENT PEC
COMPUTER: PC
COMPATING SYSTEM: «Unknown»
SOFFWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 109/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAMB/KEY: misc_feature;
LOCATION: (B) LOCATION 1...1281;
SEQUENCE DESCRIPTION: SEQ ID NO: 3518:
US-09-107-532A-3518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Enterococcus faecium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (781)893-5007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (781) 893-8277
INFORMATION FOR SEQ ID NO: 3518:
SEQUENCE CHARACTERISTICS:
LENGTH: 1281 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: circular
MOLECTUE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     844 AAGGAAACAAGTACACCC 861
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                        STATE: Massachusetts
COUNTRY: USA
ZIP: 02354
COMPUTER READABLE FORM:
                                                                                                                                                                                       NUMBER OF SEQUENCES: 7310
RESULT 97
US-09-107-532A-3518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-722-377-12/c
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Matches
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Gaps
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LOCATION: (7, 90, 93, 115, 177, 183, 217, 249, 254, 272, 356, 357)
OTHER INFORMATION: n is a or g or c or t
                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: "misc_feature
LOCATION: (364, 1017, 1037, 1041, 1458, 1616, 1641, 1861, 1879)
OTHER INFORMATION: n is a or g or c or t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 74.0%; Score 14.8; DB 3; Length 2281; Best Local Similarity 88.9%; Pred. No. 9.6e+02; Matches 16; Conservative 0; Mismatches 2; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; NAME/KEY: misc_feature
; LOCATION: (1923, 2050)
... OTHER INFORMATION: n is a or g or c or t
US-09-722-377-6
                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Hordeum vulgare
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1294 AGGAACCACGGACATCCA 1277 g

2 AGGAAACACGGACACCCA 19

Search completed: March 8, 2006, 21:07:05 Job time : 91.9223 secs

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Perfect score:

Sequence:

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Scoring table:

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Database

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Sequence 65977, A Sequence 47447, A Sequence 47477, A Sequence 896, App Sequence 937, App Sequence 2211, App Sequence 366331, Sequence 544937, Sequence 544937,
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Sequence 260, App
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Sequence 58, Appl
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Sequence 361
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Sequence 6
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US-09-925-065A-287845
US-09-925-065A-216395
US-09-925-065A-19679
US-09-925-065A-19628
US-09-925-065A-19628
US-09-925-065A-19628
US-09-925-065A-19628
US-09-925-065A-19628
US-09-925-065A-19628
US-09-925-065A-1968
US-09-925-065A-1968
US-09-925-065A-366331
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US-09-925-065A-366331
US-09-925-065A-366331
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US-09-925-065A-138739
US-09-925-065A-138739
US-09-925-065A-138739
US-09-925-065A-138739
US-09-925-065A-1387398
US-10-750-185-513198
US-10-750-185-331398
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US-09-925-065A-697075
US-09-925-065A-697076
US-10-750-185-54418
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Sequence 13286, A
Sequence 187976,
Sequence 527437,
Sequence 527438,
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Sequence 21, Appl
Sequence 31, Appl
Sequence 138, App
Sequence 156382,
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Sequence 62571, A
Sequence 62571, A
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Sequence 3, Appli
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Sequence 15797,
                                                                             9, 2006, 00:29:05 ; Search time 435.728 Seconds (without alignments) 105.905 Million cell updates/sec
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Sequence 110, App Sequence 718646, Sequence 718637, Sequence 727006, Sequence 727007, Sequence 727007, Sequence 5651, App Sequence 255, App Sequence 255, App	sequence 1805, Ap sequence 1806, Ap sequence 43374, A sequence 43374, A sequence 57537, A sequence 57537, A sequence 26296, A sequence 26, Appl Sequence 172, Ap sequence 4672, Ap	Sequence 53159, A Sequence 61625, A Sequence 61625, A Sequence 41414, Ap Sequence 44141, Ap Sequence 40075, A Sequence 37228, A Sequence 37229, A Sequence 15986, A Sequence 37876, A Sequence 61932, A Sequence 679238, A Sequence 718288, A	Sequence 25534, A Sequence 25534, A Sequence 25534, A Sequence 18348, A Sequence 1005, Ap Sequence 11658, A Sequence 11658, A Sequence 670571, Sequence 67223, Sequence 672234, Sequence 702234, Sequence 702254, Sequence 116, App Sequence 71519, Sequence 72, Appl Sequence 71, Appl
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100 1100 1100 1100 1100 1100 1100 1100	321 6 US-09-925-065A-1805 326 8 US-09-925-065A-1806 326 8 US-10-750-185-43374 326 8 US-10-750-185-57537 340 8 US-10-750-623-57537 349 9 US-11-096-56BA-26296 374 12 US-11-091-883-26 400 12 US-11-091-883-172 400 12 US-11-091-883-172 407 7 US-10-932-182A-4672	549 8 US-10-750-185-51159 564 8 US-10-750-185-51159 565 8 US-10-750-185-61625 565 8 US-10-750-182-61625 563 7 US-10-932-182A-4414 700 8 US-10-932-182A-4414 710 8 US-10-925-065A-37229 712 6 US-09-925-065A-37229 713 6 US-09-925-065A-37229 714 0 US-10-925-065A-19139 715 8 US-11-096-568A-15986 717 0 US-10-925-065A-14115 718 9 US-11-096-568A-15986 719 1 US-10-925-065A-14115 719 1 US-10-925-065A-14115 719 1 US-10-925-065A-14119 719 1 US-10-932-182A-81392 818 6 US-10-932-182A-81392 818 6 US-09-925-065A-18288 719 0 US-09-925-065A-18288	1157 8 US-10-750-185-25534 420 8 US-10-750-185-25534 420 8 US-10-750-185-38348 420 8 US-10-750-185-38348 420 8 US-10-750-185-38348 420 8 US-10-750-185-31638 420 8 US-11-075-512-1005 425 8 US-11-075-212-1005 421 6 US-09-925-065A-670570 421 6 US-09-925-065A-670233 422 0 US-09-925-065A-670233 423 6 US-09-925-065A-670233 424 6 US-09-925-065A-670233 425 12 US-11-009-840A-416 425 12 US-11-009-840A-416 425 12 US-11-009-840A-416 426 US-09-925-065A-702254 426 US-09-925-065A-702254 426 US-09-925-065A-702254 426 US-09-925-065A-702919 427 US-11-009-840A-72 428 US-10-750-185-38712 428 US-10-750-185-38712 429 US-11-009-840A-72 420 US-11-009-840A-72 421 US-11-009-840A-72 422 US-11-009-840A-72 423 US-11-009-840A-72 424 US-11-009-840A-77 425 US-11-009-873A-72 426 US-11-009-873A-72 427 US-11-099-873A-77 428 US-10-932-182A-77170 428 US-10-932-182A-77170 429 US-10-932-182A-77170
4.2 71.0 1108 6 4.2 71.0 1108 6 4.2 71.0 1162 6 4.2 71.0 1170 6 4.2 71.0 1196 6 4.2 71.0 1237 9 4.2 71.0 1314 8 4.2 71.0 1314 8 4.2 71.0 1314 8	4.2 71.0 1321 6 US-09-925-065A-1805 4.2 71.0 1321 6 US-09-925-065A-1805 4.2 71.0 1326 8 US-10-750-185-43374 4.2 71.0 1340 8 US-10-750-185-57537 4.2 71.0 1340 8 US-10-750-623-57537 4.2 71.0 1340 9 US-11-096-568A-26296 4.2 71.0 1374 6 US-09-925-065A-553137 4.2 71.0 1374 12 US-11-091-883-17 4.2 71.0 1374 12 US-11-091-883-17 4.2 71.0 1400 12 US-11-091-883-17	71.0 1549 8 US-10-750-185-53159 71.0 1569 8 US-10-750-185-61625 71.0 1569 8 US-10-750-623-61625 71.0 1569 8 US-10-750-623-61625 71.0 1593 7 US-10-932-182A-4414 71.0 1700 8 US-10-750-185-40075 71.0 1700 8 US-10-750-185-40075 71.0 1732 6 US-09-925-065A-37228 71.0 1732 6 US-09-925-065A-37229 71.0 1732 6 US-09-925-065A-37229 71.0 1732 6 US-09-925-065A-37229 71.0 1791 6 US-10-925-065A-37115 71.0 1791 8 US-10-750-185-7876 71.0 1795 8 US-10-750-182-7876 71.0 1883 6 US-09-932-182A-81392 71.0 1883 6 US-09-932-065A-679238 71.0 1883 6 US-09-925-065A-679238 71.0 1883 6 US-09-925-065A-679239	4.2 71.0 2157 8 US-10-750-185-25534 4.2 71.0 2420 8 US-10-750-623-28534 4.2 71.0 2420 8 US-10-750-623-8348 4.2 71.0 2420 8 US-10-750-623-8348 4.2 71.0 2622 9 US-11-075-185-31638 4.2 71.0 2625 8 US-10-750-623-31638 4.2 71.0 2625 8 US-10-750-623-31638 4.2 71.0 2631 6 US-09-925-065A-670570 4.2 71.0 2860 6 US-09-925-065A-670234 4.2 71.0 2860 6 US-09-925-065A-672234 4.2 71.0 2860 6 US-09-925-065A-672234 4.2 71.0 2997 6 US-09-925-065A-672234 4.2 71.0 2997 6 US-09-925-065A-672234 4.2 71.0 2997 6 US-09-925-065A-672234 4.2 71.0 3939 9 US-11-245-147-13 71.0 3122 12 US-11-009-840A-416 71.0 3122 12 US-11-009-840A-416 71.0 3122 12 US-11-009-840A-716 71.0 3607 8 US-10-750-185-38712 71.0 3607 8 US-10-750-185-38712 71.0 3607 8 US-10-750-185-38712 71.0 3618 12 US-11-009-769A-72 71.0 4236 7 US-10-932-182A-77170 71.0 4236 7 US-10-932-182A-77170 71.0 4736 7 US-10-932-182A-77170

IBM Compatible

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1, 135, 136, 137, 138, 139, 167, 203, 224, 225, 231, 232,
                                                                                                                               DB 12; Length 810;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             85.0%; Score 17; DB 7; Length 415; ilarity 100.0%; Pred. No. 63; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: LEE, MING-CHOU
APPLICANT: KONG, LILLY
APPLICANT: GROEN, JAN
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING
TITLE OF INVENTION: RHINOVIRUSES
FILE REFERENCE: FOCS-003
                                                                                                                                                                        Indels
                                                                                                                          Query Match 92.0%; Score 18.4; I
Best Local Similarity 95.0%; Pred. No. 14;
Matches 19; Conservative 0; Mismatches
                 OTHER INFORMATION: human Enterovirus
OTHER INFORMATION: strain Coxakievirus B1
OTHER INFORMATION: accession number m16560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:

APPLICANT: Miles, Vincent J.

APPLICANT: Mathews, Michael B.

APPLICANT: Witherell, Gary

APPLICANT: Witherell, Gary

APPLICANT: Watherell, Gary

TITLE OF INVENTION: METHON FOR SELECTIVE

TITLE OF INVENTION: OF VIRAL REPLICATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/10/886,517A CURRENT FILING DATE: 2004-07-06
NUMBER OF SEQ ID NOS: 74
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                      US-10-886-517A-21/c

Sequence 21, Application US/10886517A

; Publication No. US20060008810A1

; GENERAL INFORMATION:
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Publication No. US20050265975A1
                                                                                                                                                                                                              1 AAGGAAACACGGACACCCAA 20
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: 1155 Avenue of the A
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie &
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Best Local Similarity
...(810)
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                                                                                   US-11-155-478A-137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-11-195-109-31/c
LOCATION: (1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: No COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EQ ID NO 21
LENGTH: 415
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APPLICANT: UNIVERSITE LAVAL
TITLE OF INVENTION: MOLECULES METHODS AND COMPOSITIONS FOR DETECTING AND QUANTIFYING
TITLE OF INVENTION: MOLECULES METHODS AND COMPOSITIONS FOR DETECTING AND QUANTIFYING
TITLE OF INVENTION: RESPIRATORY VIRUSES.
FILE REFERENCE: 6013-146018
CURRENT APPLICATION NUMBER: US/11/155,478A
CURRENT FILING DATE: 2005-05-06
PRIOR FILING DATE: 2002-12-19
PRIOR FILING DATE: 2003-01-24
PRIOR FILING DATE: 2003-01-24
PRIOR FILING DATE: 2003-12-19
NUMBER OF SEQ ID NOS: 174
SOFTWARE: RestSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: human Rhinovirus
OTHER INFORMATION: strain 14
OTHER INFORMATION: accession number k02121
                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/10/867,798
FILING DATE: 14-0u-2004
APPLICATION NUMBER: US/10/109,368
FILING DATE: 27-Mar-2002
APPLICATION NUMBER: US/08/221,816
FILING DATE: 01-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: COTUZZI, Laura A
REGISTRATION NUMBER: 30,742
REFERRICE/DOCKET NUMBER: 7960-030
TELECOMUNICATION INFORMATION:
                                                               APPLICATION NUMBER: US/11/195,109
FILING DATE: 01-Aug-2005
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 138, Application US/11155478A Publication No. US20060014140A1 GENERAL INFORMATION:
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100.0%; P
Matches 17; Conservative 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                            (212) 790-9090
(212) 869-8864
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 627 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA ORGANISM: human Rhinovirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Boivin, Guy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         JS-11-155-478A-138/c
                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE:
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Score 16.8; DB 6; Length 585; Pred. No. 83;
                                                                                                               0; Mismatches
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NAME/KEY: misc_feature

LOCATION: (5.1526)..(51526)

OTHER INFORMATION: n is a, c, g, or US-10-857-780-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                50345 ATGGAAACACGGGCACCCAA 50326
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                                                                                                                                                                                                 85 AAGGAACAGGGACAACCAA 104
                                                                                                                                                                                                                                                                                                                           Sequence 3, Application US/10857780 Publication No. US20050272043A1 GENERAL INFORMATION:
                                                                                                                                                             1 AAGGAAACACGGACACCCAA 20
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                                                                   84.0%;
90.0%;
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Best Local Similarity 90.0%;
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: misc feature
LOCATION: (51510)..(51510)
OTHER INFORMATION: n is a,
                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA ORGANISM: Homo sapiens
                                                                                    Best Local Similarity
Matches 18; Conserv
                     US-09-925-065A-156383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 147700
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                                                                 Query Match
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                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: Identification and Mapping of Single
FILE REFERENCE: 108827.135
CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT PILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR PILING DATE: 2000-11-20
PRIOR PAPLICATION NUMBER: US 60/250,092
PRIOR PAPLICATION NUMBER: US 60/261,766
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR PRIOR DATE: 2001-01-16
PRIOR PILING DATE: 2001-01-16
PRIOR PILING DATE: 2001-01-16
PRIOR PRIOR SPELICATION NUMBER: US 60/289,846
PRIOR FILING DATE: 2001-01-16
SECTION NUMBER OF SECTION NUMBER: US 60/289,846
SOFTWARRE: PRAESEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nuclectide Polymorphisms in the Human Genome
FILE REFERENCE: 108827.135
CURRENT APPLICATION NUMBER: US/09/925.065A
CURRENT FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR PILING DATE: 2000-11-20
PRIOR FILING DATE: 2000-11-30
PRIOR FILING DATE: 2000-11-30
PRIOR FILING DATE: 2001-10-30
PRIOR FILING DATE: 2001-01-30
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                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2; Indels
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0
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                                              Mismatches
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SOFTWARE: FastSEQ for Windows Version 4.0
                     Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 156383, Application US/09925065A Publication No. US20040181048A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                    Sequence 156382, Application US/09925065A Publication No. US20040181048A1
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100.08; L
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                                                                                         4 GAAACACGGACACCCAA 20
                                                                                                                                  92 GAAACACGGACACCCAA 76
                   Similarity 100.
17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 90.0
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                           RESULT 5
US-09-925-065A-156382
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US-09-925-065A-156383
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LENGTH: 585
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                   Best Local
Matches 1
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CHARLY INCURRANT INCURATION:
CHARL INCURRANT INCURATION:
APPLICANT: RAWMERER, STEFAN M.
APPLICANT: RAWMERER, STEFAN M.
APPLICANT: RAWMERER, STEFAN M.
APPLICANT: REMEMBER, STEFAN M.
APPLICANT: REMEMBER, RIKARD HENRY
TITLE OF INVENTION: METHODS FOR IDENTIFYING RISK OF BREAST CANCER AND TREATMENTS;
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
CURRENT FILING DATE: 2004-05-28
PRIOR APPLICATION NUMBER: 10/723,681
PRIOR APPLICATION NUMBER: 60/490,234
PRIOR FILING DATE: 2003-11-25
PRIOR APPLICATION NUMBER: 60/55,239
PRIOR FILING DATE: 2003-11-25
NUMBER OF SEQ ID NOS: 4962
SOFTWARE PRICE PRICE AND SECONDERS.
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  Gaps
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Pred. No. 1.9e+02;
0; Mismatches 2; Indels 0;
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Publication No. US20060003352A1

GENERAL INFORMATION:

APPLICANT: Lipkin, W. Ian

APPLICANT: Tipkin, W. Ian

APPLICANT: Thomas, Briese

TITLE REFERENCE: 0575/71310-A

CURRENT APPLICATION NUMBER: US/11/119,231

CURRENT FILING DATE: 2005-04-28

NUMBER OF SEQ ID NOS: 131

SOFTWARE: Patentin version 3.1
Indels
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88 AAGGAAAGACGCASACCCAA 107

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LENGTH: 25

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; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-124-367A-15797
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US-11-124-367A-33200
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                                                                                                                           Length 25;
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                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Lipkin, W. Ian
APPLICANT: Lipkin, W. Ian
APPLICANT: Thomas Briese
TITLE CANT: Thomas Briese
FILE REPERENCE: 0575/71310-A
CURRENT APPLICATION NUMBER: US/11/119,231
CURRENT APPLICATION DATE: 2005-04-28
NUMBER OF SEQ ID NOS: 131
SOFTWARE: Patentin version 3.1
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                                                                                                                                                                    Indels
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TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG REI
TITLE OF INVENTION: DETECTION AND USES THEREOF
PILE REFERENCE: CL001559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       83.0%; Score 16.6; DB 12; 94.1%; Pred. No. 66;
                                                                                                                           DB 12;
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                                                         ; OTHER INFORMATION: REVERSE PRIMER FOR ENTEROVIRUS US-11-119-231-48
                                                                                                                       Query Match 83.0%; Score 16.6; I
Best Local Similarity 94.1%; Pred. No. 66;
Matches 16; Conservative 1; Mismatches
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CURRENT FILING DATE: 2004-11-24
NUMBER FILING NOS: 85702
SOFTWARE: PASTSEQ for Windows Version 4.0
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Publication No. US20050272054A1
GENERAL INFORMATION:
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Publication No. US20060003352A1
GENERAL INFORMATION:
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TYPE: DNA
ORGANISM: ARTIFICIAL SEQUENCE
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Matches 16; Conservative
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; ORGANISM: Homo sapiens
US-10-995-561-41106
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LENGTH: 201
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LENGTH: 25
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                                          FEATURE:
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TITLE OF INVENTION: Genetic Polymorphisms Associated with
CURRENT APPLICATION NUMBER: US/11/124,367A
CURRENT APPLICATION NUMBER: US 60/568,846
PRIOR PILING DATE: 2004-05-07
PRIOR FILING DATE: 2004-06-07
PRIOR FILING DATE: 2004-06-25
PRIOR FILING DATE: 2004-06-25
PRIOR FILING DATE: 2004-06-09
NUMBER: OS SEQ ID NOS: 34460
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 33200
                                                                                                                 APPLICANT: Michele Cargill
APPLICANT: Hongin Huang
TITLE OF INVENTION: Genetic Polymorphisms Associated with
TITLE OF INVENTION: Genetic Polymorphisms Associated with
TITLE OF INVENTION: Genetic Polymorphisms Associated with
TITLE OF INVENTION: Through Methods of Detection and Uses Thereof
FILE REFERENCE: CL001519.ORD
CURRENT APPLICATION NUMBER: US/11/124,367A
CURRENT FILING DATE: 2005-05-09
PRIOR APPLICATION NUMBER: US 60/568,846
PRIOR PILING DATE: 2004-05-07
PRIOR PAPLICATION NUMBER: US 60/599,554
PRIOR APPLICATION NUMBER: US 60/599,554
PRIOR APPLICATION NUMBER: US 60/599,554
PRIOR APPLICATION NUMBER: US 60/599,554
SPRIOR PILING DATE: 2004-08-09
NUMBER OF SEQ ID NOS: 34460
SEQ ID NO 15797
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85.0%; Pred. No. 1.1e+02;
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Pred. No. 1.1e+02;
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US-11-124-367A-15797/c
; Sequence 15797, Application US/11124367A
; Publication No. US20060024700A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 33200, Application US/11124367A Publication No. US20060024700A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 AAGGAAACACGGACACCCAA 20
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Best Local Similarity 94.4%;
Matches 17; Conservative
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28555 AGGAACACGCAGACCCA 28538
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; ORGANISM: Bovine 19866881638593
US-10-750-623-62571
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il Similarity 94.4%;
17; Conservative
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US-11-124-367A-5040
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Best Local Similarity
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US-11-124-367A-5040/c
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            Sequence 319374, Application US/09925065A;
Publication No. US20040181048A1
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
FILE REFERENCE: 108827.135
CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2001-08-08
FRIOR FILING DATE: 2000-10-24
PRIOR FILING DATE: 2000-11-20
FRIOR APPLICATION NUMBER: US 60/252,147
FRIOR APPLICATION NUMBER: US 60/250,092
FRIOR APPLICATION NUMBER: US 60/261,766
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; Publication No. US2050260603A1
; GENERAL INPORMATION:
APPLICANT: MMI GENOMICS, INC.
APPLICANT: DANISE, Sue K.
; APPLICANT: RERR, RIChard
APPLICANT: ROSENFELD, David
APPLICANT: HOLM, Tom
APPLICANT: HATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REPREBNICE: MMILLOO-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 82.0%; Score 16.4; DB 6; Length 578; Best Local Similarity 94.4%; Pred. No. 1.38+02; Matches 17; Conservative 0; Mismatches 1; Indels C
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Pred. No. 1.4e+02;
0; Mismatches 1; Indels (
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CURRENT FILING DATE: 2003-12-31
PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR FILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
SOFTWARE: PatentIN version 3.1
LENGTH: 778
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; ORGANISM: Bovine 19866881638593
US-10-750-185-62571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          300 AAGGAAACACGTACACCC 317
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Best Local Similarity 94.4%;
Matches 17; Conservative
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CORGANISM: Homo sapiens
US-09-925-065A-319374
US-09-925-065A-319374
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Sequence 5040, Application US/11124367A;
Publication No. US20060024700A1
GENERAL INFORMATION:
APPLICANT: Michele Cargill
APPLICANT: Hichele Cargill
APPLICANT: Hongjin Huang
TITLE OF INVENTION: Fibrosis Methods of Detection and Uses Thereof
TITLE OF INVENTION: Fibrosis Methods of Detection and Uses Thereof
TITLE OF INVENTION: Fibrosis Methods of Detection and Uses Thereof
TITLE OF INVENTION: FORDS: C1001519.ORD
CURRENT APPLICATION NUMBER: US 60/589,846
PRIOR FILING DATE: 2004-05-05
PRIOR FILING DATE: 2004-06-05
PRIOR FILING DATE: 2004-06-09
PRIOR FILING DATE: 2004-08-09
NUMBER OF SEQ ID NOS: 34460
SOFTWARE: FREESEQ for Windows Version 4.0
SEQ ID NO 5040
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                                                             Gaps
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Query Match 82.0%; Score 16.4; DB 8; Length 778; Best Local Similarity 94.4%; Pred. No. 1.4e+02; Matches 17; Conservative 0; Mismatches 1; Indels C
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Pred. No. 2.5e+02;
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Gaps
                                                TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
FILE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2001-08-08
FRIOR FILING DATE: 2000-10-24
FRIOR FILING DATE: 2000-11-20
FRIOR FILING DATE: 2000-11-30
FRIOR FILING DATE: 2000-11-30
FRIOR FILING DATE: 2000-11-30
FRIOR FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Mouleotide Polymorphisms in the Human Genome
FILE REFERENCE: 108827.135
CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR FILING DATE: 2000-10-24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 15.8; DB 6;
Pred. No. 2.5e+02;
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Pred. No. 2.5e+02;
0; Mismatches 2;
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PRIOR FILING DATE: 2000-11-20
PRIOR FILING DATE: 2000-11-30
PRIOR PELICATION NUMBER: US 60/250,092
PRIOR PELICATION NUMBER: US 60/261,766
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR PILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-01-05-09
NUMBER OF SEQ ID NOS: 957086
SOFTWARE: FRSESEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 957086
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 527437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 527438, Application US/09925065A Publication No. US20040181048A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               383 AGGAAACACGCACACCCTA 365
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 79.0%;
Best Local Similarity 89.5%;
Matches 17; Conservative
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Best Local Similarity 89.5%;
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; ORGANISM: Homo sapiens
US-09-925-065A-527437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
CORGANISM: Homo sapiens
US-09-925-065A-527438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 20
JS-09-925-065A-527438/c
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US-09-925-065A-287845/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: FastSI
SEQ ID NO 527438
LENGTH: 449
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    NAME/KEY: misc_feature
    LOCATION: (1)...(1125000)
    OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-US-10-995-561-13286

TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
TITLE OF INVENTION: DETECTION AND USES THEREOF
FILE REFERENCE: CLOO1559
CURRENT APPLICATION NUMBER: US/10/995,561
CURRENT FILING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 8570-2
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 13286
LENGTH: 1125000
TYPE: NON
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TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
CURRENT FILID STATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR FILING DATE: 2000-11-20
PRIOR PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR PRIOR APPLICATION NUMBER: US 60/260,092
PRIOR APPLICATION NUMBER: US 60/269,846
PRIOR APPLICATION NUMBER: US 60/269,846
PRIOR APPLICATION NUMBER: US 60/289,846
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
SOFTWARE: FasteSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                82.0%; Score 16.4; DB 8; Length 1125000;
85.0%; Pred. No. 3.6e+02;
tive 1; Mismatches 2; Indels 0;
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Pred. No. 2.2e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 187976, Application US/09925065A Publication No. US20040181048A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 527437, Application US/09925065A Publication No. US20040181048A1
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89.5%;
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Best Local Similarity 85.0'
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Best Local Similarity 89.5
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-187976
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 19
US-09-925-065A-527437/c
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1 AAGGAAACACGGACACCCA 19
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Best Local Similarity 89.5
Matches 17; Conservative
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US-09-925-065A-187867
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US-09-925-065A-708503
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Sequence 287845, Application US/09925065A
Fublication No. US20040181048A1
GENERAL INFORMATION:
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
FILE REFERENCE: 10897.135
CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2001-08-08
FRIOR FILING DATE: 2000-11-20
FRIOR APPLICATION NUMBER: US 60/252,147
FRIOR PILING DATE: 2000-11-30
FRIOR APPLICATION NUMBER: US 60/261,766
FRIOR APPLICATION NUMBER: US 60/26
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Fublication No. US20040181048A1

GENERAL INFORMATION:

APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single

TITLE OF INVENTION: Identification and Mapping of Single

TITLE OF INVENTION: Identification and Mapping of Single

TITLE OF INVENTION: NUALectide Polymorphisms in the Human Genome
FILE REFERENCE: 108827.135

CURRENT APPLICATION NUMBER: US 60/255, 065A

FRIOR APPLICATION NUMBER: US 60/252,147

FRIOR FILING DATE: 2000-11-20

FRIOR FILING DATE: 2000-11-30

FRIOR FILING DATE: 2000-11-30

FRIOR FILING DATE: 2001-01-16

FRIOR FILING DATE: 2001-05-09

FRIOR FILING DATE: 2001-05-09
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
79.0%; Score 15.8; DB 6;
Best Local Similarity 89.5%; Pred. No. 2.6e+02;
Matches 17; Conservative 0; Mismatches 2;
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US-09-925-065A-287845
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; ORGANISM: Homo sapiens
US-09-925-065A-216395
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                                                             GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nuclectide Polymorphisms in the Human Genome
FILE REFERENCE: 108627.135
CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR PILING DATE: 2000-11-30
PRIOR PILING DATE: 2001-01-16
PRIOR PILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 187867
LENGTH: 560
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GENERAL INFORMATION:
GENERAL INFORMATION:
ITILE OF INVENTION: Identification and Mapping of Single
ITILE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
FILE REFERENCE: 108827.135
CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT APPLICATION NUMBER: US 60/243,096
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR APPLICATION NUMBER: US 60/250,147
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR PILING DATE: 2000-11-30
PRIOR PILING DATE: 2001-11-30
PRIOR PILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 708503
LENGTH: 632
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 15.8; DB 6; Length 560;
Pred. No. 2.6e+02;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 15.8; DB 6;
Pred. No. 2.7e+02;
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Sequence 187867, Application US/09925065A Publication No. US20040181048A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 708503, Application US/09925065A Publication No. US20040181048A1 GENERAL INFORMATION:
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89.5%;
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Best Local Similarity 89.5%;
Matches 17; Conservative
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Gaps

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Indels

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0; Mismatches
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; Sequence 65977, Application US/09925065A
; Publication No. US20040181048A1
                                                                                                                                                                                             553 AAGTAAACAAGGACACCCA 571
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                                                                                                          1 AAGGAAACACGGACACCCA 19
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Best Local Similarity 89.5
Matches 17; Conservative
             17; Conservative
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US-09-925-065A-722637
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US-09-925-065A-65977
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             Matches
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APPLICART: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Sin;
TITLE OF INVENTION: Muclectide Polymorphisms in the
FILE REFERENCE: 108827.135
CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT PILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR FILING DATE: 2000-11-20
PRIOR FILING DATE: 2000-11-30
PRIOR FILING DATE: 2001-10-16
PRIOR FILING DATE: 2001-10-16
PRIOR FILING DATE: 2001-10-16
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-01-16
PRIOR REPLICATION NUMBER: US 60/289,846
PRIOR FILING DATE: 2001-01-16
PRIOR REPLICATION NUMBER: US 60/289,846
PRIOR REPLICATION UNMBER: US 60/289,846
PRIOR REPLICATION NUMBER: US 60/289,846
PRIOR REPLICATION NUMBER: US 60/289,846
PRIOR REPLICATION NUMBER: US 60/289,846
PRIOR REPLICATION UNMBER: US 60/289,846
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                       Sequence 136278, Application US/09925065A Publication No. US20040181048A1
155 AGGGAACAGGGACACCCAA 173
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89.5%;
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Matches 17; Conservative
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; ORGANISM: Homo sapiens
US-09-925-065A-879054
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Homo sapiens
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Best Local Similarity
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USCALLAGE TO SECULDATION OF SECULDATION OF SECULDATION OF SECULDATION OF USCOQUIBIO48A1

| Publication No. USCOQUIBIO48A1
| GENERAL INFORMATION:
| APPLICANT: WANG, DAVIG G.
| TITLE OF INVENTION: Uncleotide Polymorphisms in the Human Genome ITILE OF INVENTION: Nucleotide Polymorphisms in the Human Genome FILE REFERENCE: 108827.135
| CURRENT APPLICATION NUMBER: US (09/925,065A)
| CURRENT APPLICATION NUMBER: US 60/243,096
| PRIOR APPLICATION NUMBER: US 60/243,096
| PRIOR PILING DATE: 2000-10-24
| PRIOR APPLICATION NUMBER: US 60/250,147
| PRIOR APPLICATION NUMBER: US 60/250,092
| PRIOR PILING DATE: 2000-11-16
| PRIOR PILING DATE: 2001-01-16
| PRIOR PAPLICATION NUMBER: US 60/289,846
| SOFTWARE: PREASED for Windows Version 4.0
| SEC ID NO 722637
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TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
FILE REFERENCE: 100827,135
CURRENT PAPLICATION NUMBER: US/09/925,065A
CURRENT PALING DATE: 2001-08-08
PRIOR FILING DATE: 2000-10-24
PRIOR PILING DATE: 2000-11-30
PRIOR PILING DATE: 2000-11-30
PRIOR PILING DATE: 2000-11-30
PRIOR PILING DATE: 2001-11-6
PRIOR FILING DATE: 2001-01-6
PRIOR PRIOR DATE: 2001-01-6
PRIOR PRIOR DATE: 2001-01-6
PRIOR PRIOR DATE: 2001-01-6
PRIOR PILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
SOFTWARE: FastSEQ for Windows Version 4.0
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Pred. No. 2.8e+02;
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Ouery Match 79.0%; Score 15.8; DB 7; Length 137454; Best Local Similarity 89.5%; Pred. No. 5.7e+02; Matches 17; Conservative 0; Mismatches 2; Indels 0;
                                                                                                                                                                                            Sequence 896, Application US/10330773

Publication No. US20060040262A1

GENERAL INFORMATION:

APPLICANT: DAVIG W. Morris

APPLICANT: Marc Malandro

TITLE OF INVENTION: Novel Compositions and Methods in Cancer

FILE REFERENCE: 529452001300

CURRENT APPLICATION NUMBER: US/10/330,773

CURRENT FILING DATE: 2002-12-27

NUMBER OF SEQ ID NOS: 981

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 896

LENGTH. 98638
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APPLICANT: David W. Morris
APPLICANT: Marc Malandro
TITLE OF INVENTION: Novel Compositions and Methods in Cancer
FILE REFERENCE: 529452010300
CURRENT APPLICATION NUMBER: US/10/330,773
CURRENT FILING DATE: 2002-12-27
NUMBER OF SEQ ID NOS: 981
SEQ ID NO 365
LENGTH: 137454
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  0; Mismatches
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Publication No. US20060040262A1
GENERAL INFORMATION:
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                                                                                         2887 AAGGACACAGGGACACCCA 2869
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LOCATION: (1)...(98638)
OTHER INFORMATION: n = A,T,C or G
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                                                1 AAGGAAACACGGACACCCA 19
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17; Conservative
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Matches
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Sequence 47477, Application US/10750623
Publication No. US20050287531A1
GENERAL INFORMATION:
APPLICANT: MAI GENOMICS, INC.
APPLICANT: RERR, Richard
APPLICANT: ROBINEED, David
APPLICANT: ROBINEED, David
APPLICANT: FANTIN, Dennis
APPLICANT: FANTIN, Dennis
APPLICANT: FANTIN, Dennis
APPLICANT: MAITON: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
FILE REPERBENCE: MAILIO-1
CURRENT APPLICATION NUMBER: US/10/750,623
CURRENT APPLICATION NUMBER: US 60/437,482
PRIOR FILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
SOFTWARE: PatentIN version 3.1
SEQ ID NO 47447
LENGTH 3908
                                                                   Gaps
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US-10-750-185-47447/C
Sequence 4747, Application US/10750185
Publication No. US20050260603A1
GENERAL INFORMATION:
APPLICANT: MMI GENOMICS, INC.
APPLICANT: MERR, Richard
APPLICANT: ROSENFELD, David
APPLICANT: HOLM, Tom
APPLICANT: HOLM, Tom
APPLICANT: HOLM, Tom
APPLICANT: HOLM, Tom
APPLICANT: PANTIN, Dennis
TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
FILE REFERENCE: MMILLOU-2
CURRENT FILING DATE: 2003-12-31
FRICR APPLICATION NUMBER: US/10/750,185
CURRENT FILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
SEQ ID NO 47447
FUENCH: NANA
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                     79.0%; Score 15.8; DB 6; Length 1463; 89.5%; Pred. No. 3e+02; 1ve 0; Mismatches 2; Indels 0;
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                                                                                                                                                   246 AAGGAAGCACGGACACTCA 228
                                                                                                                 1 AAGGAAACACGGACACCCA 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 AAGGAAACACGGACACCCA 19
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; ORGANISM: Bovine 19866880584558
US-10-750-623-47447
                Query Match 79.03
Best Local Similarity 89.53
Matches 17; Conservative
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Best Local Similarity
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US-10-750-623-47447/c
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Indels
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Pred. No. 4.1e+02;
); Mismatches 1;
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  PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/289,846
PRIOR FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
SOFTWARE: FREESEQ for Windows Version 4.0
SEQ ID NO 86331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR PILING DATE: 2000-11-30
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/289,846
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-05-09
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SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 366333, Application US/09925065A
Publication No. US20040181048A1
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PRIOR PEPLICATION NUMBER: US 60/243,096
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 60/252,147
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94.1%;
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Best Local Similarity 94.1
Matches 16; Conservative
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Best Local Similarity 94.1%
                                                                                                                                                                                                      ORGANISM: Homo sapiens
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US-09-925-065A-366333
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SEQ ID NO 366333
LENGTH: 537
                                                                                                                                                                                    TYPE: DNA
                                                                                                                                                               LENGTH:
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Publication No. US20040181048A1
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
FILE REPERENCE: 108927.135
CURRENT APPLICATION NUMBER: US/09/925,065A
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                                                                                                                                                                                                                                                                                                                                                                                   Length 390183;
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2.9e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2211, Application US/11175859
Publication No. US20060024715A1
GENERAL INFORMATION:
APPLICANT: Affymetrix, Inc.
APPLICANT: Liu, Guoying et al.
TITLE OF INVENTION: Method of Analysis of Human Polymorphism
FILE REPERENCE: 36901
CURRENT APPLICANTION WUMBER: US/11/175,859
CURRENT FILING DATE: 2005-07-05
                       Compositions and Methods in Cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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Pred. No. 6
                                       FILE REFERENCE: 529452001300
CURRENT APPLICATION NUMBER: US/10/330,773
CURRENT FILING DATE: 2002-12-27
NUMBER OF SEQ ID NOS: 981
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 937
LENGTH: 390183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: US 60/585,352 PRIOR FILING DATE: 2004-07-02 NUMBER OF SEQ ID NOS: 116251 SOFTWARE: Patentin version 3.2 SEQ ID NO 2211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR FILING DATE: 2000-10-24
PRIOR PELING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR PLING DATE: 2000-11-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                228440 AGGAAACCCGGACACTCAA 228422
                                                                                                                                                                                                                                                                                    ; LOCATION: (1) ... (390183)
; OTHER INFORMATION: n = A,T,C or G
US-10-330-773-937
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Best Local Similarity 89.5%;
Matches 17; Conservative
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il Similarity 94.1%;
16; Conservative (
                                                                                                                                                                                                                      ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                NAME/KEY: misc_feature
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; ORGANISM: homo sapien
US-11-175-859-2211
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Best Local Similarity
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                                                                                                                                                                                                 TYPE: DNA
APPLICANT:
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Gaps
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APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Mucleotide Polymorphisms in the Human Genome
FILE REFERENCE: 108827.135
CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT APPLICATION NUMBER: 2001-08-08
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TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
FILE REFERENCE: 108827.135
CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2001-08-08
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Length 537;
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TYPE: DNA ORGANISM: Artificial Sequence
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Sequence 2902, Application US/11124368A;
Publication No. US20050287559A1
GENERAL INFORMATION:
APPLICANT: Michele Cargill
APPLICANT: James J. Devlin
APPLICANT: May Luke
TITLE OF INVENTION: Vascular Diseases, Methods of Detection and Uses Thereof
TITLE OF INVENTION: Vascular Diseases, Methods of Detection and Uses Thereof;
TITLE OF INVENTION: Vascular Diseases, Methods of Detection and Uses Thereof;
CURRENT APPLICATION NUMBER: US/11/124,368A;
CURRENT APPLICATION NUMBER: US 60/568,845;
PRIOR APPLICATION NUMBER: US 60/625,936;
PRIOR APPLICATION NUMBER: US 60/625,936;
NUMBER OF SEQ ID NOS: 21112;
SOFTWARE: FastSEQ for Windows Version 4.0
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Publication No. US2005287570A1

GENERAL INFORMATION:

APPLICANT: Wyeth

APPLICANT: Wyeth

TITLE OF INVENTION Probe Arrays For Expression Profiling of Rat Genes

TITLE OF INVENTION NUMBER: US/11/136,527

CURRENT APPLICATION NUMBER: US 60/574,294

PRIOR PILING DATE: 2005-05-26

NUMBER OF SEQ ID NOS: 362830

SOFTWARE: Patentin version 3.2

SEQ ID NO 1862

LENGTH: 4562
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                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 77.0%; Score 15.4; DB 6; Length 620; Best Local Similarity 94.1%; Pred. No. 4.2e+02; Matches 16; Conservative 0; Mismatches 1; Indels
PRIOR FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR FILING DATE: 2000-11-30
PRIOR FILING DATE: 2001-11-30
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 544937
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA ORGANISM: Rattus norvegicus
                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Homo sapiens
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US-11-124-368A-2902/c
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Sequence 49, Application US/11114798

Publication No. US20060035246A1

GENERAL INFORMATION:

APPLICANT: WU, RINA

APPLICANT: WARQUEZ, ABBEY

TITLE OF INVENTION: COMPOSITIONS

FILE REFERENCE: 0618.011.004

CURRENT APPLICATION NUMBER: 10014

CURRENT FILING DATE: 2005-04-26

PRIOR FILING DATE: 2002-06-17

PRIOR FILING DATE: 2002-06-17

PRIOR FILING DATE: 2001-09-14

NUMBER OF SEQ ID NOS: 58

SOFTWARE: PATCHING DAYE: 301-09-14

SOFTWARE: PATCHING DAYE: 301-09-14

SOFTWARE: PATCHING DAYE: 301-09-14

MUMBER OF SEQ ID NOS: 58

SEQ ID NO 49

LENGTH: 121736
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APPLICANT: WARQUEZ, ABBEY
TITLE OF INVENTION: CHROMOGENIC IN SITU HYBRIDIZATION METHODS, KITS, AND
TITLE OF INVENTION: COMPOSITIONS
TITLE OF INVENTION: COMPOSITIONS
FILE REFERENCE: 0618.011.0004
CURRENT APPLICATION NUMBER: US/11/114,798
CURRENT FILING DATE: 2005-06-16
PRIOR PILING DATE: 2002-06-17
PRIOR APPLICATION NUMBER: 09/952,851
PRIOR APPLICATION NUMBER: 09/952,851
PRIOR FILING DATE: 2001-09-14
NUMBER OF SEQ ID NOS: 58
SOFTWARE: Patentin Ver: 3.3
SEQ ID NO 58
FILING APPLICATION NUMBER: US/152
FILING DATE: 2001-09-14
SOFTWARE: Patentin Ver: 3.3
FILING PATE: 2001-09-14
FILING 
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; SEQ ID NO 2902
; LENGTH: 94035
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-124-368A-2902
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; TYPE: DNA
; ORGANISM: Human papillomavirus type 45
US-10-500-831-260
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US-10-310-914A-143
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                                                                                                                                                                                                                                                                                                                                       US-10-310-914A-143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: NELSON, MATTHEW ROBERTS
APPLICANT: RENELAND, RIKARD HENRY
APPLICANT: HOYAL-WIGHTSON, CAROLTN R.
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
CURRENT APPLICATION NUMBER: US/10/857,780
CURRENT APPLICATION NUMBER: US/10/857,780
CURRENT PILING DATE: 2004-05-28
PRIOR APPLICATION NUMBER: 60/490,234
PRIOR FILING DATE: 2003-11-25
PRIOR FILING DATE: 2003-07-24
PRIOR FILING DATE: 2003-11-25
NUMBER OF SEQ ID NOS: 4962
SEQ ID NOS: 4962
SEQ ID NOS: 4962
SEQ ID NO 1527
LENGTH: 30
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                      OTHER INFORMATION: Description of Artificial Sequence: Synthetic; OTHER INFORMATION: nucleotide sequence US-11-114-798-58
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| Publication No. US20050244813A1
| GENERAL INFORMATION:
| TITLE OF INVENTION: DETECTION OF HUMAN PAPILLCMAVIRUS E6 mRNA
| TITLE RF INVENTION: DETECTION OF HUMAN PAPILLCMAVIRUS E6 mRNA
| FILE REFERENCE: B0192.70052US00
| CURRENT APPLICATION NUMBER: US/10/500,831
| CURRENT FILING DATE: 2004-07-07
| PRIOR PLING DATE: 2002-01-07
| PRIOR PLING DATE: 2002-01-07
| PRIOR PLING DATE: 2002-01-07
| PRIOR PRIOR DATE: 2002-01-07
| NUMBER OF SEQ 1D NOS: 387
| SOFTWARE: PatentIn version 3.2
                                                                                                               / Match 77.0%; Score 15.4; DB 9; Length 318488; Local Similarity 94.1%; Pred. No. 9.7e+02; Ass. 16; Conservative 0; Mismatches 1; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                              Sequence 1527, Application US/10857780
Publication No. US20050272043A1
GENERAL INFORMATION:
APPLICANT: ROTH, RICHARD B.
APPLICANT: BRAUN, ANDREAS
APPLICANT: KAMMERER, STEFAN M.
APPLICANT: NELSON, MATTHEW ROBERTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; OTHER INFORMATION: Synthetic primer US-10-857-780-1527
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US-10-500-831-260
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Best Local S:
Matches 16
FEATURE:
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Sequence 143, Application US/10310914A
Publication No. US20060003322A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Kvuzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof
FILE REPERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT PILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: PatentIn version 3.3
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APPLICANT: Twine, Natalie
APPLICANT: Dorner, Andrew
APPLICANT: Trepicchio, William
TITLE OF INVENTION: Method for Monitoring Drug Activities In Vivo
FILE REFERENCE: AMI01080 (031896-013000)
CURRENT APPLICATION NUMBER: US/10/775,169
CURRENT FILING DATE: 2004-02-11
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  Length 55;
                                                  3; Indels
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Pred. No. 3.8e+02;
0; Mismatches 3;
Query Match 76.0%; Score 15.2; DB 8; Best Local Similarity 85.0%; Pred. No. 3.7e+02; Matches 17; Conservative 0; Mismatches 3;
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Publication No. US20050287532A9
GENERAL INFORMATION:
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SOFTWARE: Patentin version 3.2
SEQ ID NO 361
LENGTH: 81
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Best Local Similarity 85.0%;
Matches 17; Conservative
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Best Local Similarity 85.09
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US-10-775-169-361
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PRIOR APPLICATION NUMBER: US 60/250, 092
PRIOR FILING DATE: 2000-11-30
PRIOR PILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-01-16
PRIOR PILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
SEQ ID NO 102175
LENGTHARE: PastSEQ for Windows Version 4.0
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Best Local Similarity 85.0%;
Matches 17; Conservative
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; ORGANISM: Homo sapiens
US-09-925-065A-102175
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US-09-925-065A-192787
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TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH

TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF

TITLE OF INVENTION: DETECTION AND USES THEREOF

FILE REFERENCE: CL001559

CURRENT APPLICATION NUMBER: US/10/995,561

CURRENT PILING DATE: 2004-11-24

NUMBER OF SEQ ID NOS: 85702

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 9264
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TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
TITLE OF INVENTION: DETECTION AND USES THEREOF
FILE REFERENCE: CL001559
CURRENT APPLICATION NUMBER: US/10/995,561
CURRENT FILING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 85702
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 35511
LENGTH: 201
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US-09-925-065A-102175
Sequence 102175, Application US/09925065A
Publication No. US20040181048A1
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
FILE REFERENCE: 108827.135
CURRENT APPLICATION NUMBER: US/09/955,065A
CURRENT PILING DATE: 2000-1.08-08
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR PILING DATE: 2000-11-20
PRIOR FILING DATE: 2000-11-20
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                                                            Sequence 35611, Application US/10995561 Publication No. US20050272054A1 GENERAL INFORMATION:
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Publication No. US20050272054A1
GENERAL INFORMATION:
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ORGANISM: Homo sapiens
US-10-995-561-35611
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; ORGANISM: Homo sapiens
US-10-995-561-69264
                                     US-10-995-561-35611/c
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TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
FILE REFERENCE: 108827.135
CURRENT FILING DATE: 2001-08-08
FRIOR PAPLICATION NUMBER: US 60/243,096
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR PILING DATE: 2000-11-30
PRIOR PILING DATE: 2001-11-30
PRIOR FILING DATE: 2001-10-10
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-01-16
SEQ ID NO 192787
LENGHH: 54
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Publication No. US20040181048A1
GENERAL INFORMATION:
APPLICANT' Wang David G.
ITILE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
FILE REPERENCE: 108827.135
CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243,096
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Score 15.2; DB 6; Length 440;
Pred. No. 5e+02;
0; Mismatches 3; Indels
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Publication No. US20040181048A1
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Score 15.2; DB 6;
Pred. No. 5.2e+02;
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                                        PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR PLILNG DATE: 2000-11-20
PRIOR PLILNG DATE: 2000-11-30
PRIOR PLILNG DATE: 2000-11-30
PRIOR PLILNG DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR PLILNG DATE: 2001-01-16
PRIOR PLILNG DATE: 2001-01-05
PRIOR FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
SOFTWARE: FREESEQ for Windows Version 4.0
APPLICATION NUMBER: US/09/925,065A
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85.0%;
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Best Local Similarity 85.0
Matches 17; Conservative
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US-09-925-065A-138729
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                                                                                                                                                                                                                                                                                                                                        SEQ ID NO 482408
LENGTH: 550
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SEQ ID NO 138729
LENGTH: 560
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Sequence 482407, Application US/09925065A

Publication No. US20040181048A1

GENERAL INFORMATION:

APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single

TITLE OF INVENTION: UNCleotide Polymorphisms in the Human Genome

FILE REFERENCE: 108827.135

CURRENT APPLICATION NUMBER: US/09/925,065A

CURRENT FILING DATE: 2001-08-08

PRIOR PRILING DATE: 2000-11-20

PRIOR APPLICATION NUMBER: US 60/252,147

PRIOR APPLICATION NUMBER: US 60/250,092

PRIOR APPLICATION NUMBER: US 60/250,092

PRIOR APPLICATION NUMBER: US 60/261,766

PRIOR FILING DATE: 2001-01-130

PRIOR FILING DATE: 2001-01-16

PRIOR FILING DATE: 2001-01-16
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Publication No. US20040181048A1
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
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76.0%; Score 15.2; DB 6;
Best Local Similarity 85.0%; Pred. No. 5.2e+02;
Matches 17; Conservative 0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                PRIOR PILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR PILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR PILING DATE: 2001-01-16
PRIOR PILING DATE: 2001-01-06
PRIOR PILING DATE: 2001-01-06
NUMBER OF SEQ ID NOS: 957086
SOFTWARE: RESUSED FOR Windows Version 4.0
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SOFTWARE: PastSEQ for Windows Version 4.0
            LICATION NUMBER: US 60/252,147
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136 AAAGAACACTGTCACCCAA 155
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85.0%;
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Best Local Similarity 85.0°
Matches 17; Conservative
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                                                                                                                                                                                                                                                                                                          TYPE: DNA
CORGANISM: Homo sapiens
US-09-925-065A-20386
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US-09-925-065A-482407
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US-09-925-065A-482408
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LENGTH: 550
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LENGTH: 550
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Gaps

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Indels

Length 550;

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TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: UNCleotide Polymorphisms in the Human Genome
FILE REPERBNCE: 108827.135
CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2001-08-08
FRIOR PAPLICATION NUMBER: US 60/243,096
FRIOR FILING DATE: 2000-10-24
FRIOR FILING DATE: 2000-11-20
FRIOR PILING DATE: 2000-11-30
FRIOR FILING DATE: 2000-11-30
FRIOR FILING DATE: 2001-01-16
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Mismatches
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Publication No. US20040181048A1
GENERAL INFORMATION:
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136 AAAGAACACTGTCACCCAA 155
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GENERAL INFORMENTION:
GENERAL INFORMENTION:
GENERAL INFORMENTION:
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
FILE REFERENCE: 108827.135
CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR PELING DATE: 2000-11-6
PRIOR PILING DATE: 2001-01-16
PRIOR PILING DATE: 2001-01-16
PRIOR PILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
SOFTWARE: PASTESEQ for Windows Version 4.0
SEQ ID NO 794043
LENGTH: 585
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Pred. No. 5.2e+02;
0; Mismatches 3;
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Best Local Similarity 85.0%;
Matches 17; Conservative
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Best Local Similarity 85.0%;
Matches 17; Conservative
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US-09-925-065A-436621
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US-09-925-065A-794043
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TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Noticetide Polymorphisms in the Human Genome
FILE REFERENCE: 108827.135
CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/23,096
PRIOR FILING DATE: 2000-11-20
PRIOR PILING DATE: 2000-11-20
PRIOR FILING DATE: 2000-11-20
PRIOR FILING DATE: 2000-11-30
PRIOR FILING DATE: 2001-11-6
PRIOR FILING DATE: 2001-11-6
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/289,846
PRIOR FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
SEQ ID NO 412774
TITLE OF INVENTION: Identification and Mapping of Single TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
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                                         TITLE OF INVENTION:
FILE REFERENCE: 108027.135
CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2001-08-08
PRIOR PILING DATE: 2000-10-24
PRIOR FILING DATE: 2000-10-24
PRIOR FILING DATE: 2000-11-20
PRIOR FILING DATE: 2000-11-30
PRIOR FILING DATE: 2000-11-30
PRIOR FILING DATE: 2000-11-30
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2010-01-16
PRIOR FILING DATE: 2011-01-16
PRIOR FILING DATE: 2001-01-16
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US-09-925-065A-794043/c
; Sequence 794043, Application US/09925065A
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85.0%;
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Best Local Similarity 85.0
Matches 17; Conservative
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Matches 17; Conservative
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US-09-925-065A-412774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-99970
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Gaps

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Indels

Length 585;

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Sequence 436621, Application US/09925065A

Sequence 436621, Application US/09925065A

Publication No. US2004081048A1

GENERAL INFORMATION:

APPLICANT: Wang, David G.

TITLE OF INVENTION: Noclectide Polymorphisms in the Human Genome

TITLE OF INVENTION: Noclectide Polymorphisms in the Human Genome:

FILE REFERENCE: 10827.135

CURRENT APPLICATION NUMBER: US/09/925,065A

CURRENT APPLICATION NUMBER: US 60/243,096

PRIOR FILING DATE: 2000-10-24

PRIOR FILING DATE: 2000-11-20

PRIOR FILING DATE: 2000-11-30

PRIOR FILING DATE: 2000-11-6

PRIOR FILING DATE: 2001-01-16

PRIOR FILING DATE: 2001-01-16

PRIOR FILING DATE: 2001-01-6

PRIOR FILING DATE: 2001-05-09

NUMBER OF SEQ ID NOS: 957086

SEQ ID NOS: 957086

SEQ ID NO 436621
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Pred. No. 5.3e+02;
0; Mismatches 3;
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574 ATGGAAACCAGGACACCCAA 593

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GENERAL INFORMATION

APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: UNDER: US/09/925,065A
CURRENT APPLICATION NUMBER: US 60/243,096
PRIOR PELING DATE: 2000-10-24
PRIOR PELING DATE: 2000-11-20
PRIOR PELING DATE: 2000-11-30
PRIOR PLING DATE: 2000-11-30
PRIOR PLING DATE: 2000-10-16
PRIOR PLING DATE: 2000-10-16
PRIOR PLING DATE: 2000-10-16
PRIOR PLING DATE: 2000-10-16
PRIOR PLING DATE: 2001-01-16
PRIOR PLING DATE: 2001-01-16
PRIOR PLING DATE: 2001-01-16
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GENERAL INFORMATION:

TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nuclectide Polymorphisms in the Human Genome
TITLE OF INVENTION: Nuclectide Polymorphisms in the Human Genome
FILE REFERENCE: 108827.135

CURRENT APPLICATION NUMBER: US/09/925,065A

CURRENT APPLICATION NUMBER: US 60/243,096

PRIOR PILING DATE: 2000-10-24

PRIOR PILING DATE: 2000-11-20

PRIOR PILING DATE: 2000-11-20

PRIOR PILING DATE: 2000-11-16

PRIOR APPLICATION NUMBER: US 60/261,766

PRIOR PILING DATE: 2001-01-16

PRIOR PILING DATE: 2001-01-16

PRIOR PILING DATE: 2001-01-16

PRIOR PILING DATE: 2001-05-09

NUMBER OF SEQ ID NOS: 957086

SOFTWARE: FastSEQ for Windows Version 4.0

TOWNSTON OF 92481
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Pred. No. 5.3e+02;
0; Mismatches 3;
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Pred. No. 5.3e+02;
0; Mismatches 3;
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                                                                               US-09-925-065A-919664
; Sequence 919664, Application US/09925065A
; Publication No. US20040181048A1
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Publication No. US20040181048A1
GENERAL INFORMATION:
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Best Local Similarity 85.0%;
Matches 17; Conservative 0
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Best Local Similarity 85.0%;
Matches 17; Conservative
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US-09-925-065A-919664
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ORGANISM: Homo sapiens
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SEQ ID NO 919664
LENGTH: 614
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                                                                                           GENERAL INVENTALION:

GENERAL INVENTALION:

GENERAL INVENTALION:

TITLE OF INVENTION: Identification and Mapping of Single

TITLE OF INVENTION: Uncleotide Polymorphisms in the Human Genome

FILE REFERENCE: 108827.135

CURRENT APPLICATION NUMBER: US/09/925,065A

CURRENT FILING DATE: 2001-08-08

PRIOR FILING DATE: 2000-11-20

PRIOR FILING DATE: 2000-11-20

PRIOR FILING DATE: 2000-11-30

PRIOR FILING DATE: 2000-11-30

PRIOR FILING DATE: 2000-11-30

PRIOR FILING DATE: 2000-11-30

PRIOR FILING DATE: 2001-01-16

PRIOR FILING DATE: 2001-11-10

PRIOR FILING DATE: 2001-11-10

PRIOR FILING DA
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APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Indentification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
FILE REFERENCE: 108827.135

CURRENT APPLICATION NUMBER: US/09/925,065A

CURRENT PILING DATE: 2001-08-08

PRIOR PILING DATE: 2000-10-24

PRIOR PILING DATE: 2000-11-20

PRIOR PILING DATE: 2000-11-30

PRIOR PILING DATE: 2000-11-30

PRIOR PELING DATE: 2000-11-30

PRIOR PELING DATE: 2001-11-16

PRIOR PILING DATE: 2001-01-16

PRIOR PILING DATE: 2001-05-09

PRIOR PILING DATE: 2001-05-09

PRIOR PILING DATE: 2001-05-09

PRIOR PILING DATE: 2001-05-09
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Pred. No. 5
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 919663
Sequence 436622, Application US/09925065A Publication No. US20040181048A1
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Publication No. US20040181048A1
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Best Local Similarity 85.0%;
Matches 17; Conservative
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; ORGANISM: Homo sapiens
US-09-925-065A-436622
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; ORGANISM: Homo sapiens
US-09-925-065A-919663
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US-09-925-065A-919663
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Query Match 76.0%;
Best Local Similarity 85.0%;
Matches 17; Conservative
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US-09-925-065A-214200
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TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome FILE REFERENCE: 108827.135
CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR PILING DATE: 2000-11-30
PRIOR FILING DATE: 2001-11-30
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/261,766
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 820980, Application US/09925065A Publication No. US20040181048A1
                                                                                                                                                                               423 AAGGAAACACATACACACAA 442
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                                                                  1 AAGGAAACACGGACACCCAA 20
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US-09-925-065A-820980
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GENERAL INFORMATION:
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GENERAL GENERATION:
FILE OF INVENTION:
UNCLOSED TO THE Human Genome
FILE REFRENCE: 108827.135
CURRENT APPLICATION NUMBER: US 60/243,096
PRIOR PAPLICATION NUMBER: US 60/243,096
PRIOR PAPLICATION NUMBER: US 60/252,147
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR PILING DATE: 2000-11-30
PRIOR PILING DATE: 2000-11-16
PRIOR PELING DATE: 2001-01-16
PRIOR PELING DATE: 2001-01-16
PRIOR PELING DATE: 2001-01-16
PRIOR PELING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
SOFTWARE: FRAESEQ for Windows Version 4.0
SEQ ID NO 214200
LENGTH: 650
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TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
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Score 15.2; DB 6; Length 633;
Pred. No. 5.3e+02;
0; Mismatches 3; Indels
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CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2001-08-08
PRIOR PILING DATE: 2000-10-24
PRIOR FILING DATE: 2000-10-24
PRIOR FILING DATE: 2000-11-20
PRIOR FILING DATE: 2000-11-30
PRIOR FILING DATE: 2000-11-30
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
SEQ ID NO 529196
LENGTHARE: FASESED FOR WINDOWS VERSION 4.0
SEQ ID NO 529196
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; SEQ ID NO 192788
; LENGTH: 674
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-192788
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APPLICANT: Wang, David G.

ITILE OF INVENTION: Identification and Mapping of Single
ITILE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
ITILE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
ITILE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
ITILE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
CURRENT APPLICATION NUMBER: US 60/243,096
PRIOR PILING DATE: 2000-10-24
PRIOR PILING DATE: 2000-11-20
PRIOR PILING DATE: 2000-11-30
PRIOR PILING DATE: 2001-01-16
PRIOR PILING DATE: 2001-01-16
PRIOR PILING DATE: 2001-01-16
PRIOR PILING DATE: 2001-01-6
PRIOR PI
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                                                                                                    Length 654;
                                                                                                                                                               Indels
                                                                                          Query Match

76.0%; Score 15.2; DB 6;
Best Local Similarity 85.0%; Pred. No. 5.3e+02;
Matches 17; Conservative 0; Mismatches 3;
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SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 529197, Application US/09925065A Publication No. US20040181048A1
                                                                                                                                                                                                                                                             133 AAGGAGACACGGAAACTCAA 152
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Matches 17; Conservative
; ORGANISM: Homo Bapiens
US-09-925-065A-529196
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CRGANISM: Homo sapiens
US-09-925-065A-529197
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US-09-925-065A-192788
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Publication No. US2040181048A1

GRNERAL INFORMATION:

APPLICANT: Wang, David G:

ITTLE OF INVENTION:

FILE REPERBURG:

CURRENT APPLICATION NUMBER: US/09/925,065A

CURRENT APPLICATION NUMBER: US/09/925,065A

CURRENT PILING DATE: 2001-08-08

PRIOR PILING DATE: 2000-10-24

PRIOR PILING DATE: 2000-11-20

PRIOR FILING DATE: 2000-11-30

PRIOR PILING DATE: 2000-11-30

PRIOR PILING DATE: 2000-11-30

PRIOR PILING DATE: 2000-10-16

PRIOR PILING DATE: 2001-00-16

PRIOR PILING DATE: 2001-00-16

PRIOR PILING DATE: 2001-00-16

PRIOR PILING DATE: 2001-00-16

PRIOR PILING DATE: 2001-01-16

PRIOR PILING DATE: 2001-01-16
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TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
FILE REFERENCE: 108827.135
CURRENT APPLICATION WHERE: US/09/925,065A
CURRENT FILING DATE: 2001-08-08
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Length 674;
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                                                                     Indels
Score 15.2; DB 6;
Pred. No. 5.3e+02;
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Pred. No. 5.3e+02;
0; Mismatches 3;
                                                                     0; Mismatches
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PRIOR FILING DATE: 2000-10-24
PRIOR PELICATION NUMBER: US 60/252,147
PRIOR FILING DATE: 2000-11-20
PRIOR FILING DATE: 2000-11-30
PRIOR FILING DATE: 2000-11-30
PRIOR FILING DATE: 2000-11-30
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR APPLICATION NUMBER: US 60/289,846
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                                                                                                                                                                                          186 AAGGAAAAACGGACACTGAA 205
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Conservative (
                         Best Local Similarity 85.0
Matches 17; Conservative
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US-09-925-065A-192789
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Best Local Similarity
Matches 17; Conserv
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US-10-750-185-61482/c
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    SEQ ID NO 27789
LENGTH: 877
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LENGTH: 878
TYPE: DNA
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; Publication No. U52050287531A1
; GENERAL INFORMATION:
APPLICANT: DENISE, Sue K.
APPLICANT: DENISE, Sue K.
APPLICANT: ROSENFELD, David
APPLICANT: Holm Tom
TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
: TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
: TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
: CURRENT APPLICATION NUMBER: US/10/750,623
: CURRENT APPLICATION NUMBER: US 60/437,482
: PRIOR PILING DATE: 2003-12-31
: NUMBER OF SEQ ID NOS: 64922
: OTHER OF SEQ ID NOS: 64922
: OTHER OF SEQ ID NOS: 64922
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; Sequence 27789, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENPELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: BATES, Stephen
; APPLICANT: BATES, USPHEN
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
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PRIOR FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
SOFTWARE: PARTSEQ for Windows Version 4.0
SEQ ID NO 6885
LENGTH: 766
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PRIOR FILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
SEQ ID NO 27789
LENGTH: 877
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; ORGANISM: Bovine 19866881436091
US-10-750-185-27789
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                                                                                                                   TYPE: DNA
ORGANISM: Homo sapiens
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GENERAL INFORMATION:

GENERAL INFORMATION:

TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nuclectide Polymorphisms in the Human Genome
TITLE OF INVENTION: Nuclectide Polymorphisms in the Human Genome
FILE REFERENCE: 108827.135
CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT PILING DATE: 2000-10-24
PRIOR PAPLICATION NUMBER: US 60/252,147
PRIOR PILING DATE: 2000-11-24
PRIOR PILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR PILING DATE: 2000-11-6
PRIOR PILING DATE: 2001-01-16
PRIOR PILING DATE: 2001-01-16
PRIOR PILING DATE: 2001-01-6
PRIOR PILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 710789
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TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
FILE REFERENCE: 108827.135
                                                                                                                                                                    Length 925;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    76.0%; Score 15.2; DB 6; Length 925; 85.0%; Pred. No. 5.6e+02;
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                                                                                                                                                                 Score 15.2; DB 6;
Pred. No. 5.6e+02;
0; Mismatches 3;
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CURRENT FILING DATE: 2001-08-08
PRIOR PEPLICATION NUMBER: US 60/243,096
PRIOR FILING DATE: 2000-10-24
PRIOR FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR PELING DATE: 2000-11-30
PRIOR PELING DATE: 2000-11-30
PRIOR PELING DATE: 2000-11-30
PRIOR PELING DATE: 2001-0-14
PRIOR PILING DATE: 2001-0-1-16
PRIOR PILING DATE: 2001-0-1-16
PRIOR PILING DATE: 2001-0-1-16
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Publication No. US20040181048A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                              229 AAGGACACACACACCCAA 210
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; SEQ ID NO 710788
; LENGTH: 925
; TYPE: DNA
; ORGANIEM: Homo sapiens
US-09-925-065A-710788
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US-09-925-065A-710789
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Best Local Similarity
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US-09-925-065A-710789/c
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TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
FILE REPERENCE: 108827, 135
CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2000-024
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR PILING DATE: 2000-11-20
PRIOR PILING DATE: 2000-11-30
PRIOR FILING DATE: 2000-11-30
PRIOR FILING DATE: 2000-11-30
PRIOR PILING DATE: 2010-01-6
PRIOR PILING DATE: 2010-01-6
PRIOR PILING DATE: 2010-01-6
PRIOR PILING DATE: 2010-01-6
PRIOR FILING DATE: 2010-01-6
PRIOR PILING DATE: 2010-01-6
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TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
FILE REFERENCE: 108827.135
CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2001-08-08
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                                                                         Score 15.2; DB 8; Length 878;
Pred. No. 5.6e+02;
0; Mismatches 3; Indels
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PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 710787
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NUMBER OF SEQ ID NOS: 957086
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                          Sequence 710787, Application US/09925065A Publication No. US20040181048A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 710788, Application US/09925065A
Publication No. US20040181048A1
GENERAL INFORMATION:
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PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/250,092
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; ORGANISM: Bovine 19866880980307
US-10-750-623-61482
                                                                            Query Match
Best Local Similarity 85.0%;
Matches 17; Conservative
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; ORGANISM: Homo sapiens
US-09-925-065A-710787
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TYPE: DNA ORGANISM: Saccharomyces pastorianus
PRIOR FILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
SOFTWARE: PatentIN version 3.1
SEQ ID NO 59220
LENGTH: 1139
                                                                                                                                               ; TYPE: DNA
; ORGANISM: Bovine
US-10-750-185-59220
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APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
FILE REFERENCE: 108827.135

CURRENT APPLICATION NUMBER: US/09/925,065A

CURRENT PILING DATE: 2001-08-08

PRIOR PELLING DATE: 2000-10-24

PRIOR PILING DATE: 2000-11-20

PRIOR FILING DATE: 2000-11-30

PRIOR FILING DATE: 2000-11-30

PRIOR FILING DATE: 2001-11-30

PRIOR FILING DATE: 2001-10-16

PRIOR FILING DATE: 2001-01-16

PRIOR SPELICATION NUMBER: US 60/289,846

PRIOR APPLICATION NUMBER: US 60/289,846

PRIOR SPELING DATE: 2001-01-16

PRIOR FILING DATE: 2001-01-16

PRIOR FILING DATE: 2001-01-16

PRIOR PRIOR APPLICATION NUMBER: US 60/289,846

PRIOR SPELIOR APPLICATION NUMBER: US 60/289,846

PRIOR PRIOR APPLICATION NUMBER: US 60/289,846

PRIOR FILING DATE: 2001-01-16

PRIOR FILING DATE: 2001-01-16
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                                                                                                                                                                                                                                                              Score 15.2; DB 6; Length 1125;
Pred. No. 5.8e+02;
0; Mismatches 3; Indels 0,
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APPLICANT: ROSENFELD, David
APPLICANT: HOLM, Town
APPLICANT: BATES, Stephen
APPLICANT: FANTIN, Dennis
TITLE OF INVERTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
FILE REFERENCE: MM11100-2
CURRENT APPLICATION NUMBER: US/10/750,185
CURRENT FILING DATE: 2003-12-31
PRIOR FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 717601
LENGTH: 1125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-925-065A-717602/c
; Sequence 717602, Application US/09925065A
; Publication No. US20040181048A1
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Publication No. US20050260603A1
GENERAL INFORMATION:
APPLICANT: MMI GENOMICS, INC.
APPLICANT: DeNISE, Sue K.
APPLICANT: KERR, Richard
APPLICANT: ROSENFELD, David
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Best Local Similarity 85.0%;
Matches 17; Conservative
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Matches 17; Conservative
                                                                                                                                               ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-717601
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US-09-925-065A-717602
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US-10-750-185-59220/c
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Publication No. US20060046253A1

GENERAL INFORMATION:

APPLICANT: NAKAWIRA, NORIHIRA

APPLICANT: FULIMIRA, TOONOKO

APPLICANT: FULIMIRA, TOONOKO

APPLICANT: FULIMIRA, TOSHHHIKO

APPLICANT: FULIMIRA, TOSHHHIKO

TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS

FILE REPERBENGE: 200685-043

CURRENT APPLICATION NUMBER: 2004-09-02

NUMBER OF SEQ ID NOS: 197023

SOFTWARE: Patentin version 3.3

SEQ ID NO 76110
                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: MAT GENOMICS, INC.
APPLICANT: MAT GENOMICS, INC.
APPLICANT: DeNISE, Sue K.
APPLICANT: ROSENPELD, David
APPLICANT: ROSENPELD, David
APPLICANT: ROSENPELD, David
APPLICANT: BATES, Stephen
APPLICANT: PANTIN, Dennis
TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
FILE REPERENCE: MATLIOG-1
CURRENT APPLICATION NUMBER: US/10/750,623
CURRENT APPLICATION NUMBER: US 60/437,482
PRIOR PILING DATE: 2003-12-31
PRIOR PILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
SOFTWARE: PatentIN version 3.1
SEQ ID NO 59220
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                                                                               Length 1139;
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                                                                             Query Match 76.0%; Score 15.2; DB 8; Best Local Similarity 85.0%; Pred. No. 5.8e+02; Matches 17; Conservative 0; Mismatches 3;
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Publication No. US20050287531A1
GENERAL INFORMATION:
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                                                                                                                                                                                           1 AAGGAAACACGGACACCCAA 20
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; ORGANISM: Bovine 19866881082830
US-10-750-623-59220
19866881082830
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APPLICANT: HOLM, Tom
APPLICANT: BATES, Stephen
APPLICANT: FANTIN, Dennis
TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
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CURRENT FILING DATE: 2003-12-31
PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR FILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
SOFTWARE: PatentIN version 3.1
SEQ ID NO 25747
                                                                                                                                                       Sequence 25747, Application US/10750623
Publication No. US20050287531A1
                                                                                                                                                                                                                              APPLICANT: MMI GENOMICS, INC.
APPLICANT: DENISE, Sue K.
APPLICANT: KERR, Richard
APPLICANT: ROSENFELD, David
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APPLICANT: NAKAMTAA, NORIHISA
APPLICANT: KODANA, VUKINA
APPLICANT: FUJIMURA, TOMOKO
APPLICANT: ASHIKRAI, TOSHIHIKO
APPLICANT: MAHIKANI, TOSHIHIKO
TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
FILE REPERENCE: 0306685-043
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                                                      Length 1371;
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APPLICANT: FANTIN, Dennis
TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
                                                                                                      Indels
                                                 Score 15.2; DB 7;
Pred. No. 5.9e+02;
                                               Query Match 76.0%; Score 15.2; I Best Local Similarity 85.0%; Pred. No. 5.9e Matches 17; Conservative 0; Mismatches
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CURRENT FILING DATE: 2004-09-02
NUMBER OF SEQ ID NOS: 197023
SOFTWARE: PatentIn version 3.3
SEQ ID NO 76110
LENGTH: 1371
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CURRENT FILING DATE: 2003-12-31
PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR FILING DATE: 2002-12-31
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Publication No. US20060046253A1
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Publication No. US20050260603A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA ORGANISM: Saccharomyces pastorianus
                                                                                                                                                                                         154 AATGAAATACGGACACCTAA 173
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; ORGANISM: Bovine 19866880936728
US-10-750-185-25747
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SOFTWARE: PatentIN version 3.1
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APPLICANT: MMI GENOMICS, INC.
APPLICANT: DeNISE, Sue K.
APPLICANT: KERR, Richard
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US-10-932-182A-76110
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APPLICANT: FANTIN, Dennis
TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
FILE REPERENCE: MMILLOD-0.2
CURRENT APPLICATION NUMBER: US/10/750,185
CURRENT FILING DATE: 2003-12-31
                                                                                                                   Indels
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                                                                   DB 8;
                                                                   Query Match 76.0%; Score 15.2; DB 8; Best Local Similarity 85.0%; Pred. No. 6.1e+02; Matches 17; Conservative 0; Mismatches 3
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PRIOR FILING DATE: 2002-12-31
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Publication No. US20050260603A1
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                                                                                                                                                               1 AAGGAAACACGGACACCCAA 20
; ORGANISM: Bovine 19866880936728
US-10-750-623-25747
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SOFWARE: Patentin version 3.1
SEQ ID NO 33198
LENCTH: 1816
                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: MMI GENOMICS, INC.
APPLICANT: DeNISE, Sue K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                KERR, Richard
ROSENFELD, David
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Best Local Similarity
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1 AAGGAAACACGGACACCCAA 20

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Sequence 31642, Application US/10750623
Publication No. US20050287531A1
GENERAL INFORMATION:
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US-10-932-182A-1309/c
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                                                              Sequence 33198, Application US/10750623

Publication No. US20050287531A1

GENERAL INFORMATION:

APPLICANT: NMI GENOMICS, INC.

APPLICANT: RERR, Richard

APPLICANT: ROSENFELD, David

APPLICANT: ROSENFELD, David

APPLICANT: RATES, Stephen

APPLICANT: FANTIN, Dennis

TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS

FILE REFERENCE: MAILIO-1

CURRENT TRING DATE: 2003-12-31

CURRENT FILING DATE: 2003-12-31

FRIOR FILING DATE: 2002-12-31

SOFTWARE: PATCHIN VERSION 3.1

SEQ ID NO 33198

LENGTH 1816

LENGTH 1816
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; Sequence 31642, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
    APPLICANT: MI GENOMICS, INC.
    APPLICANT: RERR, Richard
    APPLICANT: RESPERED, David
    APPLICANT: HOLM, Toom
    APPLICANT: BATES, Stephen
    APPLICANT: BATES, Stephen
    APPLICANT: PANITH, Dennis
    TILLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
    TILLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
    TURRENT APPLICATION NUMBER: US/10/750,185
    CURRENT FILING DATE: 2002-12-31
    PRIOR FILING DATE: 2002-12-31
    NUMBER OF SEQ ID NOS: 64922
    SOFTWARE: PALENTIN VERSION 3.1
    SEQ ID NO 31642
    LENGTAL 12168
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TYPE: DNA
; ORGANISM: Bovine 19866880641575
US-10-750-623-33198
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; ORGANISM: Bovine 19866880775685
US-10-750-185-31642
                                                      US-10-750-623-33198/c
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US-10-750-185-31642
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RESULT 88 US-10-750-623-31642

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Publication No. US20060046253A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: NAKAMORA, NORIHISA
APPLICANT: RODAMA, YUKIKO
APPLICANT: RODAMA, YUKIKO
APPLICANT: FULIMIRA, TOOKNO
APPLICANT: AFHIKARI, TOSHIHIKO
TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
FILLE REFRENCE: 200645-043
CURRENT PILING DATE: 2004-09-02
NUMBER OF SEQ ID NOS: 197023
CURRENT FILING DATE: 2004-09-02
NUMBER OF SEQ ID NOS: 197023
SOFTWARE: Patentin version 3.3
SEQ ID NO 1309

LENGTH: 2406
APPLICANT: INCOMAILON:
APPLICANT: BORISE, Sue K.
APPLICANT: BORISE, Sue K.
APPLICANT: GRENFELD, David
APPLICANT: RERR, Richard
APPLICANT: HOLM, Tom
APPLICANT: HOLM, Tom
APPLICANT: HATES, Stephen
APPLICANT: BATES, Stephen
APPLICANT: FANTIN, Dennis
TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
FILE REFREENCE: MMILLOD 0.1
CURRENT APPLICATION NUMBER: US/10/750,623
CURRENT APPLICATION NUMBER: US 60/437,482
PRIOR PILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
SOFTWARE: PALENTIN Version 3.1
SEQ ID NO 31642
LENGTH: 2168
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Publication No. US20060046253A1
GENERAL INFORMATION:
APPLICANT: NAKAO, YOSHIHIRO
APPLICANT: KODAMA, VICKKO
APPLICANT: RUJIMURA, TOMOKO
APPLICANT: TOMINGA, TOMOKO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA ORGANISM: Saccharomyces pastorianus
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; ORGANISM: Bovine 19866880775685
US-10-750-623-31642
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Best Local Similarity 85.0°
Matches 17; Conservative
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PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR PLING DATE: 2000-11-30
PRIOR PLING DATE: 2001-11-16
PRIOR PLING DATE: 2001-01-16
PRIOR PLING DATE: 2001-01-05
PRIOR PLING DATE: 2001-01-05
NUMBER OF SEQ ID NOS: 957086
SOFTWARE: FRAESEQ for Windows Version 4.0
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Best Local Similarity 85.0%;
Matches 17; Conservative C
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SOFTWARE: Patentin version 3.1
SEQ ID NO 54418
LENCTH: 2828
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APPLICANT: MAI GENOMICS, INC.
APPLICANT: DENISE, Sue K.
APPLICANT: KERR, Richard
APPLICANT: RERR, Richard
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APPLICANT: DeNISE, Sue K.
APPLICANT: KERR, Richard
APPLICANT: ROSENPELD, David
                                                                                                                                                                                                                                                                                                                   TYPE: DNA; ORGANISM: Homo sapiens
US-09-925-065A-697076
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TYPE: DNA
; ORGANISM: Bovine
US-10-750-185-54418
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                                                                                                                                                                                                                                                                  SEQ ID NO 697076
LENGTH: 2590
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                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
FILE REPERENCE: 108827.135
CURRENT PILIAN DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR PILING DATE: 2000-10-24
PRIOR PILING DATE: 2000-11-20
PRIOR PILING DATE: 2000-11-20
PRIOR PILING DATE: 2000-11-30
PRIOR PILING DATE: 2000-11-6
PRIOR PLING DATE: 2001-11-6
PRIOR PILING DATE: 2001-11-6
PRIOR PILING DATE: 2001-11-6
PRIOR PILING DATE: 2001-01-6
                   IIILE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS FILE REFERENCE: 030685-043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Uncleotide Polymorphisms in the Human Genome
FILE REFERENCE: 108827.135
CURRENT PAPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR FILING DATE: 2000-10-24
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                                                                                                                                                                                                                                                                                                                                                 Length 2406;
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                                                                                                                                                                                                                                                                                                                                                                                                3; Indels
                                                                                                                                                                                                                                                                                                                                         Score 15.2; DB 7;
Pred. No. 6.4e+02;
0; Mismatches 3;
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        CURRENT APPLICATION NUMBER: US/10/932,182A;
CURRENT APPLICATION NUMBER: US/10/932,182A;
CURRENT PILLIG DATE: 2004-09-02;
NUMBER OF SEQ ID NOS: 197023;
SQTWARE: Patentin version 3.3;
SEQ ID NO 1309;
LENGTH: 2406;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 76.0%; Score 15.2; I Best Local Similarity 85.0%; Pred. No. 6.5e Matches 17; Conservative 0; Mismatches
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; Sequence 697076, Application US/09925065A
; Publication No. US20040181048A1
                                                                                                                                                                                                                                   ; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-10-932-182A-1309
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ASHIKARI, TOSHIHIKO
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Best Local Similarity 85.0%;
Matches 17; Conservative
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; ORGANISM: Homo sapiens
US-09-925-065A-697075
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APPLICANT:
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APPLICANT: BATES, Stephen
APPLICANT: FANTIN, Dennis
TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
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     Length 2590;
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APPLICANT: BATES, Stephen
APPLICANT: BATES, Stephen
APPLICANT: RANTIN, Dennis
FITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
FILE REFERENCE: MMI1100-2
CURRENT APPLICATION NUMBER: US/10/750,185
CURRENT FILING DATE: 2003-12-31
PRIOR RAPPLICATION NUMBER: US 60/437,482
PRIOR FILING DATE: 2002-12-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
Score 15.2; DB 6;
Pred. No. 6.5e+02;
0; Mismatches 3;
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                                                                                                                                                                                                                                                                                                        Sequence 54418, Application US/10750185
Publication No. US20050260603A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 54418, Application US/10750623
Publication No. US20050287531A1
GENERAL INFORMATION:
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; LOCATION: (1) ... (123331)
; OTHER INFORMATION: n = A,T,C or G
US-10-330-773-829
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; Sequence 916, Application US/10330773
; Publication No. US20060040262A1
; GENERAL INFORMATION:
; APPLICANT: David W. Morris
; APPLICANT: Marc Malandro
; TITLE OF INVENTION: Novel Compositions and Methods in Cancer;
; FILE REFERENCE: 529452001300
; CURRENT APPLICATION UNMER: US/10/330,773
; CURRENT FILING DATE: 2002-12-27
; NUMBER OF SEQ ID NOS: 981
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 916
; LENGTH: 23367
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Publication No. US20060040262A1
| Fabrication No. US20060040262A1
| GENERAL INFORMATION:
| APPLICANT: DAVIG W. Morris
| APPLICANT: Marc Malandro
| TITLE OF INVENTION: Novel Compositions and Methods in Cancer
| PILE REFERENCE: 529452001300
| CURRENT APPLICATION NUMBER: US/10/330,773
| CURRENT FILING DATE: 2002-12-27
| NUMBER OF SEQ ID NOS: 981
| SOFTWARE: FastSEQ for Windows Version 4.0
| SEG ID NO 829
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                                                                                                                                                                                                                                                                                                             Query Match 76.0%; Score 15.2; DB 8; Length 2828; Best Local Similarity 85.0%; Pred. No. 6.6e+02; Matches 17; Conservative 0; Mismatches 3; Indels 0
    FILE REFERENCE: MMI1100-1
CURRENT APPLICATION NUMBER: US/10/750,623
CURRENT FILING DATE: 2003-12-31
PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR FILING DATE: 2002-12-31
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// LOCATION: (1)...(23367)
// OTHER INFORMATION: n = A,T,C or G
US-10-330-773-916
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                                                                                                                                                                                                                                           ORGANISM: Bovine 19866880791558
US-10-750-623-54418
                                                                                                                     NUMBER OF SEQ ID NOS: 64922
SOFTWARE: PatentIN version 3.1
SEQ ID NO 54118
LENGTH: 2828
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ORGANISM: Homo sapiens
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                                                                                                                                                                                                                        TYPE: DNA
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Matches
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| Publication No. US2005266459A1
| GENERAL INFORMATION:
| APPLICANT: POULSEN, TIM S.
| TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
| TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
| TITLE REPERENCE: 09138 6000-00000
| CURRENT FILING DATE: 2005-05-04
| PRIOR APPLICATION NUMBER: 60/567,570
| PRIOR APPLICATION NUMBER: 60/567,570
| PRIOR PELING DATE: 2004-05-04
| NUMBER OF SEQ ID NOS: 107
| SOFTWARE: PATENTIN VERSION 3.3
| SEQ ID NO 85
                                                                                                                                                                                                                                           US-11-121-086-75
; Sequence 75, Application US/11121086
; Sequence 75, Application US/11121086
; Publication No. US20050266459A1
; GENERAL INFORMATION:
; APPLICANT: DILLEN, TIM S.
; APPLICANT: NIELELS, KIRSTEN V.
; TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
; FILE REFERENCE: 09138.6000-00000
; CURRENT FILING DATE: 2005-05-04
; FRICR APPLICATION NUMBER: 60/567,570
PRIOR FILING DATE: 2004-05-04
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: Patentin Version 3.3
; SEQ ID NO 75557
                                                   Gaps
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Length 123331;
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85.0%; Pred. No. 1.1e+03;
tive 0; Mismatches 3;
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Query Match

76.0%; Score 15.2; DB 7;
Best Local Similarity 85.0%; Pred. No. 1.1e+03;
Matches 17; Conservative 0; Mismatches 3;
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Best Local Similarity 85.04
Matches 17; Conservative
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COCANISM: Homo sapiens
US-11-121-086-75
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US-11-121-086-85
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APPLICANT: CARGILL, Michele et al.

TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH

TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF

TITLE OF INVENTION: DETECTION AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 1691140;
              Sequence 1, Application US/11091018
| Publication No. US20050287551A1
| GENERAL INPORMATION:
| APPLICANT: GretarSdottir, Solveig
| APPLICANT: Thorleifseon, Gudmar |
| APPLICANT: Thorleifseon, Gudmar |
| APPLICANT: Thorleifseon, Gudmar |
| TILE OF INVENTION: SUCCEPTIBILITY GENE FOR HUMAN STROKE;
| TILLE OF INVENTION: WETHODS OF TREATMENT |
| FILE REFERENCE: 2345, 2010-016 |
| CURRENT APPLICATION NUMBER: US/11/091,018 |
| CURRENT FILING DATE: 2005-03-25 |
| PRIOR APPLICATION NUMBER: 10/255,120 |
| PRIOR APPLICATION NUMBER: 10/419,723 |
| PRIOR FILING DATE: 2003-09-15 |
| PRIOR FILING DATE: 2003-09-16 |
| PRIOR FILING DATE: 2003-09-18 |
| PRIOR FILING DATE: 2003-09-19 |
| PRIOR FILING DATE: 2003-09-19 |
| PRIOR FILING DATE: 2001-03-19 |
| NUMBER OF SEQ ID NOS: 102 |
| SOFFWARE: FREISEQ for Windows Version 4.0
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OTHER INFORMATION: Chemically synthesized reverse primer for amplifying enteroviral COTHER INFORMATION: RNA US-10-829-474-27
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Pred. No. 7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: TSANG, SHIRLEY
APPLICANT: TSANG, SHIRLEY
APPLICANT: REICE, JAMES A.
APPLICANT: HELLYER, TOBIN J.
TITLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID
FILE REFERENCE: 020187, 0187PTUS
CURRENT APPLICATION NUMBER: US/10/760, 048
CURRENT FILING DATE: 2004-01-16
NUMBER OF SEQ ID NOS: 67
SOFTWARE: PALENTIN Ver. 3.2
SEQ ID NO 52
LENGTH: 110
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APPLICANT: TSANG, SHIRLEY
APPLICANT: PRICE, JAMES A.
APPLICANT: HELLYER, TOBIN J.
TITLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLBIC ACID
FILE REFERENCE: 020187, 0187PTUS
CURRENT APPLICATION NUMBER: US/10/760, 048
CURRENT FILING DATE: 2004-01-16
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CURRENT APPLICATION NUMBER: US/10/829,474
CURRENT FILING DATE: 2004-04-22
NUMBER OF SEQ ID NOS: 57
SSOFTWARE: Patentin version 3.2
LENGTH: 26
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SOFTWARE: Patentin Ver. 3.2
SEQ ID NO 53
LENGTH: 107
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Best Local Similarity 100.0%;
Matches 20; Conservative 0
                                                                                                                                                            ORGANISM: Artificial Sequence
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GENERAL INFORMATION:
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Best Local Similarity 100.
Matches 20; Conservative
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ORGANISM: Unknown Organism
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US-10-760-048-53/c
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6.8;
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APPLICANT: Genetics & IVF
APPLICANT: Genetics & IVF
APPLICANT: MARIANI, Brian D.
TITLE OF INVENTION: ENTEROVING PRIMERS AND PROBES
FILE REPERENCE: 043956-0121
CURRENT APPLICATION NUMBER: US/10/829,474
CURRENT FILING DATE: 2004-04-22
NUMBER OF SEQ ID NOS: 57
SOFTWARE: Patentin version 3.2
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APPLICANT: Genetics & IVF
APPLICANT: MAKIANI, Brian D.
TITLE OF INVENTION: ENTEROVIRUS PRIMERS AND PROBES
FILE REPERBUCE: 043956-0121
CURRENT APPLICATION NUMBER: US/10/829,474
VUMBER FILING DATE: 2004-04-22
SUMBER OF SEC ID NOS: 57
SOFTWARE: Patent In version 3.2
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Publication No. US20050239055A1
GENERAL INFORMATION:
APPLICANT: Genetics & IVF
APPLICANT: MARIANI, Brian D.
TITLE OF INVENTION: ENTEROVIRUS PRIMERS AND PROBES
PILE REFERENCE: 043956-0121
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Best Local Similarity 100.0%; Pred. No. 6.8
Matches 20; Conservative 0; Mismatches
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100.0%; Pred. No. 6.8
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                                                                                       Sequence 25; Application US/10829474 Publication No. US20050239055A1
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Publication No. US20050239055A1
GENERAL INFORMATION:
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Matches 20, Conservative
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LENGTH: 21
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LENGTH: 21
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105 AAGGAAACACGGACACCCAA 86
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Matches 20; Conservative
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                                                                                                               US-10-760-048-21/c
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; Sequence 18, Application US/10760048
; Publication No. US20050158710A1
; GENERAL INFORMATION:
; APPLICANT: TSANG, SHIRLEY
; APPLICANT: HELLYER, TOBIN J.
; TITLE OF INVERTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID
; FILE REFERENCE: 020187.0187PTUS
; CURRENT APPLICATION NUMBER: US/10/760,048
; CURRENT FILING DATES: 2004-01-16
; NUMBER OF SEQ ID MOS: 67
; SOFTWARE: Patentin Ver. 3.2
                                                                                          Length 110;
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; OTHER INFORMATION: Description of Unknown Organism: Viral; OTHER INFORMATION: 5'untranslated polynucleotide sequence US-10-760-048-52
                                                                                                                                      0; Indels
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US-10-760-048-55/c
| Sequence 55, Application US/10760048
| Publication US/2050158710A1
| Publication US/2050158710A1
| GENERAL INFORMATION:
| APPLICANT: TSANG, SHIRLEY
| APPLICANT: PRICE, JAMES A.
| APPLICANT: HELLYER, TOBIN J.
| TITLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID
| FILE REFERENCE: 020187.0187PTUS
                                                                                        Query Match 100.0%; Score 20; DB 9; Best Local Similarity 100.0%; Pred. No. 7; Matches 20; Conservative 0; Mismatches 0
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ORGANISM: Unknown Organism
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Best Local Similarity 100.
Matches 20; Conservative
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US-10-760-048-18
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LENGTH: 126
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LENGTH: 236
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; Sequence 11, Application US/10760048; Publication No. US20050158710A1; GENERAL INFORMATION:
; APPLICANT: TSANG, SHIRLEY; APPLICANT: PRICE, JAMES A.; APPLICANT: HELLYER, TOBIN J.; TITLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID; FILE REFERENCE: 020187108; FILE REFERENCE: 020187108; CURRENT APPLICATION NUMBER: US/10/760,048; CURRENT FILING DATE: 2004-01-16; NUMBER OF SEQ ID NOS: 67; SOFTWARE: Patentin Ver. 3.2; SEQ ID NO 21
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Publication No. US20050158710A1

GENERAL INFORMATION:

APPLICANT: TSANG, SHIRLEY

APPLICANT: PRICE, JAMES A.

APPLICANT: PRICE, JAMES A.

TITLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID

FILE REFERENCE: 020187.0187PTUS

CURRENT APPLICATION NUMBER: US/10/760,048

CURRENT FILING DATE: 2004-01-16

NUMBER OF SEQ ID NOS: 67

SOFTWARE: PATCHING UNC: 3.2

SEQ ID NO 44

LENGTH: 237
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; OTHER INFORMATION: Description of Unknown Organism: Viral; OTHER INFORMATION: 5'untranslated polynucleotide sequence US-10-760-048-60
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Best Local Similarity 100.0%; Pi
Matches 20; Conservative 0;
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US-10-760-048-60/c
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                                                                                    SEQ ID NO 57
LENGTH: 237
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APPLICANT: PRICE, JAMES A.

APPLICANT: PRICE, JAMES A.

TITLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID

FILE REFERENCE: 020187.0187PTUS

CURRENT APPLICATION NUMBER: US/10/760,048

CURRENT PILIG DATE: 2004-01-16

NUMBER OF SEQ ID NOS: 67

SOFTWARE: Patentin Ver. 3.2

LENGTH: 237

TYPE: received.
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Publication No. US20050158710A1
GENERAL INFORMATION:
APPLICANT: TRANG, SHIRLEY
APPLICANT: PRICE, JAMES A.
APPLICANT: PRICE, JAMES A.
TILLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID
FILE REFERENCE: 020187.0189PTUS
CURRENT APPLICATION NUMBER: US/10/760,048
CURRENT FLING DATE: 2004-01-16
NUMBER OF SEQ ID NOS: 67
SOUTHWARE: Patentin Ver. 3.2
                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 237;
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OTHER INFORMATION: Description of Unknown Organism: Viral:
OTHER INFORMATION: 5'untranslated polynucleotide sequence
US-10-760-048-56
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US-10-760-048-57/c
| Sequence 57, Application US/10760048
| Publication No. US2050158710A1
| GENERAL INFORMATION:
| APPLICANT: FRICE, JAMES A.
| APPLICANT: HELLY TOBIN J.
| TITLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID;
| FILE REFERENCE: 020187.0187PTUS
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7.1;
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7.1;
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100.0%; Score 20; DB
Best Local Similarity 100.0%; Pred. No. 7.1
Matches 20; Conservative 0; Mismatches
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Pred. No.
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ORGANISM: Unknown Organism
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Best Local Similarity 100.
Matches 20; Conservative
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US-10-760-048-56/c
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LENGTH: 237
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                                                                                                                                                                                                                                                                                                                                                                                      Sequence 59, Application US/10760048
Publication No. US20050158710A1
GENERAL INFORMATION:
APPLICANT: TSANG, SHIRLEY
APPLICANT: PRICE, JAMES A.
APPLICANT: PRICE, JAMES A.
TITLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID
TITLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID
CURRENT APPLICATION NUMBER: US/10/760,048
CURRENT FILING DATE: 2004-01-16
NUMBER OF SEQ ID NOS: 67
SOFTWARE: PATENTING DATE: 3.2
SEQ ID NO 59
LENGTH: 237
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; Publication No. US20050158710A1
; GENERAL INFORMATION:
; APPLICANT: FANG, SHIRLEY
; APPLICANT: PRICE, JAMES A.
; APPLICANT: HELLYER, TOBIN J.
; TITLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID
; FILE REFERENCE: 020187.0187PIG.
; CURRENT APPLICATION NUMBER: US/10/760,048
; CURRENT FILING DATE: 2004-01-16
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: Patentin Ver. 3.2
; SEQ ID NO 60
                                                                                                         Score 20; DB 9; Length 237;
Pred. No. 7.1;
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CTHER INFORMATION: Description of Unknown Organism: Viral; OTHER INFORMATION: 5'untranslated polynucleotide sequence US-10-760-048-57
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US-10-76-048-13/C
Sequence 13, Application US/10760048
Publication No. US20050158710A1
GENERAL INFORMATION:
APPLICANT: PRICE, JAMES A.
APPLICANT: PRICE, JAMES A.
APPLICANT: PRICE, TOBIN J.
TITLE OF INVENTION: DEFECTION OF ENTEROVIRUS NUCLEIC ACID
FILE REPERENCE: 020187.0187PTUS
CURRENT FILING DATE: 2004-01-16
NUMBER OF SEQ ID NOS: 67
SOFTWARR: PATENTIN Ver. 3.2
SEQ ID NO 18
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100.0%; Score 20; DB 9; Length 237;
Best Local Similarity 100.0%; Pred. No. 7.1;
Matches 20; Conservative 0; Mismatches 0: Indela
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                                                                 Sequence 66, Application US/10760048
Publication No. US20050158710A1
GENERAL INFORMATION:
APPLICANT: TSANG, SHIRLEY
APPLICANT: TRICE, JAMES A.
APPLICANT: HELLYER, TOBIN J.
TITLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID
FILE REFRENCE: 020187.0187PTUS
CURRENT APPLICATION UNBER: US/10/760,048
CURRENT FILING DATE: 2004-01-16
NUMBER OF SEQ ID NOS: 67
SOUTHARE: PATENTIN Ver. 3.2
SEQ ID NO 66
LENGTH: 237
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APPLICANT: PRICE, JAMES A.
APPLICANT: HELLYER
APPLICANT: HELLYER
TITLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID
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Sequence 63, Application US/10760048

Publication No. US20050158710A1

GENERAL INFORMATION:
APPLICANT: FRICE, JAMES A.
APPLICANT: HELLYER, TOBIN J.
TITLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID
FILE REFERENCE: 020187.0187PTUS
CURRENT APPLICATION NUMBER: US/10/760,048

CURRENT PILING DATE: 2004-01-16
NUMBER OF SEQ ID NOS: 67

SOFTWARE: Patentin Ver. 3.2

LENGTH: 237
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| Sequence 64, Application US/10760048
| Sequence 64, Application US/10760048
| Sequence 64, Application US/10760048
| Publication No. US20050158710A1
| APPLICANT: TSANG, SHIRLEY
| APPLICANT: PRICE, JAMES A. |
| APPLICANT: HELLYER, TOBIN J. |
| TITLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID |
| TITLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID |
| TITLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID |
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| TITLE OF INVENTION OF ENTEROVIRUS NUCLE ACID |
| TITLE OF INVENTION OF ENTEROVIRUS NUCLE ACID |
| TITLE OF 
100.0%; Score 20; DB 9; Length 237; 100.0%; Pred. No. 7.1; or Mismatches 0; Indels
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ORGANISM: Unknown Organism
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ORGANISM: Unknown Organism
   Query Match 100.
Best Local Similarity 100.
Matches 20; Conservative
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Best Local Similarity 100.
Matches 20; Conservative
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Sequence 33, Application US/10760048

Publication No. US20050158710A1

GENERAL INFORMATION:
APPLICANT: TSANG, SHIRLEY
APPLICANT: FRICE, JAMES A.
APPLICANT: HELLYER, TOBIN J.
TITLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID
FILE REFERENCE: 202187.0187PTUS
CURRENT APPLICATION NUMBER: US/10/760,048
NUMBER OF SEQ ID NOS: 67
SEQ ID NO 33
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Sequence 38, Application US/10760048

Publication No. US20050158710A1

GENERAL INFORMATION:
APPLICANT: TSANG, SHIRLEY
APPLICANT: HELLYER AND APPLICANT:
FILE REFERENCE: JOHN J.
TITLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID
FILE REFERENCE: 2020187.0187PTUS
CURRENT APPLICATION NUMBER: US/10/760,048
CURRENT APPLICATION NUMBER: US/10/760,048

NUMBER OF SEQ ID NOS: 67

SOFTWARE: Patentin Ver. 3.2

SEQ ID NO 38
LENGTH: 238
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                                                                                                                                100.0%; Score 20; DB 9; Length 238; 100.0%; Pred. No. 7.1;
       FEATURE: OTHER INFORMATION: Description of Unknown Organism: Viral OTHER INFORMATION: 5'untranslated polynucleotide sequence
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COTHER INFORMATION: Description of Unknown Organism: Viral:
COTHER INFORMATION: 5'untranslated polynucleotide sequence
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OTHER INFORMATION: Description of Unknown Organism: Viral
OTHER INFORMATION: 5'untranslated polynucleotide sequence
US-10-760-048-38
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ORGANISM: Unknown Organism
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ORGANISM: Unknown Organism
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Best Local Similarity
Matches 20; Conserv
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US-10-760-048-33/c
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Publication No. US20050158710A1
GENERAL INFORMATION:
APPLICANT: TSANG, SHIRLEY
APPLICANT: PRICE, JAMES A.
APPLICANT: HELIYER, TOBIN J.
TITLE OF INVENTION: EDETECTION OF ENTEROVIRUS NUCLEIC ACID
PILE REFERENCE: 020187.0187PTUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: Description of Unknown Organism: Viral OTHER INFORMATION: 5'untranslated polynucleotide sequence
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APPLICANT: PRICE, JAMES A.
APPLICANT: HELLYER, TOBIN J.
TITLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID
FILE REFERENCE: 020187.0187PTUS
FILE REFERENCE: 020187.0187PTUS
CURRENT APPLICATION NUMBER: US/10/760,048
CURRENT FILING DATE: 2004-01-16
NUMBER OF SEQ ID NOS: 67
SOFTWARE: Patentin Ver: 3.2
SEQ ID NO 15
LENGTH: 238
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CURRENT FILING DATE: 2004-01-16
NUMBER OF SEQ ID NOS: 67
SEQ ID NO 30
LENGTH: 238
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CURRENT APPLICATION NUMBER: US/10/760,048
CURRENT FILING DATE: 2004-01-16
NUMBER PEGQ ID NOS: 67
SOFTWARE: Patentin Ver. 3.2
SEQ ID NO 31
LENGTH: 238
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                                                                                                                                                                                            ORGANISM: Unknown Organism
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Best Local Similarity 100.
Matches 20; Conservative
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ORGANISM: Unknown Organism
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US-10-760-048-30/c
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; Sequence 47, Application US/10760048
; Publication No. US20050158710A1
; GENERAL INFORMATION:
; APPLICANT: TRANG, SHIRLEY
; APPLICANT: PRICE, JAMES A.
; APPLICANT: HELLYER, TOBIN J.
; TITLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID
; FILE REFERENCE: 020187.0187P0156,048
; CURRENT APPLICATION NUMBER: US/10/760,048
; CURRENT FILING DATE: 2004-01-16
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: Patentin Ver. 3.2
; SEQ ID NO 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-10-760-048-48/c
; Sequence 48, Application US/10760048
; Publication No. US20050158710A1
; GENERAL INFORMATION:
A APPLICANT: TSANG, SHIRLEY
; APPLICANT: HELLYER, TOBIN J.
; TITLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID
FILE REFERENCE: 020197.0187PTUS
; CURRENT APPLICATION NUMBER: US/10/760,048
; CURRENT FILING DATE: 2004-01-16
; NUMBER OF SEQ ID NOS: 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 100.0%; Score 20; DB 9; Length 238; Best Local Similarity 100.0%; Pred. No. 7.1; Matches 20; Conservative 0; Mismatches 0; Indels
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APPLICANT: TRANS, SHIRLEY
APPLICANT: TRANS, SHIRLEY
APPLICANT: TRICE, JAMES A.
APPLICANT: HILLYER, TOBIN J.
TITLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID
FILE REFERENCE: 020187.0187PUS
CURRENT APPLICATION NUMBER: US/10/760,048
CURRENT FILING DATE: 2004-01-16
NUMBER OF SEQ ID NOS: 67
SEQ ID NO 46
LENGTH: 238
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ORGANISM: Unknown Organism
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| Publication No. US20050158710A1
| GENERAL INFORMATION:
| APPLICANT: PRICE, JAMES A. |
| TITLE OF INVENTION DETECTION OF ENTEROVIRUS NUCLEIC ACID FILE REFERENCE: 020187.0187PUS
| CURRENT APPLICATION NUMBER: US/10/760,048 |
| CURRENT PILING DATE: 2004-01-16 |
| NUMBER OF SEQ ID NOS: 67 |
| SOFTWARR: Patentin Ver. 3.2 |
| SEQ ID NO 43 |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 20; DB 9; Length 238; 100.0%; Pred. No. 7.1; cive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                 APPLICANT: TSANG, SHIRLEY
APPLICANT: FRICE, JAMES A.
APPLICANT: HELLYER, TOBIN J.
TITLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID
FILE REFERENCE: 020187.0187PTUS
CURRENT APPLICATION NUMBER: US/10/760,048
CURRENT FILING DATE: 2004-01-16
NUMBER OF SEQ ID NOS: 67
SOFTWARE: PACENTIN Ver. 3.2
                                                                                                                                 US-10-760-048-42/c
; Sequence 42, Application US/10760048
; Publication No. US20050158710A1
; GENERAL INFORMATION:
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; Publication No. US20050158710A1
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                               105 AAGGAACACGGACACCCAA 86
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Best Local Similarity 100.
Matches 20, Conservative
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ORGANISM: Unknown Organism
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ORGANISM: Unknown Organism
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LENGTH: 238
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ORGANISM: Unknown Organism
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SOFTWARE: Patentin Ver. 3.2
SEQ ID NO 1
LENGTH: 709
                                                                       20; Conservative
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; ORGANISM: Enterovirus 71
US-10-614-283-1
                         Query Match
Best Local Similarity
Matches 20; Conserv
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; Publication No. US20050158710A1
; GENERAL INFORMATION:
; APPLICANT: PRICE, JAMES A.
; APPLICANT: PRICE, JAMES A.
; TILLE OF INVESTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID
; FILE REPERENCE: 020187.01897PTUS
; CURRENT APPLICATION NUMBER: US/10/760,048
; CURRENT FILING DATE: 2004-01-16
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: Patentin Ver. 3.2
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                                                                                                                                                                                                                     Score 20; DB 9; Length 238;
Pred. No. 7.1;
                                                                                                                              CTHER INFORMATION: Description of Unknown Organism: Viral; OTHER INFORMATION: 5'untranslated polynucleotide sequence US-10-760-048-48
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APPLICANT: PRICE, JAMES A.
APPLICANT: PRICE, JAMES A.
APPLICANT: HELLYSTA, TOBIN J.
TITLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID
FILE REPRENCE: 020187.0187PTUS
CURRENT FILING DATE: 2004-01-16
NUMBER OF SEQ ID NOS: 67
SEQ ID NOS: 67
SEQ ID NO 61
LENGTH: 238
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100.0%; Score 20; DB
Best Local Similarity 100.0%; Pred. No. 7.1
Matches 20; Conservative 0; Mismatches
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Publication No. US20050158710A1
GENERAL INFORMATION:
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ORGANISM: Unknown Organism
SOFTWARE: Patentin Ver. 3.2
                                                                                  ORGANISM: Unknown Organism
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ORGANISM: Unknown Organism
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nes 20; Conserv
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LENGTH: 238
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Best Local S:
Matches 20
                                                                  TYPE: DNA
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APPLICANT: HSU, TSU-AN
APPLICANT: HSU, TSU-AN
APPLICANT: WU, TZONG-YUAN
APPLICANT: LEE, JIN-CHING
TITLE OF INVENTION: INTERNAL RIBOSOME ENTRY SITES FOR RECOMBINANT PROTEIN
TITLE OF INVENTION: EXPRESSION
FILE REFERENCE: 08842.0002-00000
CURRENT APPLICATION NUMBER: US/10/614,283
FRIOR APPLICATION NUMBER: 60/394,269
PRIOR FILING DATE: 2002-07-09
PRIOR FILING DATE: 2002-07-09
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DB 9; Length 238; 7.1;
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                                                Indels
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APPLICANT: TSANG, SHIRLEY
APPLICANT: PRICE, JAMES A.
APPLICANT: HELLYER, TOBIN J.
TITLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID
FILE REFERENCE: 020187.0187PTUS
CURRENT PAPLICATION NUMBER: US/10/760,048
CURRENT FILING DATE: 2004-01-16
NUMBER OF SEQ ID NOS: 67
SOFTWARE: PALENTIN Ver. 3.2
SEQ ID NO 65
LENGTH: 238
                                                Mismatches
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Publication No. US20050158710A1
GENERAL INFORMATION:
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Matches 20; Conservative 0
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                             APPLICANT: Sommermeyer, Klaus
TITLE OF INVENTION: TRANSGENICALLY PRODUCED PLATELET DERIVED
TITLE OF INVENTION: GROWTH FACTOR
TITLE OF INVENTION: GROWTH FACTOR
FILE REFERENCE: 10275-120001
CURRENT APPLICATION NUMBER: US/09/884,586A
CURRENT FILING DATE: 2001-06-19
PRIOR APPLICATION NUMBER: 60/212,406
PRIOR FILING DATE: 2000-06-19
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
LENGTH: 2076
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 100.0%; Score 20; DB 6; Length 10448; Best Local Similarity 100.0%; Pred. No. 7.7; Matches 20; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 100.0%; Score 20; DB 3; Length 2076; Best Local Similarity 100.0%; Pred. No. 7.4; Matches 20; Conservative 0; Mismatches 0; Indels C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 4, Application US/10408456; Sequence 4, Application US/10408456; Publication No. US2004001364BA1; GRNERAL INFORMATION: US2004001364BA1; APPLICANT: Oxford Biomedica (UK) Limited; APPLICANT: KINGSMAN, et al., Alan John TITLE OF INVENTION: Vector System; FILE REPERBENCE: 674523-2016; CURRENT APPLICATION NUMBER: US/10/408,456; CURRENT FILING DATE: 2003-04-08; PRIOR FILING DATE: 2001-10-15; PRIOR FILING DATE: 2001-10-15; PRIOR FILING DATE: 2001-10-06; NUMBER: OF SEQ ID NOS: 34; SOFTWARR: PATENTIN Version 3.0; SEQ ID NO 4.5
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Fublication No. US20040013648A1
GERREAL INFORMATION:
APPLICANT: Oxford Biomedica (UK) Limited
APPLICANT: CAFORD STATE Alan John
TITLE OF INVENTION: Vector System
FILE REFERENCE: 674523-2016
CURRENT APPLICATION NUMBER: US/10/408,456
CURRENT FILING DATE: 2003-04-08
PRIOR PLING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: 02/4601/04433
PRIOR APPLICATION NUMBER: 02/4501/04433
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; ORGANISM: Equine Infectious Anemia Virus
US-10-408-456-4
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Meade, Harry M.
Eichner, Wolfram
                                                                                                                                                                                                                                                                                                                                                         ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-884-586A-3
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                     APPLICANT:
APPLICANT:
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APPLICANT: Atabekov, Vurii
APPLICANT: Dorokhov, Yurii
APPLICANT: Bidlackov, Maxim
APPLICANT: Ivanov, Peter
APPLICANT: Ivanov, Peter
APPLICANT: Gleba, Yuri
TITLE OF INVENTION: ELEMENTS
TITLE OF INVENTION: ELEMENTS
FILE REPRENCE: 9286,30
CURRENT FILING DATE: 2004-03-02
PRIOR FILING DATE: 2002-09-03
PRIOR FILING DATE: 2001-09-04
NUMBER OF SEQ ID NOS: 41
SOFTWARE: Patentin version 3.2
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                                                       Sequence 21, Application US/10839729;
Publication No. US20050002953A1
GENERAL INFORMATION:
TITLE OF INVENTION: SARS-CORONAVIRUS VIRUS-LIKE PARTICLES;
TITLE OF INVENTION: AND METHODS OF USE;
TITLE OF INVENTION: AND METHODS OF USE;
FILE REFERENCE: BIODANK.013A
CURRENT APPLICATION NUMBER: US/10/839,729
CURRENT FILICATION NUMBER: 60/468703
PRIOR FILICATION NUMBER: 60/468703
PRIOR FILICATION NUMBER: 60/468703
SROWENCE: 2003-05-06
SOUTHAND DATE: 2003-05-06
SOUTHAND: PASISEQ FOR WINDOWS VERSION 4.0
SEQ ID NO 21
LENGTH: 743
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 20; DB 8; Length 743; 100.0%; Pred. No. 7.3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
; ORGANISM: Mahoney Strain Poliovirus Type I
US-10-839-729-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 10, Application US/10489136; Publication No. US20050014150A1; GENERAL INFORMATION:
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; Publication No. US2030046716A1
; RENERAL INFORMATION;
; APPLICANT: Echelard, Yann
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Best Local Similarity 100.
Matches 20; Conservative
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ORGANISM: Poliovirus
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US-10-489-136-10/c
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US-09-884-586A-3/c
                                            US-10-839-729-21/c
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LENGTH: 745
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PEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic;
OTHER INFORMATION: nucleotide sequence
19.10-873-573-7
        TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                Query Match
Best Local Similarity
Matches 20; Conserv
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APPLICANT:
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                                                                                                                                                                                                Length 11058;
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100.0%; Pred. No. 7.7
tive 0; Mismatches
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TITLE OF INVENTION: Vector System
FILE REFREEMENE: 674523-201
CURRENT APPLICATION NUMBER: US/10/408,456
CURRENT FILING DATE: 2003-04-08
PRIOR APPLICATION NUMBER: PCT/GB01/04433
PRIOR FILING DATE: 2001-10-15
PRIOR PLING DATE: 2000-10-05
PRIOR FILING DATE: 2000-10-05
NUMBER OF SEQ ID NOS: 34
NUMBER OF SEQ ID NOS: 34
SOFTWARE: Patentin version 3.0
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APPLICANT: RIGKIN, JAMES
APPLICANT: KINGSMAN, SUGAN MARIE
TITLE OF INVENTION: VECTOR SYSTEM
FILE REFERENCE: 674523-2016.1
CURRENT APPLICATION NUMBER: US/10/873,573
CURRENT FILING DATE: 2004-06-21
PRIOR PRLICATION NUMBER: 10/408,456
PRIOR PELICATION NUMBER: PCT/GB01/04433
PRIOR PELICATION NUMBER: PCT/GB01/04433
                                                                                                           ; TYPE: DNA
; ORGANISM: Equine Infectious Anemia Virus
US-10-408-456-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: GB 0024550.6
PRIOR FILING DATE: 2000-10-06
NUMBER OF SEQ ID NOS: 11
                                                                                                                                                                                                                                                                                                                      3813 AAGGAAACACGACACCCAA 3794
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Publication No. US20040013648A1
GENERAL INFORMATION:
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Publication No. US20050002907A1
GENERAL INFORMATION:
APPLICANT: MITRAPHANOUS, KYRI
PRIOR FILING DATE: 2000-10-06
NUMBER OF SEQ ID NOS: 34
SOFTWARE: Patentin version 3.0
SEQ ID NO 5
LENGTH: 11058
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Matches 20; Conservative
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LENGTH: 11622
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Score 20; DB 8; Length 11622; Pred. No. 7.7;
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                                                    Indels
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APPLICANT: Juang, Jyh-Lyh
APPLICANT: Lin, Chung-Yen
FILE APPLICANT: Lin, Chung-Yen
TITLE OF INVENTION: CROSS-SPECIES NUCLEIC ACID PROBES
FILE REPERBENT: 1563-006001
CURRENT APPLICATION NUMBER: US/10/366,823
CURRENT APPLICATION NUMBER: US/00/367,541
PRIOR APPLICATION NUMBER: 2003-02-15
FRIOR PILING DATE: 2002-02-15
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5
LENGTH: 62
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1; Mismatches
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CURRENT APPLICATION NUMBER: US/10/408,519
CURRENT FILING DATE: 2003-04-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: US 09/522,417
PRIOR FILING DATE: 2000-03-09
NUMBER OF SEQ ID NOS: 5
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                      7244 AAGGAAACACGGACACCCAA 7225
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Publication No. US20030211526A1
GENERAL INFORMATION:
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Publication No. US20030228683A1
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      100.0%;
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Best Local Similarity 95.0%;
Matches 19; Conservative 1
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Bair, Chi-Horng
Wang, Shin-Hwan
                                                  Conservative
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APPLICANT: Shih, Yu-Hau
APPLICANT: Tsai, Chuan-Mei
APPLICANT: Wang, Yih-Weng
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; Sequence 35, Application US/10760048
; Publication Wo. US20050158710A1
; Publication Wo. US20050158710A1
; GENERAL INFORMATION:
A APPLICANT: TSANG, SHIRLEY
; APPLICANT: HELLYER, ADELS A.
; TITLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID
; FILE REFERENCE: 020187.0187PTUS
; CURRENT APPLICATION NUMBER: US/10/760,048
; CURRENT PILLING DATE: 2004-01-16
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: Patentin Ver. 3.2
; SEQ ID NO 35
; LENGTH: 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 238;
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22;
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                                                                                                                                     APPLICANT: TSANG, SHIRLEY
APPLICANT: PRICE, JAMES A.
APPLICANT: HELLYER, TOBIN J.
TITLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID
FILE REFERENCE: 020187.0187PTUS
CURRENT APPLICATION NUMBER: US/10/760,048
CURRENT FILING DATE: 2004-01-16
NUMBER OF SEQ ID NOS: 67
SOFTWARE: Patentin Ver. 3.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 9;
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100.0%; Pred. No.
                                                                         Sequence 34, Application US/10760048
Publication No. US20050158710A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               104 AGGAAACACGGACACCCAA 86
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Best Local Similarity 100.0
Matches 19, Conservative
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ORGANISM: Unknown Organism
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ORGANISM: Unknown Organism
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                              SEQ ID NO 34
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  ; FEATURE:
; OTHER INFORMATION: Probe from 5' ends of enterovirus genes
US-10-408-519-3
                                                                               Length 53;
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Publication No. US20050239055A1
GENERAL INFORMATION:
APPLICANT: Genetics & IVF
APPLICANT: MARIANI, Brian D.
TITLE OF INVENTION: BRIEROUS PRIMERS AND PROBES
FILE REPERBURE: 043956-0121
CURRENT APPLICATION NUMBER: US/10/829,474
CURRENT FILING DATE: 2004-04-22
NUMBER OF SEQ ID NOS: 57
SOFTWARE: PatentIn version 3.2
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APPLICANT: MARIANI, Brian D.
TITLE OF INVENTION: ENTEROVIRUS PRIMERS AND PROBES
FILE REPERENCE: 043956-0121
CURRENT APPLICATION NUMBER: US/10/829,474
CURRENT FILING DATE: 2004-04-22
NUMBER OF SEQ ID NOS: 57
SOFTWARE: Patentin version 3.2
SEQ ID NO 22
LENGTH: 19
                                                                             Query Match 100.0%; Score 20; DB 6; Best Local Similarity 95.0%; Pred. No. 17; Matches 19; Conservative 1; Mismatches 0
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100.0%; Pred. No. ...
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; Sequence 22, Application US/10829474
; Publication No. US20050239055A1
; GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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Best Local Similarity 100.
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Best Local Similarity
Matches 19; Conserv
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US-10-829-474-21
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LENGTH: 19
FEATURE:
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APPLICANT: PRICE, JAMES A.
APPLICANT: PRICE, JAMES A.
APPLICANT: HILLYST, TOBIN J.
TITLE OF INVANITON: DETECTION OF ENTEROVIRUS NUCLEIC ACID
FILE REFERENCE: 020187.0187PUS
CURRENT PAPLICATION NUMBER: US/10/760,048
CURRENT FILING DATE: 2004-01-16
NUMBER OF SEQ ID NOS: 67
SEQ ID NOS: 67
SEQ ID NO 41
LENGTH: 235
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Publication No. US20050158710A1
GENERAL INFORMATION
APPLICANT: TSANG, SHIRLEY
APPLICANT: PRICE, JAMES A.
APPLICANT: HELLYER, TOBIN J.
TITLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID
FILE REFERENCE: 020187.0187PTUS
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100.0%; Pred. No. 22;
iive 0; Mismatches
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       CURRENT APPLICATION NUMBER: US/10/332,123
CURRENT FILING DATE: 2003-09-24
FRIOR PEPLICATION NUMBER: PCT/FR01/02191
PRIOR FILING DATE: 2001-07-06
PRIOR APPLICATION NUMBER: FR00-08839
FRIOR APPLICATION NUMBER: FR00-08839
NUMBER OF SEQ ID NOS: 108
SOFWARE: Patentin version 3.2
LENGTH: 521
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CURRENT FILING DATE: 2004-01-16
NUMBER OF SEQ ID NOS: 67
SEQ ID NO 37
LENGTH: 236
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Publication No. US20050158710A1
GENERAL INFORMATION:
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US-10-332-123-53
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Best Local Similarity 95.09
Warches 19; Conservative
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ORGANISM: Unknown Organism
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Best Local Similarity
Matches 19; Conserv
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TITLE OF INVENTION: METHOD FOR CONTROLLING THE MICROBIOLOGICAL QUALITY OF AN AQUEOUS
TITLE OF INVENTION: MEDIUM AND KIT THEREFOR
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APPLICANT: HELLYER, TOBIN J.

TITLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID
FILE REPERENCE: 020187-0118FPTUS
CURRENT APPLICATION NUMBER: US/10/760,048
CURRENT FILING DATE: 2004-01-16
NUMBER OF SEQ ID NOS: 67
SOFTWARE: Patentin Ver. 3.2
SEQ ID NO 36
LENGTH: 238
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APPLICANT: PRICE, JAMES A.
TITLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID
FILE REFERENCE: 020187.0187PTUS
CURRENT PRILICATION NUMBER: US/10/760,048
CURRENT FILING DATE: 2004-01-16
NUMBER OF SEQ ID NOS: 67
SEQ ID NO 62
LENGTH: 238
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Best Local Similarity 100.0%; Pred. No. 22;
Matches 19; Conservative 0; Mismatches
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Publication No. US20050158710A1
GENERAL INFORMATION:
APPLICANT: TSANG, SHIRLEY
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Publication No. US20040072239A1
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APPLICANT: GUILLOT, Emmanuelle
APPLICANT: MABILAT, Claude
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LACROIX, Bruno
VERNET, Guy
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Matches 19; Conserv
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APPLICANT: PRICE, JAMES A.
APPLICANT: PRICE, JAMES A.
TITLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID
FILE REFERENCE: 020187.0187PTUS
CURRENT APPLICATION NUMBER: US/10/760,048
CURRENT FILING DATE: 2004-01-16
NUMBER OF SEQ ID NOS: 67
SEQ ID NO 14
LENGTH: 238
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APPLICANT: TSANG, SHIRLEY
APPLICANT: PRICE, JAMES A.
APPLICANT: HELLYER, TOBIN J.
ATTILE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID
FILE REFERENCE: 020187.0187FUS
CURRENT APPLICATION NUMBER: US/10/760,048
CURRENT FILING DATE: 2004-01-16
NUMBER OF SEQ ID NOS: 67
SOFTWARE: Patentin Ver. 3.2
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95.0%; Pred. No. 43;
tive 0; Mismatches
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                                                                                                                                             Sequence 14, Application US/10760048
Publication No. US20050158710A1
GENERAL INFORMATION:
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; Sequence 23, Application US/10760048
; Publication No. US20050158710A1
1 AAGGAAACACGGACACCCAA 20
                                      105 AAAGAACACGGACACCCAA 86
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ORGANISM: Unknown Organism
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ORGANISM: Unknown Organism
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Best Local Similarity 95.0
Matches 19; Conservative
                                                                                                     RESULT 54
US-10-760-048-14/c
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LENGTH: 238
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                                                                                                         Length 236;
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                                                                                                                                                                                                                                                                                                                                      Sequence 16, Application US/10760048
Publication No. US20050158710A1
GENERAL INFORMATION:
APPLICANT: TSANG. SHIRLEY
APPLICANT: TRANG. SHIRLEY
APPLICANT: HELLYER, TOBIN J.
TILLE REFERENCE: O2018'.0187PTUS
CURRENT APPLICATION NUMBER: US/10/760,048
CURRENT FILLING DATE: 2004-01-16
NUMBER OF SEQ ID NOS: 67
SOFTWARE: Patentin Ver. 3.2
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| Publication No US20050158710A1 |
| GENERAL INFORMATION: |
| APPLICANT: TSANG, SHIRLEY |
| APPLICANT: PRICE, JAMES A. |
| APPLICANT: PRICE, JAMES A. |
| TITLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID |
| FILE REFERENCE: 020187.0187PTUS |
| CURRENT APPLICATION UNMBER: US/10/760,048 |
| CURRENT FILING DATE: 2004-01-16 |
| NUMBER OF SEQ ID NOS: 67 |
| SOGTWARE: Patentin Ver. 3.2 |
| SEQ ID NO 32 |
                  OTHER INFORMATION: Description of Unknown Organism: Viral OTHER INFORMATION: 5'untranslated polynucleotide sequence
                                                                                                                                                    1; Indels
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                                                                                                       Score 18.4; DB 9;
Pred. No. 43;
                                                                                       92.0%; Stor.
95.0%; Pred. No. -.,
0; Mismatches
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Best Local Similarity 95.09
Matches 19; Conservative
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Best Local Similarity 95.0
Matches 19; Conservative
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US-10-760-048-16/c
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                                                            US-10-760-048-37
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LENGTH: 237
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- SOFTWARE: Patentin Ver. 3.2
SEQ ID NO 26
LENGTH: 238
                                                                        TYPE: DNA
ORGANISM: Unknown Organism
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ORGANISM: Unknown Organism
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Matches 19; Conserv
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                                         APPLICANT: PRICE, JAMES A.
APPLICANT: PRICE, JAMES A.
APPLICANT: HELLYER, TOBLN J.
TITLE OP INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID
FILE REPERENCE: 020187.0187PTUS
CURRENT APPLICATION NUMBER: US/10/760,048
CURRENT PILING DATE: 2004-01-16
NUMBER OF SEQ ID NOS: 67
SOFTWARE: Patentin Ver. 3.2
SEQ ID NO 23
LENGTH: 238
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APPLICANT: HELLYER, TOBIN J.
TITLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID
FILE REFERENCE: 0.20187, 0.187PTUS
CURRENT APPLICATION NUMBER: US/10/760, 048
CURRENT FILING DATE: 2004-01-16
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APPLICANT: HELLYER, TOBIN J.
TITLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID
FILE REFERENCE: 020187.0187PUS
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CURRENT FILING DATE: 2004-01-16
NUMBER OF SEQ ID NOS: 67
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Publication No. US20050158710A1
GENERAL INFORMATION:
APPLICANT: TSANG, SHIRLEY
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Publication No. US20050158710A1
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ORGANISM: Unknown Organism
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SOFTWARE: PatentIn Ver. 3.2
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Matches 19; Conservative
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APPLICANT: TSANG, SHIRLEY
                          SHIRLEY
GENERAL INFORMATION:
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LENGTH: 238
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APPLICANT: TSANG, SHIRLEY
APPLICANT: PRICE, JAMES A.
APPLICANT: PRICE, JAMES A.
TITLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID
FILE REPRENCE: 020187.0187PTUS
CURRENT APPLICATION NUMBER: US/10/760,048
CURRENT PILING DATE: 2004-01-16
NUMBER OF SEQ ID NOS: 67
SOFTWARE: PARENTIN Ver. 3.2
SEQ ID NO 27
LENGTH: 238
OTHER INFORMATION: Description of Unknown Organism: Viral JOTHER INFORMATION: 5'untranslated polynucleotide sequence US-10-760-048-26
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APPLICANT: FRICE, JAMES A.
APPLICANT: FRICE, JAMES A.
APPLICANT: HILLYER TOBIN J.
TITLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID
FILE REFERENCE: 020187.0187PTUS
CURRENT APPLICATION NUMBER: US/10/760,048
CURRENT FILING DATE: 2004-01-16
NUMBER OF SEQ ID NOS: 67
SEQ ID NOS: 67
SEQ ID NO 28
LENGTH: 238
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Pred. No. 43;
0; Mismatches
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Publication No. US20050158710A1
GENERAL INFORMATION:
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Publication No. US20050158710A1
GENERAL INFORMATION:
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Best Local Similarity 95.0%;
Matches 19; Conservative (
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Sequence 7, Application US/10136819
Sequence 7, Application WS/10136819
Sequence 7, Application No. US20030166593A1
GENERAL INFORMATION:
APPLICANT: Chien, Kenneth
APPLICANT: Hoshijima, Masahiko
TITLE OF INVENTION: No. US20030166593A1-viral vesicle vector for cardiac specific gen
FILE REFERENCE: 6627-PA1198
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: 60/287,423
PRIOR FILING DATE: 2001-04-30
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin version 3.1
SEQ ID NO 7
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Pred. No. 46;
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Publication No. US20050239055A1

GENERAL INFORMATION:
APPLICANT: Genetics & IVF

APPLICANT: Genetics & IVF

TITLE OF INVENTION: ENTEROVIRUS PRIMERS AND PROBES
FILE REFERENCE: 043956-0121

CURRENT APPLICATION NUMBER: US/10/829,474

CURRENT FILING DATE: 2004-04-22

NUMBER OF SEQ ID NOS: 57

SOFTWARE: Patentin version 3.2
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Pred. No. 64;
0; Mismatches
    Pred. No. 44;
0; Mismatches
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; Sequence 18, Application US/10829474
; Publication No. US20050239055A1
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95.0%;
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Best Local Similarity 95.0%;
Matches 19; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TYPE: DNA
; ORGANISM: Coxsackievirus B3
US-10-136-819-7
  Best Local Similarity 95.0%
Matches 19; Conservative
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Best Local Similarity
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APPLICANT: MABILAT, Claude
APPLICANT: MACHON, Carole
APPLICANT: MACHON, Carole
APPLICANT: LACROIX, Bruno
APPLICANT: VERNET, GUY
APPLICANT: VERNET, GUY
APPLICANT: LAFFAIRE, Philippe
ITTLE OF INVENTION: METHOD FOR CONTROLLING THE MICROBIOLOGICAL QUALITY OF AN AQUEOUS
TITLE OF INVENTION: MEDIUM AND KIT THEREFOR
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                      Score 18.4; DB 9; Length 238; Pred. No. 43;
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                                                                                                                                                                                                                                ; Sequence 29, Application US/10760048
; Publication No. US20050158710A1
; GENERAL INPORMATION:
; APPLICANT: TSANG, SHIRLEY
; APPLICANT: PRICE, JAMES A.
; APPLICANT: HELLYER, TOBIN J.
; TITLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID; FILE REFERENCE: 020187.018779105
; CURRENT APPLICATION NUMBER: US/10/760,048
; CURRENT FILING DATE: 2004-01-16
; NUMBER OF SEQ ID NOS: 67
; SOR ID NO 29
; LENGTH: 238
                                                              1; Indels
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CTHER INFORMATION: Description of Unknown Organism: Viral
CTHER INFORMATION: 5'untranslated polynucleotide sequence
US-10-760-048-29
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        92.0%; Scc...
95.0%; Pred. No. -...
0; Mismatches
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CURRENT APPLICATION NUMBER: US/10/332,123
CURRENT FILING DATE: 2003-09-24
FRIOR APPLICATION NUMBER: PR00-08839
PRIOR FILING DATE: 2001-07-06
PRIOR FILING DATE: 2000-07-06
NUMBER OF SEQ ID NOS: 108
SOFTWARE: Patentin version 3.2
LENGTH: 520
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; ORGANISM: Coxsackievirus (D00538)
US-10-332-123-54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Unknown Organism
                                                              19; Conservative
                                         Best Local Similarity
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US-10-760-048-29/c
                        Query Match
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; OTHER INFORMATION: Chemically synthesized reverse primer for amplifying enteroviral US-10-829-474-23
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                                                                                                                                                                        Length 225734;
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100.0%; Pred. No. 2e+02;
ive 0; Mismatches 0; Indels
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APPLICANT: TSANG, SHIRLEY
APPLICANT: PRICE, JAMES A.
APPLICANT: HELLYER, TOBIN J.
TITLE OF INVENTION: BETECTION OF ENTEROVIRUS NUCLEIC ACID
FILE REFERENCE: 020187.0187PTUS
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APPLICANT: Genetics & IVF
APPLICANT: MARTANI, Brian D.
TITLE OF INVENTION: ENTEROURING PRIMERS AND PROBES
FILE REPERBUCE: 043956-0121
CURRENT APPLICATION NUMBER: US/10/829,474
NUMBER OF SEQ ID NOS: 57
SOFTWARE: Patentin version 3.2
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                                                                                                                                                                                                                    Mismatches
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                                                                                                                                                                          Score 18;
Pred. No.
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; Sequence 10, Application US/10760048
; Publication No. US20050158710A1
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                                                              ; NAME/KEY: misc_feature
; LCCATION: (1)...(225734)
; OTHER INFORMATION: n = A,T,C or G
US-10-322-656-13
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Best Local Similarity 100.0%; Pi
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                                                                                                                                                                                                                18; Conservative
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Best Local Similarity 89.5
Matches 17; Conservative
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Best Local Similarity 100.
Matches 17; Conservative
TYPE: DNA ORGANISM: Mus musculus
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LENGTH: 17
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OTHER INFORMATION: Chemically synthesized reverse primer for amplifying enteroviral
OTHER INFORMATION: RNA
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APPLICANT: Malandro, Marc
TITLE OF INVENTION: NOVEL THERAPEUTIC TARGETS IN CANCER
FILE REPERENCE: 529452001200
CURRENT APPLICATION NUMBER: US/10/322,696
CURRENT FILING DATE: 2003-10-17
NUMBER OF SEQ ID NOS: 186
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 13
LENGTH: 225734
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Genetics & IVF
APPLICANT: HEAL D.
APPLICANT: WARIANI, Brian D.
TITLE OF INVENTION: ENTEROVIRUS PRIMERS AND PROBES
FILE REFERENCE: 043956-0121
CURRENT APPLICATION NUMBER: US/10/829,474
CURRENT PILING DATE: 2004-04-22
                                      APPLICANT: MARIANI, Brian D
TITLE OF INVENTION ENTEROVIRUS PRIMERS AND PROBES
FILE REFERENCE: 043956-0121
CURRENT APPLICATION NUMBER: US/10/829,474
CURRENT FILING DATE: 2004-04-22
NUMBER OF SEQ ID NOS: 57
SOFTWARE: Patentin version 3.2
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100.0%; Pred. No.
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Publication No. US20050239055A1
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SOFTWARE: PatentIn version 3.2
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Matches 18; Conservative
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nes 18; Conserv
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Best Local S:
Matches 18
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APPLICANT: Paul, John H
TITLE OF INVENTION: RAPID DETECTION OF ENTEROVIRUSES IN ENVIRONMENTAL SAMPLES BY NASB!
FILE REPERENCE: USF-114XC6
CURRENT APPLICATION NUMBER: US/10/179,082A
CURRENT FILING DATE: 2002-11-04
NUMBER OF SEQ ID NOS: 23
SOFTWARE: Patentin version 3.1
SEQ ID NO.3.
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APPLICANT: Paul, John H.

APPLICANT: Paul, John H.

APPLICANT: Paul, John H.

APPLICANT: Patterson, Stacey S.

ITLE OF INVENTION: Materials and Methods for Detection of Enterovirus and Norovirus FILE REPERENCE: USF-114XG621

CURRENT APPLICATION NUMBER: US/10/938,005

CURRENT APPLICATION NUMBER: 10/857,109

PRIOR PILING DATE: 2004-05-28

PRIOR PILING DATE: 2004-05-25

PRIOR PILING DATE: 2002-06-25

PRIOR PILING DATE: 2002-06-25

PRIOR APPLICATION NUMBER: 60/301,218

PRIOR PILING DATE: 2002-06-25

PRIOR APPLICATION NUMBER: 60/301,218

PRIOR PILING DATE: 2001-06-27

NUMBER OF SEC ID NOS: 10

SOFTWARE: Patentin version 3.2

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APPLICANT: Wimmer Prof, Eckard
TITLE OF INVENTION: Recombinant Poliovirus For The Treatment of Cancer
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100.0%; Pred. No. 2e+02;
tive 0; Mismatches 0; Indels
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100.0%; Pred. No. ...
'... 0; Mismatches
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                                        Sequence 3, Application US/10179082A Publication No. US20030186222A1 GENERAL INFORMATION:
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Best Local Similarity 100."
Matches 17; Conservative
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Best Local Similarity 100.
Matches 17; Conservative
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                      JS-10-179-082A-3/c
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APPLICANT: Patterson, Stacey S.
TITLE OF INVENTION: Materials and Methods for Detection of Enterovirus and Norovirus
TITLE REFERENCE: USF-114XC621
CURRENT APPLICATION NUMBER: US/10/938,005
CURRENT PILING DATE: 2004-09-10
PRIOR FILING DATE: 2004-05-28
PRIOR FILING DATE: 2002-06-25
PRIOR APPLICATION NUMBER: 10/179,082
PRIOR PILING APPLICATION NUMBER: 60/301,218
PRIOR FILING DATE: 2002-06-25
PRIOR PILING DATE: 2001-06-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; OTHER INFORMATION: Chemically synthesized reverse primer for amplifying enteroviral ; OTHER INFORMATION: RNA US-10-829-474-24
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100.0%; Pred. No. 2e+02;
ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                      APPLICANT: Genetics & IVF
APPLICANT: MARIANI, Brian D.
TITLE OF INVENTION: ENTEROVIRUS PRIMERS AND PROBES
FILE REPERENCE: 043956-0121
CURRENT APPLICATION NUMBER: US/10/829,474
CURRENT FILING DATE: 2044-04-22
NUMBER OF SEQ ID NOS: 57
SOFTWARE: Patentin version 3.2
SEQ ID NO 24
LENGTH: 17
                                                                                                                                            US-10-829-474-24
. Sequence 24, Application US/10829474
. Publication No. US20050239055A1
. GENERAL INFORMATION:
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Publication No. US20050048475A1
GENERAL INFORMATION:
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                                               1 GGAAACACGGACACCCA 17
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SOFTWARE: PatentIn version 3.2
SEQ ID NO LENGTH: 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 17; Conserv
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Publication No. US20050158710A1
GENERAL INFORMATION:
APPLICANT: PRICE, JAMES A.
APPLICANT: PRICE, JAMES A.
APPLICANT: PRICE, JAMES A.
TITLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID
FILE REFERENCE: 020187.0187PTUS
CURRENT APPLICATION NUMBER: US/10/760,048
CURRENT FILING DATE: 2004-01-16
NUMBER OF SEQ ID MOSS: 67
SOFTWARE: Patentin Ver. 3.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          , DB 9; Leus.
O. 2e+02;
O; Indels
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                                                                                                                                                                                     Length 92;
                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CTHER INFORMATION: Description of Unknown Organism: Viral; OTHER INFORMATION: 5'untranslated polynucleotide sequence US-10-760-048-39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: Description of Unknown Organism: Viral; OTHER INFORMATION: 5'untranslated polynucleotide sequence US-10-760-048-40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: TEALS.
APPLICANT: PRICE, JAMES A.
APPLICANT: PRICE, JAMES A.
APPLICANT: PRICE, JAMES A.
APPLICANT: PRICE, JAMES A.
APPLICANT: OF INVENTION: DESTRUCTION OF ENTEROVIRUS NUCLEIC ACID
FILE REFERENCE: 020187.0187PTUS
CURRENT FILING DATE: 2004-01-16
NUMBER OF SEQ ID NOS: 67
SECTION OF 40
LENGTH: 117
                                                                                                                                                                   DB 8; Leis.
                                                TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Enteroviral Internal Control
US-10-938-005-9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                            Query Match
Best Local Similarity 100.0%; Pred. No.
Matches 17; Conservative 0; Mismatc
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Pred. No.
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Best Local Similarity 100.0%; Pi
Matches 17; Conservative 0;
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ORGANISM: Unknown Organism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA _ ORGANISM: Unknown Organism
                                                                                                                                                                                                                                                                                                                                                                                                 US-10-760-048-39/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQ ID NO 39
LENGTH: 117
           SEQ ID NO 9
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APPLICANT: Casper, Erica T.
APPLICANT: Casper, Erica T.
APPLICANT: Paul, John H.
APPLICANT: Paul, John H.
APPLICANT: Patterson, Stacey S.
TITLE OF INVENTION: Materials and Methods for Detection of Enterovirus and Norovirus FILE REFERENCE: USF-114XC621
CURRENT APPLICATION NUMBER: 10/957,109
PRIOR APPLICATION NUMBER: 10/957,109
PRIOR FILING DATE: 2004-06-28
PRIOR FILING DATE: 2004-06-25
PRIOR FILING DATE: 2001-06-27
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PatentIn version 3.2
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                                                                                                                                                                                                                                                                                    DB 6; Length 33; 2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       85.0%; Score 17; DB 9; Length 40;
100.0%; Pred. No. 2e+02;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: TRANS, SHIRLEY
APPLICANT: PRICE, JAMES A.
APPLICANT: PRICE, JAMES A.
APPLICANT: HELLYSK, TOBIN J.
TITLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID
FILE REFERENCE: 020187.0187PTUS
CURRENT PILLING DATE: 2004-01-16
NUMBER OF SEQ ID NOS: 67
SEQ ID NO 9
LENGTH: 40
FILE REFERENCE: Recomb Poliovirus for Cancer Treatment CURRENT APPLICATION NUMBER: US/10/175,247
CURRENT FILING DATE: 2002-06-19
                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                       Score 17;
Pred. No
                                                           PRIOR APPLICATION NUMBER: US/09/129,686
PRIOR FILING DATE: 1998-08-05
NUMBER OF SEQ ID NOS: 28
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 20
LENGTH: 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 9, Application US/10760048 Publication No. US20050158710A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 9, Application US/10938005
Publication No. US20050048475A1
                                                                                                                                                                                                                                                                                  Query Match 85.0%; Sc
Best Local Similarity 100.0%; P
Matches 17; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                      1 AAGGAAACACGGACACC 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                              ; TYPE: DNA
; ORGANISM: Human rhinovirus 2
US-10-175-247-20
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Best Local Similarity 100.0
Matches 17; Conservative
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Mathews, Michael B.
                 Katze, Michael G.
Witherell, Gary
Watson, Julia C.
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Best Local Similarity 100.0%; Pr
Matches 17; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 627 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GAAACACGGACACCCAA 552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4 GAAACACGGACACCCAA 20
                                                                                                                 NUMBER OF SEQUENCES: 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: New York
COUNTRY: USA
ZIP: 10036/2711
                                                                                                                                                                                           CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEOUENCES:
                                                                                                                                                                                                                                 COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX:
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                                                                                                                                                                                       Sequence 31, Application US/10104611
Publication No. US20020160976A1
GENERAL INFORMATION:
APPLICANT: Miles, Vincent J.
Mathews, Michael B.
Katze, Michael G.
Witherell, Gary
Watson, Julia C.
TITLE OF INVENTION: METHOD FOR SELECTIVE INACTIVATION
                     Indels
 Pred. No. 2e+02;
Hismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER TOTAL
COMPUTER TADABLE PORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPUTER: IBM COMPATIBLE
COMPUTER: TABLESEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/104,611
FILING DATE: 22-Mar-2002
CLASSIFICATION AUMBER: US/08/221,816B
APPLICATION NUMBER: US/08/221,816B
FILING DATE: 01-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: COTUZZI, LBUER
REFERENCE/DOCKET NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 30,742
                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                    OF VIRAL REPLICATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear

MOLECULE TYPE: RNA
SEQUENCE DESCRIPTION: SEQ ID NO: 31:
US-10-104-611-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 627 base pairs
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US-10-112-547-31/c
; Sequence 31, Application US/10112547
; Publication No. US20020160977A1
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APPLICANT: Miles, Vincent J.
Best Local Similarity 100.0%; P
Matches 17; Conservative 0;
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                                                       4 GAAACACGGACACCCAA 20
                                                                                     102 GAAACACGGACACCCAA 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.
Matches 17; Conservative
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US-10-104-611-31/c
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Mathews, Michael B.
Katze, Michael G.
Witherell, Gary
Watson, Julia C.
TITLE OF INVENTION: METHOD FOR SELECTIVE INACTIVATION
OF VIRAL REPLICATION
TITLE OF INVENTION: METHOD FOR SELECTIVE INACTIVATION OF VIRAL REPLICATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
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                                                                                                                                                                                                                                                                                   COMPUTER: IBM COMPATIBLE
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: DOS
SOFTWARE: FBSLSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/112,547
FILLING DATE: 28-Mar-2002
CLASSIFICATION: CURKNOWN>
PRIOR APPLICATION DATA:
                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 1155 Avenue of the Americas CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION WHERE: US/08/221,816B
FILING DATE: 01-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: COTUZZI, LAULTA A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7960-030
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TOPOLOGY: linear; MOLECULE TYPE: RNA SEQUENCE DESCRIPTION: SEQ ID NO: 31: US-10-112-547-31
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ADDRESSEE: Pennie & Edmonds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (212) 790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 31, Application US/10112241 Publication No. US20020165194A1 GENERAL INFORMATION:
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Length 627;
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Watson, Julia C.
TITLE OF INVENTION: METHOD FOR SELECTIVE INACTIVATION
OF VIRAL REPLICATION
                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                     Query Match 85.0%; Score 17; DB 6; Le
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 17; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/10/109,368
FILING DATE: 27-Mar-2002
APPLICATION NUMBER: US/08/221,816
FILING DATE: 01-APR-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/867,798
FILING DATE: 14-Jun-2004
CLASSIFICATION: <UNKNOWN>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Coruzzi, Laura A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7960-030
                                                                                                                                                                                                     TOPOLOGY: linear

MOLECULE TYPE: RNA
SEQUENCE DESCRIPTION: SEQ ID NO: 31:
US-10-109-368-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT B3
US-10-867-798-31/C
is Sequence 31, Application US/10867798
is Publication No. US20040254140A1
is GENERAL INFORMATION:
i APPLICANT: Miles, Vincent J.
i APPLICANT: Mathews, Michael B.
i Katze, Michael G.
                                        TELEFAX: (212) 869-8864
INFORMATION FOR SEQ 1D NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 627 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FELEPHONE: (212) 790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 10036/2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 627 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                            568 GAACACGGACACCCAA 552
                                                                                                                                                                                                                                                                                                                                                                                                               4 GAAACACGGACACCCAA 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                 ઠ
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APPLICANT: Miles, Vincent J.
Mathews, Michael B.
Katze, Michael G.
Witherell, Gary
Watson, Julia C.
TITLE OF INVENTION: METHOD FOR SELECTIVE INACTIVATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 5; Le
2.1e+02;
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OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/109,368
FILING DATE: 27-Mar-2002
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OF VIRAL REPLICATION
                                                                                                                                                                           APPLICATION NUMBER: US/08/221,816B
FILING DATE: 01-APR-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 85.0%; Score 17; DB Best Local Similarity 100.0%; Pred. No. 2.1 Matches 17; Conservative 0; Mismatches
                                                           CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/112,241
FILING DATE: 28-Mar-2002
CLASSIFICATION: <UNKNOWN>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                  NAME: Coruzzi, Laura A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7960-030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/221,816
FILING DATE: 01-APR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: RNA
SEQUENCE DESCRIPTION: SEQ ID NO: 31:
              OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 31, Application US/10109368
Publication No. US20030144226A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Coruzzi, Laura A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
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ZIP: 10036/2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4 GAAACACGGACACCCAA 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                  TELEFAX:
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84.0%; Score 16.8; DB 9; Length 238; 90.0%; Pred. No. 2.6e+02; tive 0; Mismatches 2; Indels (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 24, Application US/10760048

Publication No. US20050158710A1

GENERAL INFORMATION:

APPLICANT: FANG, SHIRLEY

APPLICANT: PRICE, JAMES A.

TITLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID

FILE REFERENCE: 020187.0187FUS

CURRENT APPLICATION NUMBER: US/10/760,048

CURRENT FILING DATE: 2004-01-16

NUMBER OF SEQ ID NOS: 67

SOFTWARE: PatentIn Ver. 3.2

SEQ ID NO 24

LENGTH: 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; OTHER INFORMATION: 5'untranslated polynucleotide sequence US-10-760-048-24
                                                                                                                                                                                                                 APPLICANT: TRANG, SHIRLEY
APPLICANT: PRICE, JAMES A.
APPLICANT: PRICE, JAMES A.
APPLICANT: HILLYST TOBIN J.
TITLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID
FILE REFERENCE: 020187.0187PTUS
CURRENT APPLICATION NUMBER: US/10/760,048
CURRENT FILING DATE: 2004-01-16
NUMBER OF SEQ ID NOS: 67
SEQ ID NOS: 67
SEQ ID NO 22
LENGTH: 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: Description of Unknown Organism: Viral OTHER INFORMATION: 5'untranslated polynucleotide sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 88
US-10-950-009-1102/c
Sequence 1102, Application US/10950009
; Publication No. US20050069934A1
; GENERAL INFORMATION:
                                                                                                 RESULT 86
US-10-760-048-22/c
'Sequence 22, Application US/10760048
'Publication No. US20050158710A1
'GENERAL INFORMATION:
105 AAGGAAACACGGTTACCCAA 86
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ORGANISM: Unknown Organism
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Best Local Similarity 90.09
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Unknown Organism
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Matches 18; Conservative
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                                                                                                                                                                                                                                                                                                                        Sequence 173501
Sequence 173501
Sequence 173501, Application US/10425115
Sequence 173501, Application US/10425115
Sequence 173501, Application No. US2004021427241
Seneral Information No. US2004021427241
Seneral Information No. US200402162
Septicant: Language 1.
APPLICANT: Language 1.
APPLICANT: Cao, Yongwei 1.
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With 1.
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With 1.
TITLE OF INVENTION: Number: US/10/425,115
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 173501
LENGTH: 230
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 230;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 17, Application US/10760048

Publication No. US20050158710A1

GENERAL INFORMATION:

APPLICANT: TSANG, SHRLEY

APPLICANT: TRANG, SHRLEY

TITLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID

FILE REPERENCE: 020187, 01877PTUS

CURRENT APPLICATION NUMBER: US/10/760,048

CURRENT FILING DATE: 2004-01-16

NUMBER OF SEC ID NOS: 67

SOFTWARE: Patentin Ver. 3.2
                                                                                                   Length 627;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2; Indels
                                                                                                                                                 0; Indels
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                                                                                              Query Match

85.0%; Score 17; DB 8; Le
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 17; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 90.0%; Pred. No. 2.6e+02;
Matches 18; Conservative 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE: OTHER INFORMATION: Clone ID: MRT4577_89813C.1
; MOLECULE TYPE: RNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 31:
US-10-867-798-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 AAGGAAACACGGACACCCAA 20
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                                                                                                                                                                                                  4 GAAACACGGACACCCAA 20
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ORGANISM: Unknown Organism
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Best Local Similarity 90.0°
Matches 18; Conservative
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ORGANISM: Zea mays
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LENGTH: 238
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APPLICATION NUMBER: US/09/925,065A
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US-10-760-048-67/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH
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TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Incleotide Polymorphisms in the Human Genome
FILE REPERENCE: 108827,135
CURRENT PILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR PILING DATE: 2000-11-20
PRIOR PILING DATE: 2000-11-20
PRIOR PILING DATE: 2000-11-30
PRIOR FILING DATE: 2000-11-6
PRIOR PILING DATE: 2001-01-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Publication No. US20050228172A9
GENERAL INFORMATION:
APPLICANT: Warg, David G.
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
FILE REFERENCE: 108827.135
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 16.8; DB 9; Length 370; Pred. No. 2.6e+02; 0; Mismatches 2; Indels
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                                         APPLICANT: REY, Michael
TITLE OF INVENTION: Methods For Monitoring Gene Expression
FILE REPERENCE: 10541.200-US
CURRENT APPLICATION NUMBER: US/10/950,009
CURRENT FILING DATE: 2004-09-24
PRIOR APPLICATION NUMBER: 60/506,140
PRIOR PILING DATE: 2003-09-25
NUMBER OF SEQ ID NOS: 1190
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1102
LENGTH: 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 156382, Application US/09925065A Publication No. US20050228172A9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              84.0%;
90.0%;
APPLICANT: BERKA, Randy APPLICANT: BASHKIROVA, Elena
                                                                                                                                                                                                                                                                                                                                                                         ; TYPE: DNA; ORGANISM: Trichoderma reesei
US-10-950-009-1102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 90.0°
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 90.0
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
CRGANISM: Homo sapiens
US-09-925-065A-156382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
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Publication No. US20040234960A1
GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Method for determining the degree of methylation of d
TITLE OF INVENTION: cytosines in genomic DNA in the sequence context of
FILE REFERENCE: B01/1227
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 67, Application US/10760048
Publication No. US20050158710A1
GENERAL INPORMATION:
APPLICANT: TSANG, SHIRLEY
APPLICANT: PRICE, JAMES A.
APPLICANT: PRICE, TOBIN J.
TITLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID
FILE REPERENCE: 020187.0187PTUS
CURRENT FILING DATE: 2004-01-16
NUMBER OF SEQ ID NOS: 67
SOFTWARE: Patentin Ver. 3.2
SEQ ID NO 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR FILING DATE: 2000-10-24
PRIOR FILING DATE: 2000-11-20
PRIOR FILING DATE: 2000-11-20
PRIOR FILING DATE: 2000-11-30
PRIOR FILING DATE: 2000-11-30
PRIOR FILING DATE: 2000-11-6
PRIOR FILING DATE: 2000-11-6
PRIOR FILING DATE: 2001-01-6
PRIOR FILING DATE: 2001-01-6
PRIOR FILING DATE: 2001-01-6
PRIOR FILING DATE: 2001-05-09
PRIOR FILING DATE: 2001-05-09
STOWBER OF SEQ ID NOS: 957086
SOFTWARE: PRESERY FOR WINDOWS VERSION 4.0
SEQ ID NO 156383
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US-10-760-048-67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 90.0
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                      CRGANISM: Homo sapiens
US-09-925-065A-156383
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Best Local Similarity 90.0%; Pred. No. 2.7e+02; Matches 18; Conservative 0; Mismatches 2;
                                                                                                            291 AACGAAACACGAACACCCAA 272
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 3, Application US/10723681
Publication No. US20050192239A1
GENERAL INFORMATION:
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                                                                     1 AAGGAAACACGGACACCCCAA 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA ORGANISM: Artificial Sequence
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illarity 90.0%;
Conservative (
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Best Local Similarity
Matches 18; Conserval
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US-10-723-681-3/c
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Sequence 23362, Application US/10363345A

Publication No. US20040234960A1

GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Are acried an Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Actosines in genomic DNA in the sequence context of 5'-CpG-
FILE REFERENCE: E01/1227
CURRENT APPLICATION NUMBER: US/10/363,345A

NUMBER OF SEQ ID NOS: 40712

SEQ ID NO 23362

LENGTH: 906
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US-10-363-483A-23361/c
; Sequence 23361, Application US/10363483A
; Publication No. US20050064401A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Christian Piepenbrock
; TITLE OF INVENTION: illnesses
; TITLE OF INVENTION: illnesses
; TITLE OF INVENTION: illnesses
; FILE REFERENCE: 82011
; CURRENT APPLICATION NUMBER: US/10/363,483A
; NUMBER OF SEQ ID NOS: 40712
; SEQ ID NO 23361
; LENGTH: 906
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                                                                 FEATURE:
COTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
COTHER INFORMATION: CpG-island No: 23361
US-10-363-345A-23361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ) OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens); OTHER INFORMATION: CpG-island No: 23362
US-10-363-345A-23362
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OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens); OTHER INFORMATION: CpG-island No: 23361
US-10-363-483A-23361
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84.0%; Score 16.8; DB 8; Length 906;
Best Local Similarity 90.0%; Pred. No. 2.7e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0
                                                                                                                                                                           84.0%; Score 16.8; DB 8; Length 906; 90.0%; Pred. No. 2.7e+02; tive 0; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                   1 AAGGAAACACGGACACCCAA 20
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ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
                        TYPE: DNA
ORGANISM: Artificial Sequence
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Best Local Similarity
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US-10-363-345A-23362
  LENGTH: 906
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APPLICANT: ROTH, RICHARD B.
APPLICANT: BRAIN. ANDREAS
APPLICANT: BRAIN. ANDREAS
APPLICANT: BRAIN. ANDREAS
APPLICANT: RENELAND, RIKARD
TITLE OF INVENTION: METHODS FOR IDENTIFYING RISK OF BREAST CANCER AND TITLE OF INVENTION: METHODS FOR IDENTIFYING RISK OF BREAST CANCER AND TITLE OF INVENTION WHERE: US/10/723,681
CURRENT FILING DATE: 2003-11-25
PRIOR PAPLICATION NUMBER: US 60/429,136
PRIOR FILING DATE: 2002-11-25
PRIOR APPLICATION NUMBER: US 60/490,234
NUMBER OF SEQ ID NOS: 835
SOFTWARE: PALENTIN VERSION 3.2
SEQ ID NO 3
EMENCE: NUMBER OF SEQ ID NOS: 835
SEQ ID NO 3
EMENCE: NUMBER OF SEQ ID NOS: 835
                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
TITLE OF INVENTION: Diagnosis of illnesses or predisposition to certain
TITLE OF INVENTION: illnesses
TITLE OF INVENTION: illnesses
CURRENT APPLICATION NUMBER: US/10/363,483A
CURRENT APPLICATION NUMBER: US/10/363,483A
CURRENT FILING DATE: 2003-03-03
SEQ ID NO 23362
LENGTH: 906
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US-10-363-483A-23362
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84.0%; Score 16.8; DB 9; Length 906;
Best Local Similarity 90.0%; Pred. No. 2.7e+02;
Matches 18; Conservative 0; Mismatches 2; Indels
Indels
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Pred. No. 2.9e+02;
0; Mismatches 2;
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84.0%; Score 16.8; DB 9; Length 906;

Query Match

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US-10-052-482-55
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                                                                                                                                                                                                    APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
FILE REPERENCE: 108827.135
CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT PILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/234,096
PRIOR PILING DATE: 2000-10-24
PRIOR PPLICATION NUMBER: US 60/252,147
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR PILING DATE: 2000-11-20
PRIOR PILING DATE: 2000-11-30
PRIOR PILING DATE: 2000-11-6
PRIOR PILING DATE: 2001-01-6
PRIOR PILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
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LOCATION: (13629)..(13648)
OTHER INFORMATION: "n" at positions 13629 to 13648 can be any base
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OTHER INFORMATION: "n" at positions 1241 to 1975 can be any base
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APPLICANT: Engelhard, Eric
APPLICANT: Morris, David
TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR CANCER
FILE REFERENCE: 47.1087/RMS/DCF
CURRENT APPLICATION NUMBER: US/10/052,482
CURRENT FILING DATE: 2002-08-15
PRIOR APPLICATION NUMBER: US 09/747,377
PRIOR PELICATION NUMBER: US 09/798,586
PRIOR PILING DATE: 2000-12-22
PRIOR PILING DATE: 2001-03-02
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Pred. No. 4.1e+02;
0; Mismatches 1;
                                                                                                                           Sequence 319374, Application US/09925065A Publication No. US20050228172A9 GENERAL INFORMATION:
  50059 ATGGAAACACGGGCACCCAA 50040
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Publication No. US20040072264A1
GENERAL INFORMATION:
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SOFTWARE: PatentIn version 3.1
SEQ ID NO 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             82.0%;
94.4%;
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Best Local Similarity 94.4°
Matches 17; Conservative
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LOCATION: (15882)..(16151)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; UMGANISM: Homo sapiens
US-09-925-065A-319374
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LOCATION: (1241)..(197)
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                                                                                                         US-09-925-065A-319374
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OTHER INFORMATION: Chemically synthesized reverse primer for amplifying enteroviral OTHER INFORMATION: RNA
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OTHER INFORMATION: "n" at positions 15882 to 16151 can be any base
                                                                                                                                  NAME/KEY: misc_feature
LOCATION: (26226)..(26285)
OTHER INFORMATION: "n" at positions 26226 to 26285 can be any base
                                                                                         any base
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NAME/KEY: misc_feature
LOCATION: (42909)..(43118)
OTHER INFORMATION: "n" at positions 42909 to 43118 can be
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LOCATION: (31687)..(32259)
OTHER INFORMATION: "n" at positions 31687 to 32259 can be
                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: misc_feature
LOCATION: (40899)..(41095)
OTHER_INFORMATION: "n" at positions 40899 to 41095 can be
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Publication No. US20050239055A1
GENERAL INFORMATION:
APPLICANT: Genetics & IVF
APPLICANT: GENETION: Brian D.
TITLE OF INVENTION: ENTEROVIRUS PRIMERS AND PROBES
FILE REFERENCE: 049356-0121
CURRENT APPLICATION NUMBER: US/10/829,474
CURRENT FILING DATE: 2004-04-22
NUMBER OF SEQ ID NOS: 57
SOFTWARE: PATENTIN VERSION 3.2
                                                                                                                                                                                                                       NAME/KEY: misc feature
LOCATION: (30454)..(30473)
OTHER INFORMATION: "n" at positions 30454 to 30473
                                                               LOCATION: (22065)..(22084)
OTHER INFORMATION: "n" at positions 22065 to 22084
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 16.4; DB 7;
Pred. No. 4.5e+02;
0; Mismatches 1;
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100.0%; Pred. No. 6e+02;
tive 0; Mismatches 0
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Publication No. US20040214272A1
GENERAL INFORMATION:
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Best Local Similarity 94.44
Matches 17; Conservative
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                                        NAME/KEY: misc feature
LOCATION: (22065)..(220
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Best Local Similarity
Matches 16; Conserv
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APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TILE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: 18-21(53222)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
SEQ ID NOS: 369326
SEQ ID NOS: 369326
SEQ ID NOS: 369326
SEQ ID NOS: 369326
TYPE: DNA
ORGANISM: Zea mays
FRATURE:
CHENTH: HOPORMATION: Clone ID: MRT4577_176031C.1
US-10-425-115-83354
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Search completed: March 9, 2006, 08:33:39 Job time : 588.194 secs

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                                                                                                                         The invention relates to an oligonucleotide (I) consisting of: (a) the target binding sequence of an oligonucleotide chosen from any one of the 10 sequence of ABBS6771; and (b) a sequence required for selected amplification or detection reaction. Also described: (I) a kit (K1) comprising (I), and one or more container that contains (I); and (2) detecting (M1) an enterovirus target sequence, involving: (a) amplifying the target sequence using first amplification primer having a sequence consisting essentially of target binding sequence of any one of ABBS6764 to ABBS6771 and optionally a sequence required for selected amplification reaction; and (b) detecting the amplified target sequence. (I), (M1) and (X1) are useful for detecting enterovirus target sequences. (I) specifically and selectively recognizes the enterovirus genome. (I) specifically and rapidly detects fewer than 500 copies of enteroviral genome and allows detection of broad range of enterovirus serotypes. The present sequence represents a viral 5' untranslated polymucleotide sequence given in the exemplification of the present invention.
                                                                   Novel oligonucleotide comprising sequences for binding and amplifying or detecting target, useful for detecting enterovirus nucleic acids.
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                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 20; DB 14; Length 105; 100.0%; Pred. No. 9.9;
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                                                                                                                                                                                                                                                                                                                                Sequence 105 BP; 22 A; 27 C; 27 G; 29 T; 0 U; 0 Other;
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                                                                                                      Disclosure; Fig 1A-D; 34pp; English.
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            Hellyer TJ;
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                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 100.0
Matches 20; Conservative
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(PRIC/) PRICE J A.
(HELL/) HELLYER T J.
           Tsang S, Price JA,
                                 WPI; 2005-512251/52
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                                             GENBANK; S76769
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AEB56868/c
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target binding sequence of an oligonuclectide chosen from any one of the carget binding sequence of an oligonuclectide chosen from any one of the calculation of detection reaction. Also described (1) a kit (XI) comprising (I), and one or more container that contains (I); and (2) detecting (MI) an enterovirus target sequence, involving: (a) amplifying the target sequence using first amplification primer having a sequence consisting essentially of target binding sequence of any one of ABB56764 to ABB56771 and optionally a sequence required for selected amplification creation; and (b) detecting the amplified target sequence. (I), (MI) and (XI) are useful for detecting enterovirus target sequence. (I) specifically and selectively recognizes the enterovirus genome. (I) sensitively and rapidly detects fewer than 500 copies of enteroviral sensitively and allows detection of broad range of enterovirus serotypes. The present sequence represents a viral 5' untranslated polymuclectide sequence given in the exemplification of the present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel oligonucleotide comprising sequences for binding and amplifying or detecting target, useful for detecting enterovirus nucleic acids.
                                                                                   The invention relates to an oligonucleotide (I) consisting of: (a) the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to an oligonucleotide (I) consisting of: (a)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 20; DB 14; Length 106; 100.0%; Pred. No. 9.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Viral 5' untranslated polynucleotide sequence SEQ ID NO:53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 106 BP; 21 A; 26 C; 27 G; 32 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA detection; enteroviral detection; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; SEQ ID NO 53; 34pp; English.
Disclosure; Fig 1A-D; 34pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 AAGGAAACACGGACACCCAA 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      101 AAGGAAACACGGACACCCAA 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AEB56814 standard; DNA; 107 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16-JAN-2004; 2004US-00760048.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16-JAN-2004; 2004US-00760048
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22-SEP-2005 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 100. Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (TSAN/) TSANG S.
(PRIC/) PRICE J A.
(HELL/) HELLYER T J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Isang S, Price JA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2005-512251/52.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US2005158710-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-JUL-2005.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AEB56814;
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Gaps

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Indels

100.0%; Score 20; DB 14; Length 110; 100.0%; Pred. No. 10;

0; Mismatches

Conservative

Query Match Best Local Similarity Matches 20; Conserv

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to an oligonucleotide (I) consisting of: (a) the target binding sequence of an oligonucleotide chosen from any one of the 10 sequence of ABBS6771; and (b) a sequence required for selected amplification or detection reaction. Also described: (1) a kit (K1) comprising (I), and one or more container that contains (I); and (2) detecting (M1) an enterovirus target sequence, involving: (a) amplifying the target sequence using first amplification primer having a sequence consisting essentially of target binding sequence of any one of ABBS676 to ABBS6771 and optionally a sequence required for selected amplification reaction; and (b) detecting the amplified target sequence. (I), (M1) and (K1) are useful for detecting the amplified target sequence. (I), (M1) and specifically and selectively recognizes the enterovirus genome. (I)
to AEBS6771 and optionally a sequence required for selected amplification reaction; and (b) detecting the amplified target sequence. (I), (M1) and (K1) are useful for detecting enterovirus target sequences. (I) specifically and selectively recognizes the enterovirus genome. (I) sensitively and rapidly detects fewer than 500 copies of enteroviral persent sequence represents a viral S' untranslated polymucleotide sequence given in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel oligonucleotide comprising sequences for binding and amplifying or detecting target, useful for detecting enterovirus nucleic acids.
                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                100.0%; Score 20; DB 14; Length 107; 100.0%; Pred. No. 9.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Viral 5' untranslated polynucleotide sequence SEQ ID NO:52.
                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                             Sequence 107 BP; 22 A; 28 C; 28 G; 29 T; 0 U; 0 Other;
                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA detection; enteroviral detection; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; SEQ ID NO 52; 34pp; English.
                                                                                                                                                                                                                                                                      1 AAGGAAACACGGACACCCAA 20
                                                                                                                                                                                                                                                                                                         83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hellyer TJ;
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                                                                                                                                                                                                                                                                                                                                                                                             AEB56813 standard; DNA; 110 BP
                                                                                                                                                                                                                                                                                            102 AAGGAAACACGGACACCCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16-JAN-2004; 2004US-00760048.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16-JAN-2004; 2004US-00760048
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                           Query Match
Best Local Similarity 100.
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (TSAN/) TSANG S.
(PRIC/) PRICE J A.
(HELL/) HELLYER T J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Price JA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2005-512251/52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US2005158710-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                  AEB56813;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          specifically and selectively recognizes the enterovirus genome. (I) sensitively and rapidly detects fewer than 500 copies of enteroviral genome and allows detection of broad range of enterovirus serctypes. The present sequence represents a viral 5' untranslated polynucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel oligonucleotide comprising sequences for binding and amplifying or detecting target, useful for detecting enterovirus nucleic acids.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sequence given in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 20; DB 14; Length 126; Pred. No. 10;
                                                                                                                                                                                                                                 Viral 5' untranslated polynucleotide sequence SEQ ID NO:18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 126 BP; 26 A; 36 C; 31 G; 33 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                     DNA detection; enteroviral detection; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; SEQ ID NO 18; 34pp; English.
1 AAGGAAACACGGACACCCAA 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 AAGGAAACACGGACACCCAA 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     105 AAGGAAACACGGACACCCAA 86
                                 AAGGAACACGGACACCCAA 86
                                                                                                                        AEB56779 standard; DNA; 126 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                  16-JAN-2004; 2004US-00760048.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   16-JAN-2004; 2004US-00760048
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ilarity 100.0%;
Conservative (
                                                                                                                                                                                               22-SEP-2005 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (TSAN/) TSANG S.
(PRIC/) PRICE J A.
(HELL/) HELLYER T J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tsang S, Price JA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2005-512251/52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 20; Conserv
                                                                                                                                                                                                                                                                                                                                            US2005158710-A1.
                                                                                                                                                                                                                                                                                                        Unidentified
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                                                                                                                                                           AEB56779;
                                                                                      RESULT 5
AEB56779/c
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sensitively and rapidly detects fewer than 500 copies of enteroviral genome and allows detection of broad range of enterovirus serotypes. The present sequence represents a viral 5' untranslated polynucleotide

sequence given in the exemplification of the present invention.

Sequence 110 BP; 21 A; 28 C; 29 G; 32 T; 0 U; 0 Other;

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prostate, colorectal, hepatocellular, bronchial (claimed). (Updated on 15-SEP-2003 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This sequence represents domains V-VI of the internal ribosomal entry site (IRES) of PVI(prr), a recombinant, non-pathogenic oncolytic poliovirus that carries the IRES of poliovirus type I Mahoney where the terminal loop of regions of Gomain V and domain VI are substituted with the corresponding fragments of human rhinovirus type 2 (HRV2). PVI(prr) was characterized by a loss of neuropathogenicity, demonstrated by its reduced ability to propagate within cells of neuronal origin and failure to cause neurological disease in Cal55 tg mice. Oncolytic potential was demonstrated against a panel of malignant cell lines. PVI(prr) is an example of novel recombinant polioviruses (I) of the invention in which the IRES of wild-type poliovirus is exchanged with the IRES of another picornavirus, such as HRV2, and optionally the PI, P3 or 3' untranslated region is exchanged with that of Sabin poliovirus. (I) are useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           recombinant poliovirus useful for treating malignant tumors
                                                                                                                                                                Internal ribosomal entry site; IRES; picornavirus; PV1(prr); tumour; cancer; glioblastoma multiforme; medulloblastoma; mammary carcinoma; prostate carcinoma; colorectal carcinoma; hepatocellular carcinoma; bronchial carcinoma; epidermoid carcinoma; cytostatic; therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               comprises internal ribosomal entry site derived from picornaviruses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 20; DB 3; Length 176; 100.0%; Pred. No. 10; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            treating malignant tumors such as glioblastoma multiforme,
                                                                                                                                  Recombinant poliovirus PV1(prr) IRES domain V-VI region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 176 BP; 42 A; 43 C; 40 G; 0 T; 51 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (UYNY ) UNIV NEW YORK STATE RES FOUND.
                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
1. .109
                                                                                                                                                                                                                                                                                                                                                                                                                 '*tag= b
'note= "domain VI"
                                                                                                                                                                                                                                                                                                                                                          *tag= a
'note= "domain V"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 6; Fig 7; 99pp; English.
              AAZ58488 standard; RNA; 176 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99WO-US007839
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98US-00129686
                                                                                                                                                                                                                                                        Human poliovirus 1.
Human rhinovirus sp; type 2.
                                                                                  (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and epidermoid carcinomas
standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                               38. .176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           medulloblastoma, mammary,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 100.
Best Local Similarity 100.
Matches 20; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2000-205717/18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200008166-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     09-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     05-AUG-1998;
                                                                                15-SEP-2003
23-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17-FEB-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gromeier M,
                                                                                                                                                                                                                                                                                                                                          stem_loop
                                                AAZ58488;
                                                                                                                                                                                                                                                                                                                                                                                               stem_loop
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chimeric
                                                                                                                                                                                                                                                                                         Chimeric
AAZ58488/c
                                                                                                                                                                                                                                                                                                                             Key
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target binding sequence of an oligonucleotide chosen from any one of the lo sequence of ABB5672 to ABB5671; and (b) a sequence required for selected amplification or detection reaction. Also described: (1) a kit (K1) comprising (1), and one or more contains that contains (1); and (2) detecting (M1) an enterovirus target sequence, involving: (a) amplifying the target sequence, involving: (a) amplifying the target sequence using first amplification primer having a sequence consisting essentially of target binding sequence of any one of ABB5674 to ABB56771 and optionally a sequence required for selected amplification reaction; and (b) detecting the amplified target sequence. (1), (M1) and (K1) are useful for detecting enterovirus target sequence. (1) sepectically and selectively recognizes the enterovirus genome. (1) sensitively and rapidly detects fewer than 500 copies of enteroviral genome and allows detection of broad range of enterovirus serotypes. The present sequence represents a viral 5, untranslated polynucleotide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel oligonucleotide comprising sequences for binding and amplifying or detecting target, useful for detecting enterovirus nucleic acids.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to an oligonucleotide (I) consisting of: (a) the
                                                                                                                                                                                                                         Human coxsackievirus B1 5' untranslated polynucleotide sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        present sequence represents a viral 5' untranslated polynucleot
sequence given in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 180 BP; 37 A; 48 C; 47 G; 48 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                 DNA detection; enteroviral detection; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure, Fig 1A-D; 34pp; English.
  118 AAGGAAACACGGACACCCAA 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tsang S, Price JA, Hellyer TJ;
                                                                                AEB56834/c
ID AEB56834 standard; DNA; 180 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                              16-JAN-2004; 2004US-00760048.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16-JAN-2004; 2004US-00760048.
                                                                                                                                                                                                                                                                                                          Human coxsackievirus Bl.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (TSAN/) TSANG S.
(PRIC/) PRICE J A.
(HELL/) HELLYER T J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2005-512251/52
                                                                                                                                                                                                                                                                                                                                                  US2005158710-A1.
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                                                                                                                                                                                 22-SEP-2005
                                                                                                                                                                                                                                                                                                                                                                                        21-JUL-2005.
                                                                                                                                           AEB56834;
                                                             RESULT
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ö 100.0%; Score 20; DB 14; Length 180; 100.0%; Pred. No. 10; tive 0; Mismatches 0; Indels ( AAGGAACACGGACACCCAA 140 1 AAGGAAACACGGACACCCAA 20 .; 0 ABZ69931 standard; DNA; 195 BP. Local Similario, hes 20; Conservative 159 ABZ69931 Query Match ABZ69931/c ID ABZ699 XX AC ABZ699 Matches RESULT 8 g

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Gaps

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1 AAGGAAACACGGACACCCAA 20

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The invention relates to an oligomucleotide (I) consisting of: (a) the target binding sequence of an oligomucleotide chosen from any one of the target binding sequence of ABB5671; and (b) a sequence required for selected amplification or detection reaction. Also described: (I) a kit (KI) comprising (I), and one or more container that contains (I); and (2) detecting (MI) an enterovirus target sequence, involving: (a) amplifying the target sequence using first amplification primer having a sequence consisting essentially of target binding sequence of any one of ABB56764 to ABB56771 and optionally a sequence required for selected amplification reaction; and (b) detecting the amplified target sequence. (I) (MI) and (KI) are useful for detecting enterovirus target sequence. (I) specifically and selectively recognizes the enterovirus genome. (I) sensitively and rapidly detects fewer than 500 copies of enteroviral senotives and allows detection of broad range of enterovirus serotypes. The present sequence represents a viral 5' untranslated polymucleotide sequence given in the exemplification of the present invention.
                                                                                                                                                                Novel oligonucleotide comprising sequences for binding and amplifying or detecting target, useful for detecting enterovirus nucleic acids.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 20; DB 14; Length 198;
Pred. No. 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human echovirus 6 5' untranslated polynucleotide sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 198 BP; 39 A; 49 C; 52 G; 58 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA detection; enteroviral detection; ds.
                                                                                                                                                                                                                        Disclosure, Fig 1A-D; 34pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 AAGGAAACACGGACACCCAA 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 AAGGAAACACGGACACCCAA 20
                                                                         Hellyer TJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hellyer TJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AEB56858 standard; DNA; 198 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20; Conservative
TSANG S.
PRICE J A.
HELLYER T J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (TSAN/) TSANG S.
(PRIC/) PRICE J A.
(HELL/) HELLYER T J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tsang S, Price JA,
                                                                         Price JA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2005-512251/52
GENBANK; U11709.
                                                                                                             WPI; 2005-512251/52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US2005158710-A1
                                                                                                                                 GENBANK; U11710
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                                                                         Isang S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AEB56858;
                   (PRIC/)
(HELL/)
 (TSAN/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 10
AEB56858/c
ID AEB56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention relates to a method for depositing a spot on a substrate, containing a sample for study, comprising preparing the sample in a liquid vehicle together with a magnetic support, to be deposited on the surface of a substrate as a droplet. The sample bonds to the magnetic support as particles. The sample material for analysis/ detection/ quantification can be cells, organisms, viruses and bacteria, antibodies, antibody fragments, antigens, haptens, lectins, sugars, RNA and DNA, proteins, hormone receptors, natural or synthetic molecules and macro molecules, and the like. The present oligonucleotide from Poliovirus type 3 was used in an example from the invention
                                                                                                                                                                                                                                                                                                                                                                                                             Preparing a spot on a substrate surface, the sample is contained within a
liquid with magnetic particles to be deposited as a droplet, to be dried
together with a magnetic field to distribute the particles/molecules
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 20; DB 10; Length 195; 100.0%; Pred. No. 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human echovirus 9 5' untranslated polynucleotide sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 195 BP; 42 A; 51 C; 50 G; 52 T; 0 U; 0 Other;
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA detection; enteroviral detection; ds.
                                                                         Analysis; detection; quantification; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                122 AAGGAAACACGGACACCCAA 103
                                                                                                                                                                                                                                                                                                                                       Delair T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 3; Page 17; 26pp; French
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 AAGGAAACACGGACACCCAA 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26-APR-2001; 2001FR-00005639
                                                                                                                                                                                                                                                            26-APR-2001; 2001FR-00005639
                                  Poliovirus type 3 sequence
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 100.
Matches 20, Conservative
                                                                                                                                                                                                                                                                                                                                      Theretz A,
                                                                                                                                                                                                                                                                                                                                                                          WPI; 2003-186349/19.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       evenly in the spot
                                                                                                                                                  FR2824001-A1
 04-APR-2003
                                                                                                                                                                                     31-OCT-2002
                                                                                                             Poliovirus.
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RESULT 9

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Gaps

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The invention relates to an oligonucleotide (I) consisting of: (a) the target binding sequence of an oligonucleotide chosen from any one of the target binding sequence of an oligonucleotide chosen from any one of the 10 sequence of ABB56762 to ABB56771; and (b) a sequence required for selected amplification or detection. Also described: (I) a kit (KI) comprising (I), and one or more container that contains (I); and (2) detecting (MI) an enterovirus target sequence, involving: (a) amplifying the target sequence using first amplification primer having a sequence consisting essentially of target binding sequence of any one of ABB5674 to ABB56771 and optionally a sequence required for selected amplification reaction; and (b) detecting the amplified target sequence. (I), (MI) and (KI) are useful for detecting enterovirus target sequence. (I) specifically and selectively recognizes the enterovirus genome. (I) sensitively and rapidly detects fewer than 500 copies of enteroviral genome and allows detection of broad range of enterovirus serotypes. The present sequence represents a viral 5' untranslated polynucleotide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to an oligonucleotide (I) consisting of: (a) the target binding sequence of an oligonucleotide chosen from any one of the 10 sequence of AEBS6762 to AEBS6771; and (b) a sequence required for selected amplification or detection reaction. Also described: (I) a kit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               oligonucleotide comprising sequences for binding and amplifying or ring target, useful for detecting enterovirus nucleic acids.
Novel oligonucleotide comprising sequences for binding and amplifying detecting target, useful for detecting enterovirus nucleic acids.
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                                                                                                                                                                                                                                                                                                                                                                        sequence given in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 20; DB 14; Length 198;
Pred. No. 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human echovirus 11 5' untranslated polynucleotide sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 198 BP; 37 A; 47 C; 55 G; 59 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA detection; enteroviral detection; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure, Fig 1A-D; 34pp; English.
                                                       Disclosure; Fig 1A-D; 34pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; SCC.
100.0%; Pre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 AAGGAAACACGGACACCCAA 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 AAGGAAACACGGACACCCAA 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hellyer TJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AEB56863/c
ID AEB56863 standard; DNA; 198 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.(
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (TSAN/) TSANG S.
(PRIC/) PRICE J A.
(HELL/) HELLYER T J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human echovirus 11.
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(K1) comprising (I), and one or more container that contains (I); and (2) detecting (M1) an enterovirus target sequence, involving: (a) amplifying the target sequence using first amplification primer having a sequence consisting essentially of target blinding sequence of any one of AEBS6774 to AEBS6771 and optionally a sequence required for selected amplification reaction, and (b) detecting the amplified target sequence. (I), (M1) and (M1) are useful for detecting enterovirus target sequences. (I), (M1) and (M2) are useful for detecting enterovirus target sequences. (I), (M3)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               target binding sequence of an oligoniclectide chosen from any one of the 10 sequence of ABB56721; and (b) a sequence required for selected amplification or detection reaction. Also described: (1) a kit (K1) comprising (1), and one or more contains that contains (1); and (2) detecting (M1) an enterovirus target sequence, involving: (a) amplifying consisting essentially of target indication primer having a sequence consisting essentially of target hinding sequence of any one of ABB5676 to ABB56771 and optionally a sequence required for selected amplification reaction; and (b) detecting the amplified target sequence. (1), (M1) and (K1) are useful for detecting enterovirus sequence. (1), sepecifically and selectively recognizes the enterovirus genome. (1) sensitively and rapidly detects fewer than 500 copies of enteroviral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel oligonucleotide comprising sequences for binding and amplifying or detecting target, useful for detecting enterovirus nucleic acids.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to an oligonucleotide (I) consisting of: (a) the
                                                                                                                                               specifically and selectively recognizes the enterovirus genome. (I) sensitively and rapidly detects fewer than 500 copies of enteroviral genome and allows detection of broad range of enterovirus serotypes.
                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                  present sequence represents a viral 5' untranslated polynucleotide sequence given in the exemplification of the present invention.
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                                                                                                                                                                                                                                                                                                                          Score 20; DB 14; Length 198; Pred. No. 10;
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                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                  Sequence 198 BP; 41 A; 49 C; 50 G; 58 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA detection; enteroviral detection; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                      121 AAGGAAACACGGACACCCAA 102
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                                                                                                                                                                                                                                                                                                                                              100.08;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AEB56854 standard; DNA; 198
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                                                                                                                                                                                                                                                                                                                                                                    20; Conservative
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(PRIC/) PRICE J A.
(HELL/) HELLYER T J.
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                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human echovirus 4.
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The invention relates to an oligonucleotide (1) consisting of: (a) the target binding sequence of an oligonucleotide chosen from any one of the consequence of ABBS6772 to ABBS6771; and (b) a sequence required for selected amplification or detection reaction. Also described: (1) a kit (K1) comprising (1), and one or more container that contains (1); and (2) detecting (M1) an enterovirus target sequence, involving: (a) amplifying the target sequence using first amplification primer having a sequence consisting essentially of target binding sequence of any one of ABBS6764 to ABBS6771 and optionally a sequence required for selected amplification reaction; and (b) detecting the amplified target sequence. (1), (M1) and (K1) are useful for detecting enterovirus target sequence. (1) specifically and selectively recognizes the enterovirus genome. (1) sensitively and rapidly detects fewer than 500 copies of enteroviral sensitively and allows detection of broad range of enterovirus serotypes. The present sequence represents a viral 5' untranslated polymucleotide greunce given in the exemplification of the present invention.
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genome and allows detection of broad range of enterovirus serotypes. The present sequence represents a viral 5' untranslated polynucleotide sequence given in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel oligonucleotide comprising sequences for binding and amplifying or detecting target, useful for detecting enterovirus nucleic acids.
                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 20; DB 14; Length 236; 100.0%; Pred. No. 11; ive 0; Mismatches 0; Indels 0
                                                                                                                     100.0%; Score 20; DB 14; Length 198; 100.0%; Pred. No. 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Viral 5' untranslated polynucleotide sequence SEQ ID NO:55.
                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 236 BP; 59 A; 51 C; 46 G; 80 T; 0 U; 0 Other;
                                                                                Sequence 198 BP; 43 A; 48 C; 50 G; 57 T; 0 U; 0 Other;
                                                                                                                                     , Pred. No. 10;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA detection; enteroviral detection; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure, SEQ ID NO 55; 34pp; English.
                                                                                                                                                                                                                     1 AAGGAAACACGGACACCCAA 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Isang S, Price JA, Hellyer TJ;
                                                                                                          Query Match
Best Local Similarity 100.0%;
Watches 20; Conservative 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16-JAN-2004; 2004US-00760048.
                                                                                                                                                                                                                                                                                                                                  AEB56816 standard; DNA; 236
                                                                                                                                                                                                                                                                                                                                                                                                               22-SEP-2005 (first entry)
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(PRIC/) PRICE J A.
(HELL/) HELLYER T J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unidentified.
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                                                                                                                                                                                                                                                                                                                                                                         AEB56816;
                                                                                                                                                                                                                                                                                            RESULT 13
AEB56816/c
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The invention relates to an oligonucleotide (I) consisting of: (a) the target binding sequence of an oligonucleotide chosen from any one of the 10 sequence of ABB5671; and (b) a sequence required for selected amplification or detection reaction. Also described: (I) a kit (K1) comprising (I), and one or more container that contains (I); and (2) detecting (M1) an enterovirus target sequence, involving: (a) amplifying the target sequence using first amplification primer having a sequence consisting essentially of target binding sequence of any one of ABB56764 to ABB56771 and optionally a sequence required for selected amplification reaction; and (b) detecting the amplified target sequence. (I), (M1) and (K1) are useful for detecting enterovirus target sequence. (I), specifically and selectively recognizes the enterovirus genome. (I) specifically and selectively recognizes the enterovirus genome. (I) sensitively and rapidly detects fewer than 500 copies of enteroviral genome and allows detection of broad range of enterovirus recorring.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel oligonucleotide comprising sequences for binding and amplifying or detecting target, useful for detecting enterovirus nucleic acids.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                 Human coxsackievirus B2 5' untranslated polynucleotide sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 237 BP; 46 A; 54 C; 66 G; 71 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                     DNA detection; enteroviral detection; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure, Fig 1A-D; 34pp; English.
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1 AAGGAAACACGGACACCCAA 20
                               105 AAGGAAACACGGACACCCAA 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tsang S, Price JA, Hellyer TJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AEBS6862/c
ID AEBS6862 standard; DNA; 237 BP.
XX
                                                                                                                            BP.
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                                                                                                                            AEB56837 standard; DNA; 237
                                                                                                                                                                                                 (first entry)
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                                                                                                                                                                                                                                                                                                         Human coxsackievirus B2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (TSAN/) TSANG S.
(PRIC/) PRICE J A.
(HELL/) HELLYER T J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2005-512251/52
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                                                                                                                                                                                                 22-SEP-2005
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                                                                                        RESULT 14
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Gaps

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Best Local Similarity 100. Matches 20; Conservative

Query Match

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target binding sequence of an oligonuclectide chosen from any one of the losquence of ABB5762 to ABB5671; and (b) a sequence required for selected amplification or detection reaction. Also described: (1) at kit (X1) comprising (1), and one or more container that contains (1); and (2) detecting (M1) an enterovirus target sequence, involving: (a) amplifying the target sequence using first amplification primer having a sequence of the target sequence using first amplification primer having a sequence consisting essentially of target binding sequence of any one of ABB5674 to ABB56771 and optionally a sequence required for selected amplification creation; and (b) detecting the amplified target sequence. (1) (M1) and (X1) are useful for detecting enterovirus target sequence. (1) specifically and selectively recognizes the enterovirus genome. (1) sensitively and rapidly detects fewer than 500 copies of enteroviral present sequence represents a viral 5' untranslated polymuclectide sequence represents a viral 5' untranslated polymuclectide sequence given in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel oligonucleotide comprising sequences for binding and amplifying or detecting target, useful for detecting enterovirus nucleic acids.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to an oligonuclectide (I) consisting of: (a) the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 20; DB 14; Length 237; 100.0%; Pred. No. 11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
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ID AEB56881 standard; DNA; 237 BP.
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Les 20; Conservative
                                                                                                                                                                                                                                                                                             (TSAN/) TSANG S.
(PRIC/) PRICE J A.
(HELL/) HELLYER T J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2005-512251/52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human poliovirus 3.
                               US2005158710-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENBANK; K01392
                                                                                             21-JUL-2005.
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to an oligonucleotide (1) consisting of: (a) the target binding sequence of an oligonucleotide chosen from any one of the 10 sequence of ABB567762 to ABB56771; and (b) a sequence required for selected amplification or detection reaction. Also described: (1) a kit (K1) comprishing (1), and one or more container that contains (1); and (2) detecting (M1) an enterovirus target sequence, involving: (a) amplifying the target sequence using first amplification primer having a sequence consisting essentially of target binding sequence of any one of ABB56764 to ABB56771 and optionally a sequence required for selected amplification reaction; and (b) detecting the amplified target sequence. (1), (M1) and (K1) are useful for detecting enterovirus target sequences. (1) sensitively and selectively recognizes the enterovirus genome. (1) sensitively and rapidly detects fewer than 500 copies of enteroviral contains and contains and contains a fewer than 500 copies of enterovirus contains and contain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel oligonucleotide comprising sequences for binding and amplifying or detecting target, useful for detecting enterovirus nucleic acids.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human poliovirus 3 5' untranslated polynucleotide sequence.
                                                                                                                      Human echovirus 9 5' untranslated polynucleotide sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                           DNA detection; enteroviral detection; ds
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1 Similarity 100.0%; P:
20; Conservative 0;
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(PRIC/) PRICE J A.
(HELL/) HELLYER T J.
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                                                                                                                                                                                                                                                             Human echovirus 9.
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US2005158710-A1
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AEB56875/c
                                                                                                                                                                                                                                                                   Matches
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                                                                                                                                            The invention relates to an oligonucleotide (1) consisting of: (a) the target binding sequence of an oligonucleotide chosen from any one of the target binding sequence of ABB5671; and (b) a sequence required for selected amplification or detection reaction. Also described: (1) a kit (K1) comprising (1), and one or more container that contains (1); and (2) detecting (M1) an enterovirus target sequence, involving: (a) amplifying the target sequence using first amplification primer having a sequence consisting essentially of target binding sequence of any one of ABB56764 to ABB56771 and optionally a sequence required for selected amplification reaction; and (b) detecting the amplified target sequence. (1), (M1) and (K1) are useful for detecting enterovirus target sequences. (1) specifically and selecting enterovirus target sequences. (1) specifically and selection of broad range of enterovirus serotypes. The present sequence represents a viral 5 untranslated polymucleotide sequence given in the exemplification of the present invention.
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                                                                                              Novel oligonucleotide comprising sequences for binding and amplifying or
                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                         detecting target, useful for detecting enterovirus nucleic acids
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                                                                                                                                                                                                                                                                                                                                                  Score 20; DB 14; Length 237; Pred. No. 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Viral 5' untranslated polynucleotide sequence SEQ ID NO:66.
                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                 Sequence 237 BP; 54 A; 56 C; 65 G; 62 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA detection; enteroviral detection; ds.
                                                                                                                           Disclosure; Fig 1A-D; 34pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                         161 AAGGAAACACGGACACCCAA 142
                                                                                                                                                                                                                                                                                                                                                                                              1 AAGGAAACACGGACACCCAA 20
                                          Hellyer TJ;
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TSANG S.
PRICE J A.
HELLYER T J.
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PRICE J A.
HELLYER T J.
                                         Tsang S, Price JA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Price JA,
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                                                                          SENBANK; X00925
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(HELL/) |
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(HELL/)
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 (TSAN/)
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The invention relates to an oligonucleotide (I) consisting of: (a) the target binding sequence of an oligonucleotide chosen from any one of the 10 sequence of ABBS6771; and (b) a sequence required for selected amplification or detection reaction. Also described: (I) a kit (XI) comprising (I), and one or more container that contains (I); and (2) detecting (MI) an enterovirus target sequence, involving: (a) amplifying the target sequence using first amplification primer having a sequence consisting essentially of target binding sequence of any one of AEBS6764 consisting essentially of target binding sequence of any one of AEBS6764 consisting and optionally a sequence required for selected amplification reaction; and (b) detecting the amplified target sequence. (I), (MI) and (XI) are useful for detecting enterovirus target sequences. (I) specifically and selectively recognizes the enterovirus genome. (I) specifically and rapidly detects fewer than 500 copies of enteroviral genome and allows detection of broad range of enterovirus serotypes. The presents sequence represents a viral 5, untranslated polymuclectide.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
detecting target, useful for detecting enterovirus nucleic acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 237 BP; 53 A; 58 C; 55 G; 71 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA detection; enteroviral detection; ds.
                                                                                      Disclosure; SEQ ID NO 66; 34pp; English.
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nes 20; Conservative
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(PRIC/) PRICE J A.
(HELL/) HELLYER T J.
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detecting (M1) an enterovirus target sequence, involving: (a) amplifying the target sequence using first amplification primer having a sequence consisting essentially of target binding sequence of any one of ARBS6764 to ARBS6771 and optionally a sequence required for selected amplification reaction; and (b) detecting the amplified target sequence. (1), (M1) and specifically and selecting enterovirus target sequence. (1), (M1) and specifically and selectively recognizes the enterovirus genome. (I) sensitively and rapidly detects fewer than 500 copies of enteroviral genome and allows detection of broad range of enterovirus serostypes. The segmence given in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to an oligonucleotide (I) consisting of: (a) the target binding sequence of an oligonucleotide chosen from any one of the 10 sequence of ABBS6762 to ABBS6771; and (b) a sequence required for selected amplification or detection reaction. Also described: (1) a kit (K1) comprising (I), and one or more container that contains (I); and (2) detecting (M1) an enterovirus target sequence, involving: (a) amplifying the target sequence using first amplification primer having a sequence consisting essentially of target binding sequence of any one of ABBS6764 to ABBS6771 and optionally a sequence required for selected amplification exaction, and (b) detecting the amplified target sequence. (I), (M1) and (K1) are useful for detecting enterovirus target sequence. (I) sepecifically and selectively recognizes the enterovirus genome. (I) sensitively and rapidly detects fewer than 500 copies of enteroviral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel oligonucleotide comprising sequences for binding and amplifying or detecting target, useful for detecting enterovirus nucleic acids.
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                                                                                                                                                                                                                                                                                     Score 20; DB 14; Length 237; Pred. No. 11; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human poliovirus 1 5' untranslated polynucleotide sequence.
                                                                                                                                                                                                                                               Sequence 237 BP; 57 A; 54 C; 62 G; 64 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA detection; enteroviral detection;
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                                                                                                                                                                                                                                                                                                                                                                                                161 AAGGAAACACGGACACCCAA 142
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                                                                                                                                                                                                                                                                  Query Match 100.0%; Sc
Best Local Similarity 100.0%; Pr
Conservative 0;
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(PRIC/) PRICE J A.
(HELL/) HELLYER T J.
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5' untranslated polynucleotide
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present sequence represents a viral 5' untranslated polynucleotide sequence given in the exemplification of the present invention.
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100.0%; Score 20; DB 14; Length 237;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 20; Conservative 0; Mismatches 0; Indels 0
                                                                                           Length 237;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel oligonucleotide comprising sequences for binding and detecting target, useful for detecting enterovirus nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                Human poliovirus 3 5' untranslated polynucleotide sequence.
                                                                                                                              0; Indels
                                                    Sequence 237 BP; 56 A; 54 C; 63 G; 64 T; 0 U; 0 Other;
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                                                                                       ; Score 20; DB 14;
; Pred. No. 11;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA detection; enteroviral detection; ds.
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                                                                                                                                                                                        161 AAGGAAACACGGACACCCAA 142
                                                                                                                                                                 1 AAGGAAACACGGACACCCAA 20
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                                                                                           100.08;
                                                                                                              100.08;
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                                                                                                                              20; Conservative
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(PRIC/) PRICE J A.
(HELL/) HELLYER T J.
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                                                                                                            Sest Local Similarity
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AEB56880/c
                                                                                                                              Matches
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Novel oligonucleotide comprising sequences for binding and amplifying or detecting target, useful for detecting enterovirus nucleic acids.
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                                                          Viral 5' untranslated polynucleotide sequence SEQ ID NO:44
                                                                                                     DNA detection; enteroviral detection; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; SEQ ID NO 44; 34pp; English.
                                                                                                                                                                                                                                                                      16-JAN-2004; 2004US-00760048
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                   22-SEP-2005 (first entry)
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(PRIC/) PRICE J A.
(HELL/) HELLYER T J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2005-512251/52
                                                                                                                                                                                      US2005158710-A1
                                                                                                                                               Unidentified.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to an oligonucleotide (I) consisting of: (a) the target binding sequence of an oligonucleotide chosen from any one of the consequence of ABBS6712 to ABBS671; and (b) a sequence required for selected amplification or detection. Also described: (I) a kit (KI) comprising (I), and one or more container that contains (I); and (2) detecting (MI) an enterovitus target sequence, involving: (a) amplifying the target sequence using first amplification primer having a sequence consisting essentially of target binding sequence of any one of AEBS676 to ABBS671 and optionally a sequence required for selected amplification reaction; and (b) detecting the amplified target sequence. (I), (MI) and (KI) are useful for detecting enterovirus target sequence. (I) specifically and selectively recognizes the enterovirus genome. (I) specifically and selectively recognizes the enterovirus genome. (I) genome and allows detection of broad range of enterovirus serotypes. The presents sequence represents a viral 5, untranslated polymorleotide.
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                                                                                                                                                                                                                                                                    Viral 5' untranslated polynucleotide sequence SEQ ID NO:64.
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                                                                                                                                                                                                                                                                                                           DNA detection; enteroviral detection; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; SEQ ID NO 64; 34pp; English.
                            161 AAGGAAACACGGACACCCAA 142
20
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1 AAGGAAACACGGACACCCAA
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                                                                                                                                          AEB56825 standard; DNA; 237
                                                                                                                                                                                                                          (first entry)
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Les 20; Conservative
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(PRIC/) PRICE J A.
(HELL/) HELLYER T J.
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                                                                                                   RESULT 22
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Hellyer TJ;

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target binding sequence of an oligonucleotide chosen from any one of the target binding sequence of an oligonucleotide chosen from any one of the 10 sequence of ABB5762 to ABB5671; and (b) a sequence required for selected amplification or detection reaction. Also described: (1) at kit (XI) comprising (II), and one or more container that contains (I); and (2) detecting (MI) an enterovirus target sequence, involving: (a) amplifying the target sequence using first amplification primer having a sequence or onsisting essentially of target binding sequence of any one of ABB5674 to ABB5671 and optionally a sequence required for selected amplification reaction; and (b) detecting the amplified target sequence. (I) (MI) and (XI) are useful for detecting enterovirus target sequence. (I) specifically and selectively recognizes the enterovirus genome. (I) sensitively and rapidly detects fewer than 500 copies of enteroviral present sequence represents a viral 5' untranslated polymucleotide represents a viral 5' untranslated polymucleotide sequence given in the exemplification of the present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 237 BP; 54 A; 53 C; 56 G; 74 T; 0 U; 0 Other;
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100.0%;
Best Local Similarity 100.0%;
Matches 20; Conservative 0
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Gaps

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0; Indels

0; Mismatches

100.08;

Matches

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AEB56805 standard; DNA; 237 BP.

AEB56805,

AEB56805

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The invention relates to an oligonucleotide (I) consisting of: (a) the target binding sequence of an oligonucleotide chosen from any one of the 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for selected amplification or detection reaction. Also described: (1) a kit (K1) comprising (I), and one or more container that contains (I); and (2) detecting (M1) an enterovirus target sequence, involving: (a) amplifying the target sequence using first amplification primer having a sequence consisting essentially of target binding sequence of any one of AEB56764 to AEB56771 and optionally a sequence required for selected amplification reaction; and (b) detecting the amplified target sequence. (I), (M1) and (K1) are useful for detecting enterovirus target sequences. (I), (M1) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           specifically and selectively recognizes the enterovirus genome. (I) sensitively and rapidly detects fewer than 500 copies of enteroviral genome and allows detection of broad range of enterovirus serotypes. The
                                                                                                                                                                       Novel oligonucleotide comprising sequences for binding and amplifying or detecting target, useful for detecting enterovirus nucleic acids.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          present sequence represents a viral 5' untranslated polynucleotide sequence given in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 20; DB 14; Length 237;
Pred. No. 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Viral 5' untranslated polynucleotide sequence SEQ ID NO:45.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 237 BP; 54 A; 57 C; 63 G; 63 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA detection; enteroviral detection; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; SEQ ID NO 45; 34pp; English
                                                                                                                                                                                                                                                                Disclosure; Fig 1A-D; 34pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 161 AAGGAAACACGGACACCCAA 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20
                              Hellyer TJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AEB56806/c
ID AEB56806 standard; DNA; 237 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 AAGGAAACACGGACACCCAA
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(PRIC/) PRICE J A.
(HELL/) HELLYER T J.
                              Price JA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2005-512251/52.
                                                                                     WPI; 2005-512251/52
                                                                                                                       GENBANK; AJ132961
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21-JUL-2005.
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                              Tsang S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to an oligonuclectide (I) consisting of: (a) the target binding sequence of an oligonuclectide chosen from any one of the 10 sequence of ABS5715 to ABS571; and (b) a sequence required for cleared amplification or detection. Also described: (I) a kit (KI) comprising (I), and one or more container that contains (I); and (2) detecting (MI) an enterovirus target sequence, involving: (a) amplifying the target sequence using first amplification primer having a sequence consisting essentially of target binding sequence of any one of ABS576 to ABS571 and optionally a sequence required for selected amplification reaction; and (b) detecting the amplified target sequence. (I), (MI) and (KI) are useful for detecting enerovirus target sequences. (I) specifically and selectively recognizes the enterovirus genome. (I) specifically and rapidly detects fewer than 500 copies of enteroviral genome and allows detection of broad range of enterovirus presents equence represents a viral 5' untranslated polynucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel oligonucleotide comprising sequences for binding and amplifying or detecting target, useful for detecting enterovirus nucleic acids.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequence given in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ouery Match
100.0%; Score 20; DB 14; Length 237;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 20; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human poliovirus 1 5' untranslated polynucleotide sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 237 BP; 50 A; 55 C; 59 G; 73 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA detection; enteroviral detection; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; SEQ ID NO 57; 34pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 AAGGAAACACGGACACCCAA 20
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                                                                                                                                                                                                                                                                                                                    Hellyer TJ;
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                                                                         16-JAN-2004; 2004US-00760048
                                                                                                                                         16-JAN-2004; 2004US-00760048
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                                                                                                                                                                                             (TSAN/) TSANG S.
(PRIC/) PRICE J A.
(HELL/) HELLYER T J.
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PRICE J A.
HELLYER T J.
                                                                                                                                                                                                                                                                                                                 Tsang S, Price JA,
                                                                                                                                                                                                                                                                                                                                                                           WPI; 2005-512251/52
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AEB56873;

BBBXBXBXBXSXXXXBXBXBXXX

AEB56873/c RESULT 25

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(PRIC/) (HELL/) (TSAN/)

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Gaps

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        The invention relates to an oligonucleotide (I) consisting of: (a) the target binding sequence of an oligonucleotide chosen from any one of the 10 sequence of ABBS6712 to ABBS6711, and (b) a sequence required for selected amplification or detection reaction. Also described: (I) a kit (KI) comprising (I), and one or more container that contains (I); and (2) detecting (MI) an enterovirus target sequence, involving: (a) amplifying the target sequence using first amplification primer having a sequence consisting essentially of target binding sequence of any one of ABBS676 to ABBS6771 and optionally a sequence required for selected amplification reaction; and (b) detecting the amplified target sequence. (I) (MI) and (XI) are useful for detecting enterovirus target sequences. (I) specifically and selectively recognizes the enterovirus genome. (I) specifically and rapidly detects fewer than 500 copies of enteroviral senome and allows detection of broad range of enterovirus serotypes. The present sequence represents a viral 5 untranslated polymucleotide sequence given in the exemplification of the present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to an oligonucleotide (I) consisting of: (a) the target binding sequence of an oligonucleotide chosen from any one of the 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for selected amplification or detection reaction. Also described: (1) a kit (K1) comprising (I), and one or more container that contains (I); and (2) detecting (M1) an enterovirus target sequence, involving: (a) amplifying the target sequence using first amplification primer having a sequence consisting essentially of target binding sequence of any one of AEB56764
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel oligonucleotide comprising sequences for binding and amplifying or detecting target, useful for detecting enterovirus nucleic acids.
                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                       100.0%; Score 20; DB 14; Length 237; 100.0%; Pred. No. 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human echovirus 9 5' untranslated polynucleotide sequence.
                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                             Sequence 237 BP; 54 A; 53 C; 56 G; 74 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA detection; enteroviral detection; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Fig 1A-D; 34pp; English.
                                                                                                                                                                                                                                                                                                                           1 AAGGAAACACGGACACCCAA 20
                                                                                                                                                                                                                                                                                                                                         105 AAGGAAACACGGACACCCAA 86
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                 20; Conservative
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(PRIC/) PRICE J A.
(HELL/) HELLYER T J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tsang S, Price JA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2005-512251/52.
                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human echovirus 9.
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                                                                                                                                                                                                                                                                    Query Match
Best Local S
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                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                              RESULT 27
                                                                                                                                                                                                                                                                                                                                                                                                            AEB56861/
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trarget binding sequence of an oligonucleotide (1) cubisticing of the target binding sequence of an oligonucleotide chosen from any one of the 10 sequence of ABB5672 to ABB5671; and (b) a sequence required for selected amplification or detection reaction. Also described: (1) a kit (X1) comprising (1), and one or more container that contains (1); and (2) detecting (M1) an enterovirus target sequence, involving: (a) amplifying the target sequence using first amplification primer having a sequence of the target sequence using first amplification primer having a sequence (1) consisting essentially of target binding sequence of any one of ABB5674 to ABB5671 and optionally a sequence required for selected amplification reaction, and (b) detecting the amplified target sequence. (1) (M1) and (X1) are useful for detecting enterovirus target sequences. (1) specifically and selectively recognizes the enterovirus genome. (1) specifically and selectively recognizes the enterovirus genome. (1) sensitively and rapidly detects fewer than 500 copies of enteroviral present sequence represents: a viral 5' untranslated polynucleotide sequence represents: a viral 5' untranslated polynucleotide sequence civen seamplification of the present invention.
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to AEB56771 and optionally a sequence required for selected amplification reaction, and (b) detecting the amplified target sequence. (1), (M1) and (K1) are useful for detecting enterovirus target sequences. (1) specifically and selectively recognizes the enterovirus genome. (1) sensitively and rapidly detects fewer than 500 copies of enteroviral genome and allows detection of broad range of enterovirus serotypes. The present sequence represents a viral 5' untranslated polynucleotide sequence given in the exemplification of the present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Score 20; DB 14; Length 237; ; Pred. No. 11; 0; Mismatches 0; Indels C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Viral 5' untranslated polynucleotide sequence SEQ ID NO:56.
                                                                                                                                                                                                                                                                                                                                                                                     Sequence 237 BP; 48 A; 54 C; 65 G; 70 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 237 BP; 52 A; 56 C; 58 G; 71 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA detection; enteroviral detection; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; SEQ ID NO 56; 34pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            160 AAGGAAACACGGACACCCAA 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 AAGGAAACACGGACACCCAA 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%;
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(PRIC/) PRICE J A.
(HELL/) HELLYER T J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 28
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Human enterovirus 70 5' untranslated polynucleotide sequence

(first entry)

22-SEP-2005

AEB56871;

AEB56871 standard; DNA; 237 BP

RESULT 30 AEB56871/c

DNA detection; enteroviral detection; ds.

Human enterovirus 70

US2005158710-A1.

21-JUL-2005.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to an oligonucleotide (I) consisting of: (a) the target binding sequence of an oligonucleotide chosen from any one of the 10 sequence of ABB56772 to ABB56771; and (b) a sequence required for selected amplification or detection reaction. Also described: (1) a kit (K1) comprising (I), and one or more container that contains (I); and (2) detecting (M1) an enterovirus target sequence, involving: (a) amplifying the target sequence using first amplification primer having a sequence consisting essentially of target binding sequence of any one of ABB56764 to ABB56771 and optionally a sequence required for selected amplification reaction, and (b) detecting the amplified target sequence. (I), (M1) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Jonucleotide comprising sequences for binding and amplifying or target, useful for detecting enterovirus nucleic acids.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            genome and allows detection of broad range of enterovirus serotypes. The present sequence represents a viral 5' untranslated polynuclectide sequence given in the exemplification of the present invention.
                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         reaction; and (b) detecting the amplified target sequence. (I), (K1) are useful for detecting enterovirus target sequences. (I) specifically and selectively recognizes the enterovirus genome.
                                                 ö
              Length 237;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 20; DB 14; Length 237; larity 100.0%; Pred. No. 11; Conservative 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                               Viral 5' untranslated polynucleotide sequence SEQ ID NO:59
                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 237 BP; 50 A; 53 C; 60 G; 74 T; 0 U; 0 Other;
                                                 ö
              DB 14;
100.0%; Scc...
100.0%; Pred. No. ...
                                                                                                                                                                                                                                                                                                                                                  DNA detection; enteroviral detection; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; SEQ ID NO 59; 34pp; English.
                                                                                1 AAGGAAACACGGACACCCAA 20
                                                                                                             105 AAGGAAACACGGACACCCAA 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hellyer TJ;
                                                                                                                                                                                                            ВР
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16-JAN-2004; 2004US-00760048.
                                                                                                                                                                                    AEB56820/c
ID AEB56820 standard; DNA; 237
                                                                                                                                                                                                                                                                            (first entry)
         Query Match
Best Local Similarity 100.
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel oligonucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (TSAN/) TSANG S.
(PRIC/) PRICE J A.
(HELL/) HELLYER T J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Price JA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2005-512251/52
                                                                                                                                                                                                                                                                                                                                                                                                                       US2005158710-A1.
                                                                                                                                                                                                                                                                                                                                                                                    Unidentified
                                                                                                                                                                                                                                                                              22-SEP-2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                          21-JUL-2005.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            detecting
                                                                                                                                                                                                                                           AEB56820;
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Novel oligonucleotide comprising sequences for binding and amplifying or detecting target, useful for detecting enterovirus nucleic acids.

Price JA, Hellyer TJ;

reang S,

WPI; 2005-512251/52

SENBANK; D00820

(TSAN/) TSANG S. (PRIC/) PRICE J A. (HELL/) HELLYER T J.

16-JAN-2004; 2004US-00760048 16-JAN-2004; 2004US-00760048 Disclosure; Fig 1A-D; 34pp; English

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   to AEBS6771 and optionally a sequence required for selected amplification reaction; and (b) detecting the amplified target sequence. (I), (M1) and (K1) are useful for detecting enterovirus target sequences. (I)
                                                                                                                                                                                                                                                                                                                                                The invention relates to an oligonucleotide (I) consisting of: (a) the target binding sequence of an oligonucleotide chosen from any one of the 10 sequence of ABB56762 to ABB56771; and (b) a sequence required for selected amplification or detection reaction. Also described: (1) a kit (K1) comprising (I), and one or more container that contains (I); and (2) detecting (M1) an enterovirus target sequence, involving: (a) amplifying the target sequence using first amplification primer having a sequence consisting essentially of target binding sequence of any one of ABB56764
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     specifically and selectively recognizes the enterovirus genome. (I) sensitively and rapidly detects fewer than 500 copies of enteroviral genome and allows detection of broad range of enterovirus serotypes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         l range of enterovirus serotypes.
5' untranslated polynucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sequence given in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 20; DB 14; Length 237; Pred. No. 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Viral 5' untranslated polynucleotide sequence SEQ ID NO:60.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 237 BP; 54 A; 52 C; 60 G; 71 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          161 AAGGAAACACGGACACCCAA 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 AAGGAAACACGGACACCCAA 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          represents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AEB56821 standard; DNA; 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          present sequence
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AEB56821/c
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AC AEB568
XX
XX
XX
XX
DE Viral
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Gaps

1 AAGGAAACACGGACACCCAA 20

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Local Similarity nes 20; Conserv

Best Loca Matches

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Score 20; DB 14; Length 237; Pred. No. 11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 237 BP; 54 A; 56 C; 64 G; 63 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA detection; enteroviral detection; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            161 AAGGAAACACGGACACCCAA 142
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                                                                                                                                  Hellyer TJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AEB56782 standard; DNA; 237 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.08;
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Best Local Similarity 100.0%;
Matches 20; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16-JAN-2004; 2004US-00760048
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PRICE J A.
HELLYER T J.
                                      TSANG S.
PRICE J A.
HELLYER T J.
                                                                                                                                  feang S, Price JA,
                                                                                                                                                                           WPI: 2005-512251/52
                                                                                                                                                                                                  GENBANK; AJ132960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US2005158710-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-JUL-2005.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (TSAN/)
(PRIC/)
(HELL/)
                                                                (PRIC/)
(HELL/)
                                           (TSAN/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AEB56782/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 용
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ਨੇ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to an oligonucleotide (I) consisting of: (a) the target binding sequence of an oligonucleotide chosen from any one of the 10 sequence of ABBS6712 to ABBS6712 and (b) a sequence required for selected amplification or detection reaction. Also described: (I) a kit (KI) comprising (I), and one or more container that contains (I); and (2) detecting (MI) an enterovirus target sequence, involving: (a) amplifying the target sequence using first amplification primer having a sequence consisting essentially of target binding sequence of any one of ABBS674 to ABBS6771 and optionally a sequence required for selected amplification reaction; and (b) detecting the amplified target sequence. (I) (MI) and (KI) are useful for detecting enterovirus target sequences. (I) specifically and selecting enterovirus target sequences. (I) specifically and selecting enterovirus target sequence. (I) specifically and selecting enterovirus target sequence. (I) sensitively and rapidly detects fewer than 500 copies of enteroviral senome and allows detection of broad range of enterovirus serotypes. The present sequence represents a viral 5' untranslated polymucleotide sequence given in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel oligonucleotide comprising sequences for binding and amplifying or detecting target, useful for detecting enterovirus nucleic acids.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 20; DB 14; Length 237; 100.0%; Pred. No. 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human poliovirus 1 5' untranslated polynucleotide seguence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 237 BP; 49 A; 51 C; 61 G; 76 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA detection; enteroviral detection; ds.
DNA detection; enteroviral detection; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; SEQ ID NO 60; 34pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 AAGGAAACACGGACACCCAA 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          105 AAGGAAACACGGACACCCAA 86
                                                                                                                                                                                                                                                                                                                                                       Hellyer TJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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                                                                                                                                                                                                                    16-JAN-2004; 2004US-00760048.
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                                                                                                                                                                                                                                                              (TSAN/) TSANG S.
(PRIC/) PRICE J A.
(HELL/) HELLYER T J.
                                                                                                                                                                                                                                                                                                                                                       Isang S, Price JA,
                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2005-512251/52
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                                                                                       US2005158710-A1
                                           Unidentified.
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Matches
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AEB56872/c
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Gaps

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0; Indels

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The invention relates to an oligonucleotide (I) consisting of: (a) the target binding sequence of an oligonucleotide chosen from any one of the 10 sequence of ABBS6712 to ABBS6713, and (b) a sequence required for selected amplification or detection reaction. Also described: (I) a kit (K1) comprising (I), and one or more container that contains (I); and (2) detecting (M1) an enterovirus target sequence, involving: (a) amplifying the target sequence using first amplification primer having a sequence consisting essentially of target binding sequence of any one of ABBS6764 to ABBS6771 and optionally a sequence required for selected amplification reaction; and (b) detecting enterovirus target sequence. (I), (M1) and (K1) are useful for detecting enterovirus target sequences. (I) specifically and selectively recognizes the enterovirus genome. (I) sensitively and rapidly detects fewer than 500 copies of enteroviral genome and allows detection of broad range of enterovirus serocrypes.
                                                                                                                                                                                                                                                                  Novel oligonucleotide comprising sequences for binding and amplifying or detecting target, useful for detecting enterovirus nucleic acids.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sequence given in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                       Disclosure; Fig 1A-D; 34pp; English
                   16-JAN-2004; 2004US-00760048
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                                                                                                                The invention relates to an oligonucleotide (1) consisting of: (a) the target binding sequence of an oligonucleotide chosen from any one of the 10 sequence of ABS5775 to ABS5771; and (b) a sequence required for calcated amplification or detection reaction. Also described: (1) a kit (K1) comprising (1), and one or more container that contains (1); and (2) detecting (M1) an enterovirus target sequence, involving: (a) amplifying the target sequence using first amplification primer having a sequence consisting essentially of target binding sequence of any one of ABS5764 to ABS5771 and optionally a sequence required for selected amplification reaction; and (b) detecting the amplified target sequence. (1), (M1) and (K1) are useful for detecting enterovirus target sequence. (1) specifically and selectively recognizes the enterovirus genome. (1) specifically and relatively tecognizes the enterovirus genome. (1) specifically and relatively the amplified target sequence. (1) specifically and relatively and rapidly detects fewer than 500 copies of enteroviral genome and allows detection of broad range of enterovirus serotypes. The presents sequence represents a viral 5, untranslated polymorlectide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                    Novel oligonucleotide comprising sequences for binding and amplifying or detecting target, useful for detecting enterovirus nucleic acids.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to an oligonucleotide (I) consisting of: (a) the target binding sequence of an oligonucleotide chosen from any one of the 10 sequence of ABB56762 to ABB56771; and (b) a sequence required for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel oligonucleotide comprising sequences for binding and amplifying or detecting target, useful for detecting enterovirus nucleic acids.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                            sequence given in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 20; DB 14; Length 237; 100.0%; Pred. No. 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Viral 5' untranslated polynucleotide sequence SEQ ID NO:63.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 237 BP; 46 A; 52 C; 61 G; 78 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA detection; enteroviral detection; ds.
                                                                                     Disclosure; SEQ ID NO 21; 34pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hellyer TJ
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ID AEB56824 standard; DNA; 237 BP
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Matches 20; Conservative
                                   Novel oligonucleotide
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(PRIC/) PRICE J A.
(HELL/) HELLYER I J.
WPI; 2005-512251/52
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selected amplification or detection reaction. Also described: (1) a kit (K1) comprising (1), and one or more container that contains (1); and (2) detecting (M1) an enterovirus target sequence, involving: (a) amplifying the target sequence is the target sequence are amplifying the target sequence using first amplification primer having a sequence consisting essentially of target binding sequence of any one of ABB5676 to ABB56771 and optionally a sequence required for selected amplification reaction; and (b) detecting the amplified target sequence. (1), (M1) and (K1) are useful for detecting the emplified target sequence. (1) specifically and selectively recognizes the enterovirus genome. (1) sensitively and rapidly detects fewer than 500 copies of enteroviral genome and allows detection of broad range of enterovirus serotypes. The sequence represents a viral 5' untranslated polynucleotide sequence given in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        target binding sequence of an object of the sequence from any one of the lose sequence of ABBS672 to ABBS671; and (b) a sequence required for selected amplification or detection reaction. Also described: (1) a kit (K1) comprising (I), and one or more container that contains (I); and (2) detecting (M1) an enterovirus target sequence, involving: (a) amplifying the target sequence using first amplification primer having a sequence consisting essentially of target binding sequence of any one of ABBS674 to ABBS6771 and optionally a sequence required for selected amplification reaction; and (b) detecting the amplified target sequence. (I), (M1) and (K1) are useful for detecting the amplified target sequences. (I), (M1) and specifically and selectively recognizes the enterovirus genome. (I)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel oligonucleotide comprising sequences for binding and amplifying or detecting target, useful for detecting enterovirus nucleic acids.
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                            Score 20; DB 14; Length 237; Pred. No. 11;
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                                                                                                                                                                                                                                                                                                                                               Sequence 237 BP; 53 A; 59 C; 55 G; 70 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                        100.0%; Scc...
100.0%; Pred. No. 11,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 AAGGAAACACGGACACCCAA 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AEB56791 standard; DNA; 238 BP
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1es 20; Conservative
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(PRIC/) PRICE J A.
(HELL/) HELLYER T J.
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AEB56791/c
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The invention relates to an oligonucleotide (1) consisting of: (a) the target binding sequence of an oligonucleotide chosen from any one of the target binding sequence of ABBS6771; and (b) a sequence required for selected amplification or detection reaction. Also described: (1) a kit (K1) comprising (1), and one or more container that contains (1); and (2) detecting (M1) an enterovirus target sequence, involving: (a) amplifying the target sequence using first amplification primer having a sequence consisting essentially of target binding sequence of any one of ABBS6764 to ABBS6771 and optionally a sequence required for selected amplification reaction; and (b) detecting the amplified target sequence. (1), (M1) and (X1) are useful for detecting enterovirus target sequences. (1) specifically and selectively recognizes the enterovirus genome. (1) sensitively and rapidly detects fewer than 500 copies of enteroviral cgenome and allows detection of broad range of enterovirus serotypes. The present sequence represents a viral 5' untranslated polymucleotide sequence given in the exemplification of the present invention.
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genome and allows detection of broad range of enterovirus serotypes. The present sequence represents a viral 5' untranslated polynucleotide sequence given in the exemplification of the present invention.
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                                                                                                                                                                                                                             100.0%; Score 20; DB 14; Length 238; 100.0%; Pred. No. 11; ive 0; Mismatches 0; Indels (
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                                                                                                                                                       Sequence 238 BP; 54 A; 52 C; 58 G; 74 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA detection; enteroviral detection; ds.
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                                                                                                                                                                                                                                                                                                                                                                                     1 AAGGAAACACGGACACCCAA 20
                                                                                                                                                                                                                                                                                                                                                                                                                            105 AAGGAAACACGGACACCCAA 86
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Best Local Similarity 100.09
Matches 20; Conservative
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(PRIC/) PRICE J A.
(HELL/) HELLYER T J.
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The invention relates to an oligonucleotide (I) consisting of: (a) the target binding sequence of an oligonucleotide chosen from any one of the target binding sequence of ABBS6772 to ABBS6771; and (b) a sequence required for selected amplification or detection. Also described: (1) a kit (K1) comprising (I), and one or more container that contains (I); and (2) detecting (M1) an enterovirus target sequence, involving: (a) amplifying the target sequence using first amplification primer having a sequence consisting essentially of target binding sequence of any one of ABBS6764 to ABBS6771 and optionally a sequence required for selected amplification reaction; and (b) detecting the amplified target sequence. (I) (M1) and (K1) are useful for detecting enterovirus genome. (I) specifically and rapidly detects fewer than 500 copies of enteroviral sensitively and rapidly detects fewer than 500 copies of enteroviral spenance represents a viral 5' untranslated polymucleotide present sequence given in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel oligonucleotide comprising sequences for binding and amplifying or detecting target, useful for detecting enterovirus nucleic acids.
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                 1 AAGGAAACACGGACACCCAA 20
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AEB56846 standard; DNA; 238 BP.
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                                                                                                                    AEB56849 standard; DNA; 238
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nes 20; Conservative
                                                                                                                                                                                                                                                                                           Human coxsackievirus B5.
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(PRIC/) PRICE J A.
(HELL/) HELLYER T J.
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ID AEB56
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Query Match
100.0%; Score 20; DB 14; Length 238;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 20; Conservative 0; Mismatches 0; Indels

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target binding sequence of an oilgonucleotide chosen from any one of the sequence of ABB5072 to ABB5071; and (b) a sequence required for selected amplification or detection reaction. Also described: (l) a kit (KI) comprising (l), and one or more contains that contains (l); and (2) detecting (MI) an enterovirus target sequence, involving: (a) amplifying the target sequence using first amplification primer having a sequence consisting essentially of target binding sequence of any one of ABB56774 to ABB56771 and optionally a sequence required for selected amplification reaction; and (b) detecting the amplified target sequence. (l) (MI) and specifically and selecting enterovirus target sequence. (l) sensitively and rapidly detects fewer than 500 copies of enteroviral genome and allows detection of broad range of enterovirus serotypes. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ange of enterovirus serotypes. The untranslated polynucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel oligonucleotide comprising sequences for binding and amplifying or detecting target, useful for detecting enterovirus nucleic acids.
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les 20; Conservative
                                                                                                                                                                                                                              (TSAN/) TSANG S.
(PRIC/) PRICE J A.
(HELL/) HELLYER T J.
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel oligonucleotide comprising sequences for binding and amplifying or detecting target, useful for detecting enterovirus nucleic acids.
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                                                                                            Human coxsackievirus B4 5' untranslated polynucleotide sequence
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                                                                                                                                                  DNA detection; enteroviral detection; ds.
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                                           22-SEP-2005 (first entry)
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(PRIC/) PRICE J A.
(HELL/) HELLYER T J.
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GENBANK; D00149.
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                                                                                                                                              The invention relates to an oligonucleotide (I) consisting of: (a) the target binding sequence of an oligonucleotide chosen from any one of the 10 sequence of ABBS6712 to ABBS671; and (b) a sequence required for selected amplification or detection reaction. Also described: (I) a kit (KI) comprising (I), and one or more container that contains (I); and (2) detecting (MI) an enterovirus target sequence, involving: (a) amplifying the target sequence using first amplification primer having a sequence consisting essentially of target binding sequence of any one of ABBS6764 to ABBS6771 and optionally a sequence required for selected amplification reaction; and (b) detecting the amplified target sequence. (I) (MI) and (XI) are useful for detecting enterovirus target sequences. (I) specifically and selectively recognizes the enterovirus genome. (I) specifically and rapidly detects fewer than 500 copies of enteroviral sensitively and rapidly detects fewer than 500 copies of enteroviral present sequence represents a viral 5° untranslated polynucleotide present sequence given in the exemplification of the present invention.
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                                                                                         Novel oligonucleotide comprising sequences for binding and amplifying or detecting target, useful for detecting enterovirus nucleic acids.
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                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
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                                                                                                                            Disclosure; SEQ ID NO 58; 34pp; English.
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                                              Hellyer TJ;
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ID AEB56807 standard; DNA; 238
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TSANG S.
PRICE J.A.
HELLYER T J.
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Best Local Similarity
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(PRIC/) PRICE J A.
(HELL/) HELLYER T J.
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                                              Price JA,
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           (PRIC/)
(HELL/)
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The invention relates to an oligonuclectide (I) consisting of: (a) the target binding sequence of an oligonuclectide chosen from any one of the 10 sequence of ARB56762 to ARB5671; and (b) a sequence required for selected amplification or detection. Also described: (I) a kit (KI) comprishing (I), and one or more container that contains (I); and (2) detecting (MI) an enterovirus target sequence, involving: (a) amplifying the target sequence using first amplification primer having a sequence consisting essentially of target binding sequence of any one of ARB5674 to ARB56771 and optionally a sequence required for selected amplification reaction; and (b) detecting the amplified target sequence. (I), (MI) and (KI) are useful for detecting enterovirus target sequences. (I) specifically and selectively recognizes the enterovirus genome. (I) sensitively and rapidly detects fewer than 500 copies of enteroviral manner and application and the fourty fewer than 500 copies of enteroviral manner and application and the fourty and rapidly characterial and selectively an
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Pred. No. 11;
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Disclosure; SEQ ID NO 46; 34pp; English
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Best Local Similarity 100.0%;
Matches 20; Conservative (
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(PRIC/) PRICE J A.
(HELL/) HELLYER T J.
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Sequence 238 BP; 57 A; 50 C; 55 G; 76 T; 0 U; 0 Other;

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consisting essentially of target binding sequence of any one of AEBS6764 to AEBS6771 and optionally a sequence required for selected amplification reaction, and (b) detecting the amplified target sequence. (1), (M1) and (K1) are useful for detecting enterovirus target sequences. (1) specifically and selectively recognizes the enterovirus genome. (1) sensitively and rapidly detects fewer than 500 copies of enteroviral genome and allows detection of broad range of enterovirus serotypes. The present sequence represents a viral 5' untranslated polynucleotide sequence given in the exemplification of the present invention.
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Matches 20, Conservative
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(PRIC/) PRICE J A.
(HELL/) HELLYER T J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2005-512251/52
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AEB56799;
                                                                                                                                                                                                                                                                   Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to an oligonucleotide (I) consisting of: (a) the target binding sequence of an oligonucleotide chosen from any one of the 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for selected amplification or detection. Also described: (1) a kit (XI) comprising (I), and one or more container that contains (I); and (2) detecting (MI) an enterovirus target sequence, involving: (a) amplifying the target sequence using first amplification primer having a sequence consisting essentially of target binding sequence of any one of AEB56764 to AEB56771 and optionally a sequence required for selected amplification reaction; and (b) detecting the amplified target sequence. (I), (MI) and (MI) are useful for detecting enterovirus target sequences. (I), (MI) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel oligonucleotide comprising sequences for binding and amplifying or detecting target, useful for detecting enterovirus nucleic acids.
                                                            Gaps
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  Length 238;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human poliovirus 1 5' untranslated polynucleotide sequence.
                                                         Indels
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  DB 14;
                                 . 11;
                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA detection; enteroviral detection; ds.
     Score 20;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure, Fig 1A-D; 34pp; English.
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                                                                                                              20
                                                                                                                                                 105 AAGGAAACACGGACACCCAA 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20
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                                                                                                              1 AAGGAAACACGGACACCCAA
100.08;
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                                                       20; Conservative
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(PRIC/) PRICE J A.
(HELL/) HELLYER T J.
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Query Match
Best Local Similarity
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les 20; Conserv
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                                                         Matches
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Novel oligonucleotide comprising sequences for binding and amplifying or detecting target, useful for detecting enterovirus nucleic acids.
Consensus viral 5' untranslated polynucleotide sequence.
                                                   DNA detection; enteroviral detection; da
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                                                                                                                                                                                                                                                                                                                          16-JAN-2004; 2004US-00760048.
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(PRIC/) PRICE J A.
(HELL/) HELLYER T J.
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                                                                                                                                                              JS2005158710-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel oligonucleotide comprising sequences for binding and amplifying or detecting target, useful for detecting enterovirus nucleic acids.
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                                                                                                                                                                                                                                                                       Viral 5' untranslated polynucleotide sequence SEQ ID NO:42.
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                                                                                                                                                                                                                                                                                                                          DNA detection; enteroviral detection; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; SEQ ID NO 42; 34pp; English.
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                                                                                                        AEB56803 standard; DNA; 238 BP.
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Best Local Similarity 100.
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (TSAN/) TSANG S.
(PRIC/) PRICE J A.
(HELL/) HELLYER T J.
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                                                                                                                                                                                                                                                                                                                                                                                Unidentified
                                                                                                                                                                                                                 22-SEP-2005
                                                                                                                                                              AEB56803;
                                                                         ABB55803/6

11D ABB55

AAC ABB56

AAC ABB56

ABS7

AXX ABB56

ABS7

AXX ABB56

ABS7

ABS7
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Hellyer TJ;

Price JA,

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The invention relates to an oligonucleotide (I) consisting of: (a) the target binding sequence of an oligonucleotide chosen from any one of the 10 sequence of ABS5672 to ABS5671; and (b) a sequence required for selected amplification or detection reaction. Also described: (I) a kit (KI) comprising (I), and one or more container that contains (I); and (2) detecting (MI) an enterovirus target sequence, involving: (a) amplifying the target sequence using first amplification primer having a sequence consisting essentially of target binding sequence of any one of ABS56764 to ABS5671 and optionally a sequence required for selected amplification reaction; and (b) detecting the amplified target sequence. (I), (MI) and (XI) are useful for detecting encerovirus target sequence. (I) specifically and selectively recognizes the enterovirus genome. (I) specifically and rapidly detects fewer than 500 copies of entercoviral sensitively and rapidly detects fewer than 500 copies of entercoviral present sequence represents a consensus viral 5' untranslated polynucleotide sequence given in the exemplification of the present
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 238 BP; 51 A; 55 C; 65 G; 67 T; 0 U; 0 Other;
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Disclosure; Fig 1A-D; 34pp; English.
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ilarity 100.0%;
Conservative 0
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Best Local Similarity
Matches 20; Conserv
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AEB56829 standard; DNA; 238

RESULT 46

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(first entry)

22-SEP-2005

AEB56829;

AEB56829/c ID AEB56 XX AC AEB56 XX DT 22-SI

Isang S,

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The invention relates to an oligonucleotide (1) consisting of: (a) the target binding sequence of an oligonucleotide chosen from any one of the consequence of ABS677; and (b) a sequence required for selected amplification or detection reaction. Also described: (1) a kit (K1) comprising (1), and one or more container that contains (1); and (2) detecting (M1) an enterovirus target sequence, involving: (a) amplifying the target sequence using first amplification primer having a sequence consisting essentially of target binding sequence of any one of ABB5674 to ABB56771 and optionally a sequence required for selected amplification reaction; and (b) detecting the amplified target sequence. (1), (M1) and (K1) are useful for detecting enterovirus target sequence. (1), specifically and selectively recognizes the enterovirus genome. (1) specifically and rapidly detects fewer than 500 copies of enteroviral sensitively and rapidly detects fewer than 500 copies of enteroviral segmence represents a viral 5' untranslated polymucleotide present sequence represents a viral 5' untranslated polymucleotide sequence given in the exemplification of the present invention.
                                                                                   Novel oligonucleotide comprising sequences for binding and amplifying or detecting target, useful for detecting enterovirus nucleic acids.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 20; DB 14; Length 238; 100.0%; Pred. No. 11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA detection; enteroviral detection; ds.
                                                                                                                                                                          Disclosure; SEQ ID NO 31; 34pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AEB56864 standard; DNA; 238 BP
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(PRIC/) PRICE J A.
(HELL/) HELLYER T J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US2005158710-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-JUL-2005.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AEB56864;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         rsang S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to an oligonucleotide (I) consisting of: (a) the target binding sequence of an oligonucleotide chosen from any one of the 10 sequence of ABBS6712 to ABBS671; and (b) a sequence required for selected amplification or detection reaction. Also described: (I) a kit (K1) comprising (I), and one or more container that contains (I); and (2) detecting (M1) an enterovirus target sequence, involving: (a) amplifying the target sequence using first amplification primer having a sequence consisting essentially of target binding sequence of any one of ABBS674 to ABBS6771 and optionally a sequence required for selected amplification reaction; and (b) detecting the amplified target sequences. (I), (M1) and (X1) are useful for detecting enterovirus target sequences. (I) specifically and selecting enterovirus target sequences. (I) specifically and selecting enterovirus target sequence. (I) specifically and rapidly detects fewer than 500 copies of enteroviral senome and allows detection of broad range of enterovirus serotypes. The present sequence represents a viral 5 untranslated polymucleotide sequence given in the exemplification of the present invention.
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                                                                                                                                                                                                                                                                                                                                                                             Novel oligonucleotide comprising sequences for binding and amplifying or detecting target, useful for detecting enterovirus nucleic acids.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 238 BP; 59 A; 51 C; 54 G; 74 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; SEQ ID NO 13; 34pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Scc
100.0%; Pre
ative 0; 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        105 AAGGAAACACGGACACCCAA 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hellyer TJ;
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ID AEB56792 standard; DNA; 238 BP.
                        16-JAN-2004; 2004US-00760048
                                                                             16-JAN-2004; 2004US-00760048
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1es 20; Conservative
                                                                                                                                  (TSAN/) TSANG S.
(PRIC/) PRICE J A.
(HELL/) HELLYER T J.
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(PRIC/) PRICE J A.
(HELL/) HELLYER T J.
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                                                                                                                                                                                                                                                              Price JA,
                                                                                                                                                                                                                                                                                                                      WPI; 2005-512251/52
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Query Match

Matches

ð 셤 Tsang S,

(TSAN/)

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Gaps

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target binding sequence of an oligonucleotide chosen from any one of the 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for selected amplification or detection reaction. Also described: (l) a kit (K1) comprising (l), and one or more containe that contains (l); and (2) detecting (M1) an enterovirus target sequence, involving: (a) amplifying the target sequence using first amplification primer having a sequence consisting essentially of target binding sequence of any one of AEB56764 to AEB56771 and optionally a sequence required for selected amplification reaction; and (b) detecting the amplified target sequence. (l), (M1) and (K1) are useful for detecting enterovirus target sequences. (l), (M1) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to an oligonucleotide (I) consisting of: (a) the target binding sequence of an oligonucleotide chosen from any one of the 10 sequence of ABB56762 to ABB56712. As sequence required for selected amplification or detection reaction. Also described: (1) a kit (K1) comprising (I), and one or more contains (I); and (2) detecting (M1) an enterovirus target sequence, involving: (a) amplifying the target sequence using first amplification primer having a sequence to consisting essentially of target binding sequence of any one of ABB56774 to ABB56771 and optionally a sequence required for selected amplification reaction; and (b) detecting the amplified target sequence. (I), (M1) and
                                                                                                                                                                                                      specifically and selectively recognizes the enterovirus general sensitively and rapidly detects fewer than 500 copies of enteroviral generatively and rapidly detects fewer than 500 copies of enteroviral senseme and allows detection of broad range of enterovirus serotypes. The present sequence represents a viral 5' untranslated polynucleotide sequence given in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              oligonucleotide comprising sequences for binding and amplifying or
                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 20; DB 14; Length 238; 100.0%; Pred. No. 11; 0; Indels 0
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                                                                                                                                                                                                                                                                                                                                  Sequence 238 BP; 50 A; 55 C; 64 G; 69 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA detection; enteroviral detection; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              161 AAGGAAACACGGACACCCAA 142
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ID AEB56877 standard; DNA; 238
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                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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PRICE J A.
HELLYER T J.
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Best Local Similarity
Matches 20; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               S, Price JA,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human poliovirus 2.
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(PRIC/) I
(HELL/) F
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 50
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           d range of enterovirus serotypes. The 5' untranslated polynucleotide
                specifically and selectively recognizes the enterovirus genome. (I) sensitively and rapidly detects fewer than 500 copies of enteroviral genome and allows detection of broad range of enterovirus serotypes. The present sequence represents a viral 5' untranslated polynucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel oligonucleotide comprising sequences for binding and amplifying or detecting target, useful for detecting enterovirus nucleic acids.
                                                                                                                                                                                                                         Gaps
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useful for detecting enterovirus target sequences. (I)
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                                                                                                 sequence given in the exemplification of the present invention
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                                                                                                                                                                             100.0%; Score 20; DB 14; Length 238; 100.0%; Pred. No. 11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Viral 5' untranslated polynucleotide sequence SEQ ID NO:33.
                                                                                                                                                                                                                         Indels
                                                                                                                                          Sequence 238 BP; 56 A; 56 C; 63 G; 63 T; 0 U; 0 Other;
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                                                                                                                                                                                                                         0; Mismatches
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                                                                                                                                                                                                                                                                                       161 AAGGAAACACGGACACCCAA 142
                                                                                                                                                                                                                                                                1 AAGGAAACACGGACACCCAA 20
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                                                                                                                                                                                                                                                                                                                                                                                                     AEB56794 standard; DNA; 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                    Local Similarity 100.
nes 20; Conservative
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(PRIC/) PRICE J A.
(HELL/) HELLYER T J.
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Matches
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Viral 5' untranslated polynucleotide sequence SEQ ID NO:15.

22-SEP-2005 (first entry)

AEB56776;

AEB56776 standard; DNA; 238 BP.

**AEB56776/** 

DNA detection; enteroviral detection; ds

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            specifically and selectively recognizes the enterovirus genome. (I) sensitively and rapidly detects fewer than 500 copies of enteroviral genome and allows detection of broad range of enterovirus serotypes. The present sequence represents a viral 5' untranslated polymuclectide sequence given in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel oligonucleotide comprising sequences for binding and amplifying or detecting target, useful for detecting enterovirus nucleic acids.
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                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 20; DB 14; Length 238; 100.0%; Pred. No. 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 for detecting enterovirus target sequences.
                                                                                                                                                                                                                                                                            Human echovirus 6 5' untranslated polynucleotide sequence.
                   Indels
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 red. No. 11;
Mismatches
                                                                                                                                                                                                                                                                                                              DNA detection; enteroviral detection; ds.
 Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Fig 1A-D; 34pp; English.
                                                20
                                                                                  105 AAGGAAACACGGACACCCAA 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hellyer TJ;
ilarity 100.0%; P
Conservative 0;
                                                                                                                                                                         AEB56859 standard; DNA; 238 BP
                                                    1 AAGGAAACACGGACACCCAA
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                                                                                                                                                                                                                                          (first entry)
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(PRIC/) PRICE J A.
(HELL/) HELLYER T J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2005-512251/52.
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                Human echovirus 6.
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                  20;
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                  Matches
                                                                                                                                        RESULT 52
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Novel oligonucleotide comprising sequences for binding and amplifying or detecting target, useful for detecting enterovirus nucleic acids.

Tsang S, Price JA, Hellyer TJ,

WPI; 2005-512251/52

(TSAN/) TSANG S. (PRIC/) PRICE J A. (HELL/) HELLYER T J.

16-JAN-2004; 2004US-00760048 16-JAN-2004; 2004US-00760048

US2005158710-A1. Unidentified

21-JUL-2005.

Disclosure; SEQ ID NO 15; 34pp; English.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   genome and allows detection of broad range of enterovirus serotypes. The present sequence represents a viral 5' untranslated polynucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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Pred. No. 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Viral 5' untranslated polynucleotide sequence SEQ ID NO:48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              105 AAGGAAACACGCACACCCAA
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les 20; Conserv
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0; Gaps

0; Indels

0; Mismatches

1 Similarity 100.0%; 20; Conservative 0

Local Similarity

Best Loca Matches

161 AAGGAAACACGGACACCCAA 142

1 AAGGAAACACGGACACCCAA 20

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(TSAN/) TSANG S.
(PRIC/) PRICE J A.
(HELL/) HELLYER T J.
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(PRIC/) PRICE J A.
(HELL/) HELLYER T J.
                                                                            WPI; 2005-512251/52
GENBANK; U05876.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-JUL-2005.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AEB56808;
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                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 56
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                                                                                                                                                                                                                                                                       The invention relates to an oligonucleotide (I) consisting of: (a) the target binding sequence of an oligonucleotide chosen from any one of the 10 sequence of AEBS6771 and (b) a sequence required for selected amplification or detection reaction. Also described: (I) a kit (KI) comprising (I), and one or more container that contains (I); and (2) detecting (MI) an enterovirus target sequence, involving: (a) amplifying the target sequence using first amplification primer having a sequence consisting essentially of target binding sequence of any one of AEBS6764 to AEBS671 and optionally a sequence required for selected amplification reaction; and (b) detecting the amplified target sequence. (I) (MI) and (KI) are useful for detecting enterovirus target sequences. (I) sensitively and selectively recognizes the enterovirus genome. (I) sensitively and rapidly detects fewer than 500 copies of enteroviral genome and allows detection of broad range of enteroviral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                  Novel oligonucleotide comprising sequences for binding and amplifying or detecting target, useful for detecting enterovirus nucleic acids.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                         5' untranslated polynucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human coxsackievirus A16 5' untranslated polynucleotide sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  sequence given in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 20; DB 14; Length 238; 100.0%; Pred. No. 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 238 BP; 53 A; 54 C; 55 G; 76 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                    Disclosure, SEQ ID NO 48; 34pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA detection; enteroviral detection;
                                                                                                                                                                                                                                                                                                                                                                                                                                         viral
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                                                                                                                                                                      Hellyer TJ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                         sequence represents a
                                                                              L6-JAN-2004; 2004US-00760048
                                                                                                  16-JAN-2004; 2004US-00760048
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                                                                                                                        (TSAN/) TSANG S.
(PRIC/) PRICE J A.
(HELL/) HELLYER T J.
                                                                                                                                                                      fsang S, Price JA,
                                                                                                                                                                                             WPI; 2005-512251/52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 20; Conserv
                                US2005158710-A1.
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         Unidentified.
                                                      21-JUL-2005.
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The invention relates to an oligonucleotide (I) consisting of: (a) the target binding sequence of an oligonucleotide chosen from any one of the consisting sequence of ABBS6771; and (b) a sequence required for selected amplification or detection reaction. Also described: (I) a kit (KI) comprising (I), and one or more container that contains (I); and (2) detecting (MI) an enterovirus target sequence, involving: (a) amplifying the target sequence using first amplification primer having a sequence consisting essentially of target binding sequence of any one of ABBS674 to ABBS6771 and optionally a sequence required for selected amplification reaction; and (b) detecting the amplified target sequence. (I), (MI) and (KI) are useful for detecting enterovirus target sequence. (I) specifically and selectively recognizes the enterovirus genome. (I) specifically and rapidly detects fewer than 500 copies of enteroviral sensitively and rapidly detects fewer than 500 copies of enteroviral spenome and allows detection of broad range of enterovirus serotypes. The present sequence represents a viral 5' untranslated polymucleotide sequence given in the exemplification of the present invention.
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                                                                                                                                                                                                                 Novel oligonucleotide comprising sequences for binding and amplifying or detecting target, useful for detecting enterovirus nucleic acids.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 238 BP; 51 A; 55 C; 64 G; 68 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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                                                                                                                                                                                                                                                                                                                                                  Disclosure, Fig 1A-D; 34pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            161 AAGGAAACACGGACACCCAA 142
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Isang S, Price JA, Hellyer TJ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AEB56808 standard; DNA; 238 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.08;
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les 20; Conservative C
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target binding sequence of an oligonucleotide chosen from any one of the losequence of AEB5672 to AEB5771; and (b) a sequence required for selected amplification or detection reaction. Also described: (1) and kit (X1) comprising (I), and one or more container that contains (1); and (2) detecting (M1) an enterovirus target sequence, involving: (a) amplifying the target sequence using first amplification primer having a sequence consisting essentially of target binding sequence of any one of AEB5674 to AEB56771 and optionally a sequence required for selected amplification reaction; and (b) detecting the amplified target sequence. (1), (M1) and (X1) are useful for detecting enterovirus target sequences. (1) specifically and selectively recognizes the enterovirus genome. (1) sensitively and rapidity detects fewer than 500 copies of enteroviral senome and allows detection of broad range of enterovirus serotypes. The present sequence represents a viral 5' untranslated polymucleotide sequence given in the exemplification of the present invention.
Novel oligonucleotide comprising sequences for binding and amplifying or detecting target, useful for detecting enterovirus nucleic acids.
                                                                                                                                                        The invention relates to an oligonucleotide (I) consisting of: (a) the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 238 BP; 53 A; 54 C; 55 G; 76 T; 0 U; 0 Other;
                                                                                       Disclosure; SEQ ID NO 47; 34pp; English
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86 1 AAGGAAACACGGACACCCAA 20 105 AAGGAAACACGGACACCCAA ઠે 셤

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Gaps ö

Indels

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Local Similarity 100.0%; Pred. No. 11; nes 20; Conservative 0; Mismatches

100.08;

Query Match

Best Loc Matches

Score 20; DB 14; Length 238; Pred. No. 11;

AEB56882 standard; DNA; 238 BP RESULT 57 AEB56882/

AEB56882; 

(first entry) 22-SEP-2005 Human poliovirus 3 5' untranslated polynucleotide sequence.

DNA detection; enteroviral detection; ds

Human poliovirus 3

US2005158710-A1

21-JUL-2005.

16-JAN-2004; 2004US-00760048.

16-JAN-2004; 2004US-00760048

(TSAN/) TSANG S. (PRIC/) PRICE J A. (HELL/) HELLYER T J.

Hellyer TJ Price JA, Tsang S,

2005-512251/52 GENBANK; X04468 Novel oligonucleotide comprising sequences for binding and amplifying or detecting target, useful for detecting enterovirus nucleic acids. Disclosure; Fig 1A-D; 34pp; English.

The invention relates to an oligonuclectide (I) consisting of: (a) the target binding sequence of an oligonuclectide chosen from any one of the 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for selected amplification or detection reaction. Also described: (1) a kit

The invention relates to an oligonucleotide (1) consisting of: (a) the target binding sequence of an oligonucleotide chosen from any one of the 10 sequence of ABB56762 to ABB5671; and (b) a sequence required for selected amplification or detection reaction. Also described: (1) a kit (XI) comprising (1), and one or more container that contains (1); and (2) detecting (MI) an enterovirus target sequence, involving: (a) amplifying the target sequence using first amplification primer having a sequence consisting essentially of target binding sequence of any one of ABB56764 to ABB5671 and optionally a sequence required for selected amplification reaction; and (b) detecting the amplified target sequence. (1), (MI) and (XI) are useful for detecting enterovirus target sequences. (1) specifically and selectively recognizes the enterovirus genome. (1) sensitively and rapidly detects fewer than 500 copies of enteroviral genome and allows detection of broad range of enterovirus serotypes. The ö to ABB56771 and optionally a sequence required for selected amplification reaction, and (b) detecting the amplified target sequence. (I), (M1) and (K1) are useful for detecting enterovirus target sequences. (I) specifically and selectively recognizes the enterovirus genome. (I) sensitively and rapidly detects fewer than 500 copies of enteroviral genome and allows detection of broad range of enterovirus serotypes. The present sequence represents a viral 5' untranslated polynucleotide detecting (MI) an enterovirus target sequence, involving: (a) amplifying the target sequence using first amplification primer having a sequence consisting essentially of target binding sequence of any one of AEB56764 Novel oligonucleotide comprising sequences for binding and amplifying or detecting target, useful for detecting enterovirus nucleic acids. comprising (I), and one or more container that contains (I); and Gaps . 0 sequence given in the exemplification of the present invention Viral 5' untranslated polynucleotide sequence SEQ ID NO:43. 0; Indels Score 20; DB 14; Length Pred. No. 11; Sequence 238 BP; 57 A; 54 C; 62 G; 65 T; 0 U; 0 Other; Mismatches DNA detection; enteroviral detection; ds. Disclosure; SEQ ID NO 43; 34pp; English. 161 AAGGAAACACGGACACCCAA 142 20 0 Tsang S, Price JA, Hellyer TJ; 1 AAGGAAACACGGACACCCAA 100.0%; 16-JAN-2004; 2004US-00760048. 16-JAN-2004; 2004US-00760048 AEB56804/c ID AEB56804 standard; DNA; 238 Query Match Best Local Similarity 100.' Matches 20, Conservative (TSAN/) TSANG S. (PRIC/) PRICE J A. (HELL/) HELLYER T J. WPI; 2005-512251/52. US2005158710-A1. 22-SEP-2005 Unidentified 21-JUL-2005. AEB56804; RESULT 58 ઠે g 

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WPI; 1994-101191/12.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 polycistronic vecto
of A- and B-chains.
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ses 20; Conserv
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25-MAR-2003
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AAQ58715/c
                                                                                                                                                                                                                                                                                                                               Key
5'UTR
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Matches
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                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chimeric recombinant poliovirus useful for treating malignant tumors comprises internal ribosomal entry site derived from picornaviruses.
                                                                                                                                                                                        Internal ribosomal entry site; IRES; picornavirus; tumour; cancer; glioblastoma multiforme; medulloblastoma; mammary carcinoma; prostate carcinoma; colorectal carcinoma; hepatocellular carcinoma;
                                                                                                                                                                                                               bronchial carcinoma; epidermoid carcinoma; cytostatic; therapy; ss.
present sequence represents a viral 5' untranslated polynucleotide sequence given in the exemplification of the present invention.
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                                     DB 14; Length 238;
                                                     Indels
                      Sequence 238 BP; 48 A; 52 C; 60 G; 78 T; 0 U; 0 Other;
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                                     Score 20; DB
Pred. No. 11;
                                                    0; Mismatches
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/*tag= c
/note= "domain III"
132. 338
                                                                                                                                                                          Poliovirus IRES domain II-VI region.
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/*tag= g
/note= "domain V"
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                                                                                                                                                                                                                                                             a
"domain II"
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note= "domain IV"
                                                                   1 AAGGAAACACGGACACCCAA 20
                                                                                 86
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                                                                                                                487/c
AAZ58487 standard; RNA; 514 BP.
                                                                            105 AAGGAAACACGGACACCCAA
                                     100.0%;
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/*tag= b
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                                             Best Local Similarity 100.
Matches 20; Conservative
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23-MAY-2000
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                                     Query Match
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This sequence represents domains II-VI of the internal ribosomal entry site (IRES) of wild-type poliovirus type 1 Mahoney. The invention provides non-pathogenic, oncolytic, recombinant polioviruses (I) in which the IRES of the wild-type poliovirus is exchanged with the IRES of another picornavirus, such as human rhinovirus type 2, and optionally the Pl, P3 or 3 untranslated region is exchanged with that of Sabin poliovirus. (I) may contain a composite IRES encompassing IRES domains from both wild-type poliovirus and from another virus. (I) are useful for treating malignant tumors such as glioblastoma multiforme, medulloblastoma, mammary, prostate, colorectal, hepatocellular, bronchial and epidermoid carcinomas (claimed). (Updated on 15-SEP-2003 to
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Heterodimer platelet-derived-growth factor (PDGF) prodn. - using a polycistronic vector system in mammalian host cells for equimolar prodn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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/note= "wild-type C has been substituted by G"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 20; DB 3; Length 514; 100.0%; Pred. No. 11;
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PDGF-A chain; PDGF-B chain;
                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 514 BP; 122 A; 134 C; 132 G; 0 T; 126 U; 0 Other;
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H;
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(GBFB ) GBF GES BIOTECH FORSCHUNG GMBH.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     bicistronic vector system; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 92DE-04228457
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(revised)
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Wirth M, Hauser
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expression unit in which a sequence responsible for internal translation start (designated "IRES") is located between cistrons coding for the PDGF-B and PDGF-A chains. The preferred IRES sequence for inclusion in the bicistronic construct is the 5. UTR from Poliovirus type 1 Mahoney strain of sequence AAQS8715. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Heterodimeric proteins can be recombinantly produced using a multicistronic (esp. bicistronic) expression unit in which a sequence responsible for internal translation start (designated "IRRS") is located between cistrons coding for the different subunits. The preferred IRRS sequence is the 5. UTR from Poliovirus type 1 Mahoney strain of sequence AAGS8726. (Updated on 25-MAR-2003 to correct PN field.) (Updated on 27-ANG-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                - for producing equimolar amts. of
                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                              internal translation start; initiation; 5'-untranslated region; ss
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                                                                                                                                                                                                                                                                                                                                   Multicistronic expression unit; recombinant protein production
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/note= "wild-type C has been substituted by
                                                                                                  Score 20; DB 2; Length 628;
Pred. No. 11;
                                                                             Sequence 628 BP; 143 A; 165 C; 162 G; 158 T; 0 U; 0 Other;
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ive 0; Mismatches
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polypeptide(s) in mammalian cells as hosts.
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Mielke H;
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(GBFB ) GBF GES BIOTECH FORSCHUNG GMBH
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Doerschner A, Meyer-Ingold W,
                                                                                                                                                                                                                      AAQ58726 standard; DNA; 628 BP
                                                                                                  100.08;
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                                                                                             Query Match
Best Local Similarity 100.(
Matches 20, Conservative
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5'UTR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention relates to a new bicistronic retroviral vector. These are used for (over) expression of proteins, suppressing expression of fnon-) viral RNA and/or proteins by the antisense technique, e.g. to suppress a dominant-negative phenotype, also infectious viral particles that contain the vectors, in gene therapy, particularly for control of guest versus host disease, especially where haematopoietic cells are transduced with the vector or where T cells are transduced, for adoptive immunotherapy, but also for treating severe combined immune deficiency syndrome and for expression cloning of genes. The present sequence is a vector sequence fragment shown in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bicistronic retroviral vector, useful in gene therapy, particularly of graft versus host disease, contains components of both murine embryonic stem cell and myeloproliferative sarcoma viruses.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 immunosuppressive; gene therapy; vector; bicistronic retroviral vector; severe combined immune deficiency syndrome; protein expression;
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  Length 628;
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100.0%; Score 20; DB 2;
100.0%; Pred. No. 11;
ive 0; Mismatches 0.
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                                                                                                                                                               565 AAGGAAACACGCACACCCAA 546
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unidentified.
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                                                                                                                                                                                                                                                                                                                                                                                                       26-AUG-2004
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                                                                                                                                                                                                                                                                                                                                                    ADP74707;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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                                 Local
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24-MAR-2005 (first entry)
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Best Local Similarity 100.
Matches 20; Conservative
                                                                                                                                             Hsu I, Wu I, Lee J;
                                                                                                                                                                       WPI; 2005-371616/38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human poliovirus 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (HERO/) HEROLD J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US2005002953-A1.
                                                                                             WU T.
LEB J.
                                                                              HSU T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   06-JAN-2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADW37919;
                                                                                                            (LEEJ/)
                                                                              (HSUT/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Herold
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADW37919/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 65
   %XCCCCCCCCCXXX11111XXXX1XAXXXXXXXX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention provides a new isolated or recombinant virus called Prima7 (which belong to enteroviral species) comprising a nucleic acid sequence or its functional part, derivative or analogue of the said virus. The invention is useful for detecting and/or identifying a Prima7 enterovirus in a sample and for diagnosing an enteroviral genus related disease. The vaccine or medicament prepared from the Prima7 virus is useful for preventing and/or treating a Prima7-related disease. The invention is also useful in gene therapy. The present sequence is Prima7 virus 5. UTR region DNA.
                                                               Enteroviral genus related disease; Prima7-related disease; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                       capable of specifically binding the virus in a sample, and as a vaccine or medicament for treating or preventing Prima7-related disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    vector; neurological disease; ds; gene therapy;
internal ribosome entry site; cystic fibrosis; cns-gen.;
respiratory-gen.; factor VIII deficiancy; hemostatic; genetic disorder;
factor IX deficiency; Duchenne dystrophy; muscular-gen.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Enterovirus 71 5' untranslated region internal ribosome entry site DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                     New isolated or recombinant virus, useful for detecting a molecule
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Becker's disease, cancer, cytostatic, neoplasm, acquired immune deficiency syndrome, anti-hiv; infectious disease,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 20; DB 13; Length 682; 100.0%; Pred. No. 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 682 BP; 176 A; 157 C; 159 G; 190 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. 11;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human enterovirus 71; strain TW/2086/98
                                                                                                                                                                                                                                                                                                       Mang R;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Example; SEQ ID NO 39; 51pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               504 AAGGAAACACGGACACCCAA 485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 AAGGAAACACGGACACCCAA 20
                             Prima7 virus 5' UTR region DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BP
                                                                                                                                                                                                                                                                                                       Van Den Broek PJM,
                                                                                                                                                                                                          21-MAY-2003; 2003EP-00076529
                                                                                                                                                                                                                                        21-MAY-2003; 2003EP-00076529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AEA00424 standard; DNA; 709
(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 100.
Les 20; Conservative
                                                                                                                                                                                                                                                                        (PRIM-) PRIMAGEN HOLDING
                                                                                                                                                                                                                                                                                                                                       WPI; 2004-823915/82
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                                                                                                             Prima7 virus.
                                                                                                                                             EP1479761-A1
10-FEB-2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28-JUL-2005
                                                                                                                                                                         24-NOV-2004.
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                                                                                                                                                                                                                                                                                                       Maas HCGI,
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Matches

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The present invention relates to a nucleic acid vector for the expression of at least two cistrons. The vector comprises a promoter operably linked to a nucleotide sequence comprising at least two cistrons and at least cone nucleotide sequence comprising at least two cistrons and at least cone nucleotide sequence comprising an internal ribosome entry site (IRES) selected from Human enterovirus 71 (EV71), Hepatitis C virus (HCV), or Encephalomyocarditis virus (EMCV). The invention also provides a method to screening of anti-viral compounds using the IRES. The invention is useful for the genetic treatment of patients with cystic fibrosis, hemophilia A or B, Duchenne or Becker type myopathy, cancer, AIDS and other bacterial or infectious diseases due to a pathogenic organism and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New nucleic acid vector for the expression of at least two cistrons comprising a nucleotide sequence comprising an internal ribosome entry site (IRES) e.g. enterovirus 71 (EV71), useful for treating a patient having e.g. AIDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SARS-coronavirus virus-like particle; SARS-COV-VLP; cellular immune response; humozal immune response; vaccine; immunogenicity; cytotoxic T-lymphocyte; internal ribosomal entry site;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Poliovirus type 1 strain mahoney internal ribosomal entry site cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              in gene therapy. The present sequence is the enterovirus 71 Sountranslated region (UTR) IRES DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 20; DB 14; Length 709;
Pred. No. 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 709 BP; 165 A; 185 C; 172 G; 187 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 2; SEQ ID NO 1; 23pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            534 AAGGAAACACGGACACCCAA 515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 AAGGAAACACGGACACCCAA 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        06-MAY-2003; 2003US-0468703P
08-JUL-2003; 2003US-00614283.
                                                                             09-JUL-2002; 2002US-0394269P.
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The present invention provides a system for making SARS-coronavirus virus -like particles (SARS-COV-VLPs) comprising one or more recombinant vectors that expresses the SARS-COV E (small membrane)-protein, SARS-COV M (membrane)-protein and SARS-COV E (spike)-protein. The invention is useful for inducing cellular and/or humoral immune response. The invention is also useful to reduce the symptoms of SARS-COV infections and in vaccine preparations. The present sequence is Poliovirus type I strain mahoney internal ribosomal entry site (IRES) conva. This convacence is used in the preparation of plasmid for the expression of SARS
                                                   New system comprising one or more recombinant vectors that expresses the SARS-CoV E-protein, SARS-CoV M-protein, and SARS-CoV S-protein, useful for making SARS-coronavirus virus-like particles.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 743 BP; 175 A; 185 C; 181 G; 202 T; 0 U; 0 Other;
                                                                                                                                                      Example 2; SEQ ID NO 21; 111pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                               CoV M, E and S proteins
WPI; 2005-065191/07
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14; Length 743; B Score 20; DB Pred. No. 11; 100.0%; Query Match Best Local Similarity Matches 20; Conserv

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Gaps

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Indela

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Mismatches

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Conservative

ò 셤 RESULT

197/c ACC48197 standard; cDNA; 745 ACC48197; ACC48197, 

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(first entry) 11-AUG-2003

Poliovirus internal ribosome entry site-containing mRNA 5' UTR.

Internal ribosome entry site; IRES; translation; ss

Poliovirus

Location/Qualifiers /\*tag= Key 5'UTR

WO2003020927-A2.

13-MAR-2003

03-SEP-2002; 2002WO-EP009843.

04-SEP-2001; 2001DE-01043237

(ICON-) ICON GENETICS INC.

Gleba ď Ivanov Ivanov P, Skulachev M, Dorokhov Y, WPI; 2003-313089/30. Atabekov J,

Creating nucleic acid sequence for carrying out translation by internal ribosome entry site element and expressing nucleotide sequence of interest in eukaryotic cell, by creating a nucleic acid having adeninerich block.

Disclosure; Fig 3; 48pp; English.

The present sequence is that of a known internal ribosome entry site (IRES) element contained in the 5' untranslated region of poliovirus mRNA. The invention provides a method of creating an artificial IRES element having an adenine-rich (40-100 mol\*) nucleic acid block of at

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The invention relates to the production of platelet-derived growth factor (PDGF) comprising a transgenic mammal whose somatic and germ cells comprising a transgenic mammal whose somatic and germ cells comprise a nucleic acid sequence (I) encoding PDGF, operably linked to a promoter directing expression into mammalian gland epithelial cells, and obtaining the milk from the transgenic mammal where at least 30% of the PDGF in the milk is as a dimer. Also described is a method of producing a transgenic mammal cappable of expressing an active PDGF molecule in milk. Pharmaceutical compositions can be obtained from this milk and can be transgenic pode to enhance the wound healing process, in particular diabetic foot ulcers, decubitus ulcers and venous stasis ulcers.

Transgenic PDGF (II) can also be used in the treatment of periodontal regeneration, stimulation of bone formation, ophthalmic diseases or healing of prosthetic vascular grafts. (II) can also be used for nonmedical applications, e.g., as a supplement for cell culture media or as a component of diagnostic kits. The present sequence represents the platelet-derived growth factor expression cassette insert used in pBC701 vector of the invention
                                                                                                                                                                                                                                                         ô
least 25 nucleotides and capable of causing cap-independent translation of a downstream nucleotide sequence of interest in eukaryotic cells, such as plant, animal or yeast cells (claimed). A method of identifying nucleic acid elements having IRES activity involving genome database searches is also provided. The methods allow the creation or identification of IRES elements that are universal with cross-kingdom and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Platelet-derived growth factor expression cassette insert used in pBC701.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Platelet-derived growth factor; PDGF; transgenic; milk; gene; devoud healing; diabetic foot ulcer; decubitus ulcer; ophthalmic disease; venous stasis ulcer; periodontal regeneration; bone formation; prosthetic vascular graft; pBC701; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Production of platelet derived growth factor (PDGF) comprises expression in the milk of a non-human transgenic animal.
                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                              Score 20; DB 8; Length 745;
Pred. No. 11;
                                                                                                                                                                       G; 187 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                         Indels
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                                                                                                                                                                     Sequence 745 BP; 163 A; 202 C; 193
                                                                                                                                                                                             100.0%; Sco
100.0%; Pre
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ID ABK14791 standard; DNA; 2076 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 1; Fig 1; 59pp; English.
                                                                                                                                                                                                                                                                                              1 AAGGAAACACGGACACCCAA
                                                                                                                                                                                                                                                                                                                                    568 AAGGAAACACGGACACCCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19-JUN-2001; 2001WO-US041044.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19-JUN-2000; 2000US-0212406P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           08-MAY-2002 (first entry)
                                                                                                                                                                                                                               Best Local Similarity 100.
Matches 20; Conservative
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                                                                                                                            tailor-made activity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABK14791;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This invention describes a novel nucleic acid (I) comprising elements that encode a signal peptide (SP) that provides transfer of expressed polypeptide into the endoplasmic reticulum, a fragment (FI) of HIV gp41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New nucleic acid encoding membrane-anchored gp41 fusion protein, useful for gene therapy of human immunodeficiency virus (HIV) infection,
                                                             Gaps
                                                                                                                                                                                                                                                                                                                                             Transmembrane anchor; gene therapy; endoplasmic reticulum; gp41; antiviral; HIV replication inhibitor; T lymphocyte; viral infection; hematopoietic stem cell; ds.
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                             Length 2076;
Sequence 2076 BP; 441 A; 612 C; 607 G; 416 T; 0 U; 0 Other;
                                                             Indels
                                                             ö
                             100.0%; Score 20; DB 6; 100.0%; Pred. No. 12;
                                                            Mismatches
                                                                                                                                                                                                                                                                                                               Vector containing HIV gp41 DNA SEQ ID 1.
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1438. .1773
/*tag= a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        prevents entry of virus into cells.
                                                                                                            1317 AAGGAAACACGGACACCCAA 1298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 11; Page 28-30; 39pp; German
                                                                                            1 AAGGAAACACGGACACCCAA 20
                                                             ;
0
                                                                                                                                                                                                       AAH20890 standard; DNA; 4148 BP.
                                                                                                                                                                                                                                                                                                                                                                                                            Human immunodeficiency virus 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99DE-01057838
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24-NOV-2000; 2000WO-EP011733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (PETT-) PETTE INST HEINRICH
                                                                                                                                                                                                                                                                    (revised)
(first entry)
                                                             Conservative
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                                          Similarity
20; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200137881-A2.
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                                                                                                                                                                                                                                                                  11-SEP-2003
24-AUG-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Von Laer M;
                                                                                                                                                                                                                                     AAH20890;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                              Query Match
                                               Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             field)
                                                                                                                                                                         RESULT 68
AAH20890/c
                                                               Matches
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Viral vector that expresses single-chain interleukin-12 and costimulator, useful for treatment of tumors, viral infections, e.g. human immunodeficiency virus, and prion diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention relates to a viral vector that includes a nucleic acid encoding a single-chain interleukin-12 (In-12) and a co-stimulatory protein. Viral vectors and virus particles derived from them are useful for treatment of tumours, infectious diseases (e.g. HIV, hepatitis A, B or C, cytomegalovirus or human papilloma virus), or prion diseases. The present sequence is a tricistronic expression cassette used in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      immunosuppressive; gene therapy; vector; bicistronic retroviral vector; severe combined immune deficiency syndrome; protein expression;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                        Tricistronic expression cassette containing murine coding sequences.
                                                                                                                                                                                                  cytostatic; virucide; anti-HIV; hepatotropic; neuroprotective; immunostimulant; expression cassette; viral vector; interleukin-12; co-stimulatory protein; cancer; infection; ds; gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 5252 BP; 1347 A; 1386 C; 1300 G; 1219 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel bicistronic retroviral vector related vector #1.
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 2359 AAGGAAACACGGACACCCAA 2340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAGGAAACACGGACACCCAA 2834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Fig 18; 129pp; German
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 AAGGAAACACGGACACCCAA 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADP74699 standard; DNA; 7185 BP.
                                                                             BP.
                                                                                                                                                                                                                                                                                                                                                                                                                        11-OCT-2002; 2002DE-01048141.
                                                                             ADO07652 standard; DNA; 5252
                                                                                                                                                                                                                                                                                                                                                                                           10-OCT-2003; 2003WO-EP011252.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Schnieders F;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity 100.
hes 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2004-357221/33.
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                                                                                                                                                                                                                                                                                                                              WO2004035799-A2
                                                                                                                                                                                                                                                                                               Unidentified
                                                                                                                                          15-JUL-2004
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Synthetic.
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                                                                                                           AD007652
                                              RESULT 69
ADO07652/c
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Gaps

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0; Indels

Mismatches

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Conservative

Local Similarity nes 20; Conserv

Matches

1 AAGGAAACACGGACACCCAA 20

100.0%; Score 20; DB 5; Length 4148; 100.0%; Pred. No. 13;

misc RNA

CDS

LIR

5' UTR

Key LTR

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Bicistronic retroviral vector, useful in gene therapy, particularly of graft versus host disease, contains components of both murine embryonic stem cell and myeloproliferative sarcoma viruses.
                              immunosuppressive; gene therapy; vector; bicistronic retroviral vector; severe combined immune deficiency syndrome; protein expression;
Novel bicistronic retroviral vector related vector #3.
                                                                                                                                                                                                                                                                                 product= "HSV-TK splice variant"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Heberlein C, Gindullis F, Hannemann J,
                                                                                                                                                                                 /*tag= a
/standard_name= "5/-LTR"
995. .1487
                                                                                                                                                                                                                                                                                                                                                                                                                                     /standard_name= "3'-LTR"
                                                                                                                                                                                                                                                                                                                                 standard name= "IRES"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (CELL-) CELLTECH GMBH BIOTECHNOLOGIE.
                                                                                                                                                  Location/Qualifiers
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product= "neo'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    09-DEC-2002; 2002EP-00027555.
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                                                                                                                                                                                                                                   b. 2615
                                                                                                                                                                                                                                                                                                  626. .3250
                                                                                                                                                                                                                                                                                                                                                                                                    1345. .4931
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                                                                                                                                                                   . 994
                                                                                                                                                                                                                                                                   *tag=
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                                                                   antisense; ds; gene.
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                                                                                                Synthetic.
Unidentified.
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                                                                                                                                                                                                                                                                                                misc_RNA
                                                                                                                                                                                                                 5'UTR
                                                                                                                                                Key
LTR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bicistronic retroviral vector, useful in gene therapy, particularly of graft versus host disease, contains components of both murine embryonic stem cell and myeloproliferative sarcoma viruses.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Heberlein C, Gindullis F, Hannemann J,
                                                                                                                                                                                                                                                                                                                                                 'standard_name= "3'-LTR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (CELL-) CELLTECH GMBH BIOTECHNOLOGIE.
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                                                               ocation/Qualifiers
                                                                                                                                                            .488. .2615
*tag= c
product= "HSV-TK"
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ADP74701/c
ID ADP74701 standard; DNA; 7185 BP.
XX
AC ADP74701;
XX
DT 26-AUG-2004 (first entry)
XX
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standard name=
                                                                                                                                                                                                                                               standard name=
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0
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/*tag= f
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                                                                                                                                                                                                            2626. 3250
/*tag= d
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/*tag= e
                                                                                                                             5. .1487
                                                                                . .994
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1es 20; Conservative
                                                                                                                                                  tag=
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            Synthetic.
Unidentified.
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Strathmann G;

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The present invention relates to a new bicistronic retroviral vector. These are used for (over) expression of proteins, suppressing expression of finon-) viral RNA and/or proteins by the antisense technique, e.g. to suppress a dominant-negative phenotype, also infectious viral particles that contain the vectors, in gene therapy, particularly for control of guest versus host disease, especially where haematopoietic cells are transduced with the vector or where T cells are transduced with the vector or where T cells are transduced, for adoptive immunotherapy, but also for treating severe combined immune deficiency syndrome and for expression cloning of genes. The present sequence is a vector sequence shown in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 7185 BP; 1581 A; 2013 C; 1942 G; 1649 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADP74714 standard; DNA; 7235 BP.
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ID ADP747
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Query Match

Best Loca Matches

셤 8

immunosuppressive; gene therapy; vector; bicistronic retroviral vector;

Novel bicistronic retroviral vector related vector #7.

(first entry)

26-AUG-2004 ADP74715;

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ADP74715 standard; DNA; 7235

RESULT 73

ADP74715/

severe combined immune deficiency syndrome; protein expression;

antisense; ds; gene.

Synthetic. Unidentified.

Location/Qualifiers

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The present invention relates to a new bicistronic retroviral vector. These are used for (over) expression of proteins, suppressing expression of fnon-) viral RNA and/or proteins by the antisense technique, e.g. to suppress a dominant-negative phenotype, also infectious viral particles that contain the vectors, in gene therapy, particularly for control of guest versus host disease, especially where haematopoietic cells are transduced with the vector or where T cells are transduced, for adoptive immunotherapy, but also for treating severe combined immune deficiency syndrome and for expression cloning of genes. The present sequence is a vector sequence shown in the exemplification of the invention.
                                                                                                                                                     immunosuppressive; gene therapy; vector; bicistronic retroviral vector; severe combined immune deficiency syndrome; protein expression;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      particularly of
murine embryonic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 7235 BP; 1594 A; 2025 C; 1950 G; 1666 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bicistronic retroviral vector, useful in gene therapy, graft versus host disease, contains components of both stem cell and myeloproliferative sarcoma viruses.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Strathmann G;
                                                                                                      Novel bicistronic retroviral vector related vector #6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "HSV-TK splice variant"
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3348. .4148
/*tag= e
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                                                                                                                                                                                                                                                                                                                                              ocation/Qualifiers
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/standard_n
995. .1537
/*tag= b
                                                    (first entry)
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                                                                                                                                                                                                               antisense; ds; gene.
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                                                                                                                                                                                                                                                                 Synthetic.
Unidentified
                                                    26-AUG-2004
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ADP74714;
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These are used for (over) expression of proteins, suppressing expression of (non-) viral RNA and/or proteins by the antisense technique, e.g. to suppress a dominant-negative phenotype, also infectious viral particles that contain the vectors, in gene therapy, particularly for control of guest versus host disease, especially where haematopoietic cells are transduced with the vector or where T cells are transduced, for adoptive immunotherapy, but also for traating severe combined immune deficiency syndrome and for expression cloning of genes. The present sequence is a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bicistronic retroviral vector, useful in gene therapy, particularly of graft versus host disease, contains components of both murine embryonic stem cell and myeloproliferative sarcoma viruses.
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                                                                                                                                                                                                                    "HSV-TK splice variant"
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                                                                                   name=
                                                                                                                                                                                                                                                                                                                                                                                 'product= "neo"
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                                                                                                                                                                .2665
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                                                                                                          .1537
                                                                                                                                                                                                                    product=
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                                                                          standard
                            . . 994
                                                                                                                                         *tag=
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                                                   *tag=
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                                                                                                                                                                                                                                             misc_RNA
                                                                                                          5'UTR
Key
                                                                                                                                                                CDS
                                                                                                                                                                                                                                                                                                                                SOS
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Score 20; DB 12; Length 7235; Pred. No. 13;

100.0%; 100.0%;

Query Match Best Local Similarity

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Gaps

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0; Indels

Mismatches

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Conservative

Local Similarity hes 20; Conserv

Best Loc Matches

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Query Match

100.0%; Score 20; DB 12; Length 7235; 100.0%; Pred. No. 13;

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EP1428886-A1
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                                                                                                                                                                                                                       ADP74713;
                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             misc RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                        5' UTR
                                                                                                                                                                   RESULT 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CDS
                                                                                                                                                                                                                                                                                                                                                                                                     Key
LTR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention relates to a new bicistronic retroviral vector. These are used for (over) expression of proteins, suppressing expression of fon-) viral RNA and/or proteins by the antisense technique, e.g. to suppress a dominant-negative phenotype, also infectious viral particles that contain the vectors, in gene therapy, particularly for control of guest versus host disease, especially where haematopoietic cells are transduced with the vector or where T cells are transduced, for adoptive immunotherapy, but also for treating severe combined immune deficiency syndrome and for expression cloning of genes. The present sequence is a vector sequence shown in the exemplification of the invention.
                                                                                                                                                                                                                                   immunosuppressive; gene therapy; vector; bicistronic retroviral vector; severe combined immune deficiency syndrome; protein expression;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bicistronic retroviral vector, useful in gene therapy, particularly of graft versus host disease, contains components of both murine embryonic stem cell and myeloproliferative sarcoma viruses.
  Gaps
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  Indels
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                                                                                                                                                                                                      Novel bicistronic retroviral vector related vector #2.
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 Mismatches
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/standard_name= "5'-LTR"
995, 1537
7-tag= b
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'standard_name= "3'-LTR'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /standard_name= "IRES"
1348. .4148
'*tag= e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 60-62; 91pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (CELL-) CELLTECH GMBH BIOTECHNOLOGIE.
                                                                                                                                                                                                                                                                                                                                ocation/Qualifiers
                                                   3238 AAGGAAACACGGACACCCAA 3219
                                                                                                                                                                                                                                                                                                                                                                                                                                        product= "HSV-TK"
                            1 AAGGAAACACGGACACCCAA 20
                                                                                                          ADP74700/C
ID ADP74700 standard; DNA; 7235 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          product= "neo"
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                                                                                                                                                                                                                                                                                                                                                                                                                 .2665
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1395. .4981
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Heberlein C, Gindullis F,
                                                                                                                                                                              (first entry)
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 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                               *tag=
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                                                                                                                                                                                                                                                              antisense; ds; gene
                                                                                                                                                                                                                                                                                      Synthetic.
Unidentified
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                                                                                                                                                                             26-AUG-2004
20;
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                                                                                                                                                  ADP74700;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        misc RNA
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention relates to a new bicistronic retroviral vector. These are used for (over) expression of proteins, suppressing expression of (non-) viral RNA and/or proteins by the antisense technique, e.g. to suppress a dominant-negative phenotype, also infectious viral particles that contain the vectors, in gene therapy, particularly for control of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      immunosuppressive; gene therapy; vector; bicistronic retroviral vector; severe combined immune deficiency syndrome; protein expression;
                                                                                               Gaps
Sequence 7235 BP; 1592 A; 2025 C; 1951 G; 1667 T; 0 U; 0 Other;
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                                                DB 12; Length 7235;
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel bicistronic retroviral vector related vector #5.
                                                                                               Mismatches
                                              Score 20;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gindullis F, Hannemann J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "S' -LTR'
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348. ,4148
*tag≃ e
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (CELL-) CELLTECH GMBH BIOTECHNOLOGIE.
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124. .994
                                                                                                                                                                                    3238 AAGGAAACACGGACACCCAA 3219
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                                                                                                                                        1 AAGGAAACACGGACACCCAA 20
                                                                                                                                                                                                                                                                                                         BP.
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                                           Query Match 100.0%; S
Best Local Similarity 100.0%; P
Matches 20; Conservative 0;
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standard_r
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              antisense; ds; gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic.
Unidentified.
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14-AUG-1998;
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Matches
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guest versus host disease, especially where haematopoietic cells are transduced with the vector or where T cells are transduced, for adoptive immunotherapy, but also for treating severe combined immune deficiency syndrome and for expression cloning of genes. The present sequence is a vector sequence shown in the exemplification of the invention.
                                                                                                                                                                                                                                            Coxsackie virus strain VD2921; diabetogenic coxsackie B virus-4; CBV-4; strain VD2921; VD1; VP2; VP3; VP4; P2A; P2B; P2C; P3A; P3B; P3C; P3D; diabetes; diabetogenic entervoirus; beta cell loss; blindness; renal failure; leg amputation; ds.
                                                                                           Gaps
                                                      Sequence 7235 BP; 1593 A; 2025 C; 1950 G; 1667 T; 0 U; 0 Other;
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                                                                                                                                                                                                                            Diabetogenic coxsackie B virus 4 (CBV-4) strain VD2921 genome.
                                                                       100.0%; Score 20; DB 12; Length 7235; 100.0%; Pred. No. 13;
                                                                                                                                                                                                                                                                                                                             *tag= a
note= "Specifically claimed in claim 16"
                                                                                                                                                                                                                                                                                                                                                      /*tag= b
/note= "Specifically claimed in claim 19"
513. 742
                                                                                                                                                                                                                                                                                                                                                                                                          *tag= d
note= "Specifically claimed in claim 25"
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note= "Specifically claimed in claim 26"
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'note= "Specifically claimed in claim 29"
.727. .2441
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*tag= 1
notes "Specifically claimed in claim 35"
3297. 3737
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          note= "Specifically claimed in claim 41"
1034. .5029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'note = "Specifically claimed in claim 44"
                                                                                                                                                                                                                                                                                                                                                                                *tag= c
note= "Specifically claimed in claim 22"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   *tag= h
note= "Specifically claimed in claim 32"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        *tag= j
note= "Specifically claimed in claim 38"
                                                                                         0; Indels
                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                              "Polyprotein"
                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                    3238 AAGGAAACACGGACACCCAA 3219
                                                                                                           1 AAGGAAACACGGACACCCAA 20
                                                                                                                                                                        ABX12440 standard; DNA; 7392 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .1726
                                                                                                                                                                                                                                                                                                                                                                                                                            . 7303
                                                                                                                                                                                                                                                                                                                                                                                                                                              /product= '743. .952
                                                                                                                                                                                                           (first entry)
                                                                                         20; Conservative
                                                                                                                                                                                                                                                                                                                                             88. .512
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                                                                                                                                                                                                                                                                                                                   1. .87
/*tag=
                                                                       Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                         Coxsackievirus
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                                                                                                                                                                                         ABX12440;
                                                                                                                                                      RESULT 76
ABX12440/c
                                                                                          Matches
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The invention describes a polymerase chain reaction (PCR) and primers for detecting nucleic acids from the diabetogenic coxsackie B virus-4 (CBV-4) strain VD221, (particularly VP1, VP2, VP3, VP3, P2A, P2A, P2B, P2C, P3A, P3B, P3C and P3D nucleic acids). The methods and primers are used for the detection of CBV-4 strain VD2921 which is associated with diabetes (diabetogenic enterovirus). Early detection of the diabetes e.g. detection of diabetogenic enterovirus by allowing treatment e.g. with antiviral drugs, to prevent further loss of beta cells and severe long term consequences of diabetes including blindness, renal failure and leg amputations. This sequence represents the genome of diabetogenic coxsackie B virus 4 (CBV-4) strain VD2921
                                                                                                                                                                                                                                                                                                                                                                                                                                             Polymerase chain reaction and primers for detecting nucleic acids from the diabetogenic coxsackie B virus-4 strain VD2921.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
2693. .2710
/*tag= a
/note= "Nucleotides in this position replace the wild-
/pe nucleotide sequence of strain Taiwan Yu-Li (see
AAZ98717)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 7392 BP; 2095 A; 1724 C; 1809 G; 1764 T; 0 U; 0 Other;
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Taiwan Yu-Li strain; foot and mouth disease; coxsackie virus;
differentiation; vaccine; prevent; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           / Match 100.0%; Score 20; DB 8; Length 7392; Local Similarity 100.0%; Pred. No. 13; or Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 5; Page 64-66; 79pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           568 AAGGAAACACGAACACCCAA 549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAZ98719 standard; cDNA; 7400 BP.
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                                                                                                                                                                                                      (INNO-) INNOVENTUS PROJECT AB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Swine vesicular disease virus
                                                                                                                                                                                                                                                                          Yin H;
                                                               19-JUN-2002; 2002WO-IB003278.
                                                                                                                                   20-JUN-2001; 2001SE-00002198.
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                                                                                                                                                                                                                                                                          Tuvemo HT, Frisk GE,
                                                                                                                                                                                                                                                                                                                                      WPI; 2003-278229/27.
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27-DEC-2002
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gene sequence from the SVDV strain Taiwan Yu-Li. SVDV is the
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                                                                                                                                                                                       Query Match 100.0%; Best Local Similarity 100.0%; Matches 20; Conservative (
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                                                                                                                                                                                                 (SDVD) gene sequence from the SVDV strain N3. SVDV is the causative agent of swine vesicular disease, which is very similar to foot and mouth disease. The invention relates to the wild-type Taiwan Yu-Li strain CDNA sequence, and the gene sequences of the mutant SVDV strains N3, H21 and SVDY. The mutant SVDV mucleotide sequence can be used in a vaccine for the prophylaxis of swine vesicular disease. The invention also includes a method for differentiating the mutant SVDV nucleotide sequences from the wild type strain of SVDV, coxsackie virus and foot-and-mouth disease is not present in the specification, but has been derived from the wild-type Taiwan Yu-Li strain SVDV gene sequence (see AAZ98717) shown on pages
                                                                                                       Mutant strains of swine vesicular disease virus (SVDV) used in vaccines to prevent swine vesicular disease.
                                                                                                                                                                                     This sequence represents the full length Swine vesicular disease virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 7400 BP; 2084 A; 1786 C; 1862 G; 1668 T; 0 U; 0 Other;
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Taiwan Yu-Li strain; foot and mouth disease; coxsackie virus;
                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 20; DB 3; Length 7400; 100.0%; Pred. No. 13; cive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Swine vesicular disease virus (SVDV) gene sequence.
                                            Chang EL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Taiwan Yu-Li strain, foot and mouth di
differentiation, vaccine, prevent, ss.
                                          Yang Y, Jeng K,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          568 AAGGAAACACGGACACCCAA 549
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ID AAZ98717 standard; cDNA; 7400 BP.
           (BIOT-) DEV CENT BIOTECHNOLOGY
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                                                                                                                                                    Claim 4; Page; 66pp; English.
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                                                                          WPI; 2000-258616/23
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Query Match

Best Loc Matches

AAZ98717;

RESULT 78

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Mutant strains of swine vesicular disease virus (SVDV) used in vaccines

to prevent swine vesicular disease.

Hwong CL,

Claim 1; Page 34-38; 66pp; English

This sequence represents the full length Swine vesicular disease virus

ö foot This sequence represents the full length Swine vesicular disease virus (SDVD) gene sequence from the SVDV strain H21. SVDV is the causative agent of swine vesicular disease, which is very similar to foot and mouth disease. The invention relates to the wild-type Taiwan Yu-Li strain CDNA sequence, and the gene sequences of the mutant SVDV strains N3, H31 and SP7. The mutant SVDV nucleotide sequence can be used in a vaccine for the prophylaxis of swine vestcular disease. The invention also includes a method for differentiating the mutant SVDV nucleotide sequences from the wild type strain of SVDV, coxeackie virus and foot-and-mouth disease virus through the use of polymerase chain reaction. Note: This sequence is not present in the specification, but has been derived from the wild-/\*tag= a /note= "Nucleotides in this position replace the wild-type nucleotide sequence of strain Taiwan Yu-Li AAZ98717" foot-andcausative agent of swine vesicular disease, which is very similar to foo and mouth disease. The invention relates to the wild-type Taiwan Yu-Li strain cDNA sequence, and the gene sequences of the mutant SVDV strains N3, H21 and SP7. The mutant SVDV nucleotide sequence can be used in vaccine for the prophylaxis of swine vesicular disease. The invention also includes a method for differentiating the mutant SVDV nucleotide sequences from the wild type strain of SVDV, coxsackievirus and foot-and mouth disease virus through the use of polymerase chain reaction Mutant strains of swine vesicular disease virus (SVDV) used in vaccines Gaps Swine vesicular disease virus (SVDV) H21 mutant strain gene sequence Sequence 7400 BP; 2082 A; 1786 C; 1862 G; 1670 T; 0 U; 0 Other; ö Swine vesicular disease virus; SVDV; swine vesicular disease; Taiwan Yu-Li strain; foot and mouth disease; coxsackie virus; differentiation; vaccine; prevent; ss. Score 20; DB 3; Length 7400; Pred. No. 13; 0; Indels Mismatches Chang Location/Qualifiers 2705. .2710 to prevent swine vesicular disease. 环, 568 AAGGAAACACGGACACCCAA 549 BP. 20 ö Jeng (BIOT-) DEV CENT BIOTECHNOLOGY. AAZ98718/c ID AAZ98718 standard, cDNA; 7400 1 AAGGAAACACGGACACCCAA

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This sequence represents the full length Swine vesicular disease virus (SDVD) gene sequence from the SVDV strain SP7. SVDV is the causative agent of swine vesicular disease, which is very similar to foot and mouth disease. The invention relates to the wild-type Taiwan Yu-Li strain cDNA sequence, and the gene sequences of the mutant SVDV strains N3, H21 and SP7. The mutant SVDV nucleotide sequence can be used in a vaccine for the prophylaxis of swine vesicular disease. The invention also includes a method for differentiating the mutant SVDV nucleotide sequences from the wild type strain of SVDV, coxsackie virus and foot-and-mouth disease virus through the use of polymerase chain reaction. Note: This sequence is not present in the specification, but has been derived from the wild-type Taiwan Yu-Li strain SVDV gene sequence (see AAZS8717) shown on pages 34-38 of the specification
                                                                                                                                                                                                  /*tag= a
//note= "Nucleotides in this position replace the
nucleotides at position 2705-2710 of the SVDV wild-type
Taiwan Yu-Li strain (see AAZ98717)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               strains of swine vesicular disease virus (SVDV) used in vaccines
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                  Swine vesicular disease virus (SVDV) SP7 mutant strain gene sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 7421 BP; 2090 A; 1792 C; 1867 G; 1672 T; 0 U; 0 Other;
                                                 Swine vesicular disease virus; SVDV; swine vesicular disease;
Taiwan Yu-Li strain; foot and mouth disease; coxsackie virus;
differentiation; vaccine; prevent; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 20; DB 3; Length 7421; 100.0%; Pred. No. 13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chang EL;
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                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      to prevent swine vesicular disease.
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                                                                                                                              Swine vesicular disease virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 5; Page; 66pp; English.
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16-APR-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               plasmid containing the gene; (2) preparation of the gene and its variant; and (3) a vaccine comprising the gene or its variant. The new gene is useful for the treatment of vesicular disease. The present sequence represents a specifically claimed SVDV nucleotide sequence from the
type Taiwan Yu-Li strain SVDV gene sequence (see AAZ98717) shown on pages 34-38 of the specification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention describes a native swine vascular disease virus (SVDV) gene and its variant. Also described are: (1) an expression
                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Native swine vascular disease virus gene and its variant - useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 7400 BP; 2082 A; 1786 C; 1862 G; 1670 T; 0 U; 0 Other;
                                                      Seguence 7400 BP; 2082 A; 1785 C; 1863 G; 1670 T; 0 U; 0 Other;
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                                                                                        Length 7400;
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                                                                                        Score 20; DB 3;
Pred. No. 13;
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AAA29863 standard; cDNA; 7400 BP.
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Gaps

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Indels

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RESULT 81 AAZ98720/

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91AU-00076128 91GB-00007552

29-APR-1991; 10-APR-1991;

15-OCT-1992

AU9176128-A

genome is 5 non-coding reg by uracil and adenine etc.

Macadam AJ, Minor PD,

WPI; 1992-399255/49.

ALMOND J W. MINOR P D. MACADAM A J.

(ALMO/)

(MACA/) MACADAM A (STON/) STONE D M.

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The CDNA sequence is that of a true RNA virus, i.e. the CDNA directs the produ. of a viable RNA virus which is phenotypically similar to the source virus. Viral RNA was isolated from a virus pellet obtd. from a culture of primary monkey kidney cells infected with an attenuated strain a culture of primary monkey kidney cells infected with an attenuated strain 23 poliovirus. The RNA was sequenced and compared to the published 1539-43 (1984). Two nucleotide differences were observed; at position 2493 a T in the Stanway sequence was replaced by a U(T). The viral DNA was then correct to produce a capta isolated from the synthesis of 48 control of 68 control
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                                                                                                                                                                                                                                                New vaccine against infectious polio-virus comprises RNA virus - for producing RNA virus cDNA and viable RNA virus.
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ID AAN20042 standard; cDNA; 7440 BP.
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                                                                       (UYCO ) UNIV COLUMBIA NEW YORK
                                                                                                                                                                                                                                                                                                                       Claim 7; Fig 6; 110pp; English
                                                                                                                          Tatem JM,
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P-PSDB; AAR22210:
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20-AUG-1990;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This is an attenuated poliovirus type 3 Leon strain in which the 5' non-coding region of the genome is modified by substitution with U at posn. 472, and A at posn. 537. The attenuated poliovirus may be used in a vaccine against polioviruses. They may be administered orally, as a nasal spray, or parenterally. A dose corresp. to the amt. admin. for a conventional live virus vaccine, such as up to 10power6 TCID50 for a sabin vaccine strain in the case of poliovirus may be admin. (Updated on 24-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New attenuated polio:virus for vaccines - in which 5-non-coding region of genome is 5 non-coding region of polio-virus type 3 Leon strain modified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 7431 BP; 2148 A; 1738 C; 1749 G; 1796 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 100.0%; Score 20; DB 2; Length 7431; Best Local Similarity 100.0%; Pred. No. 13; Matches 20; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                        Almond JW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /*tag= a
/note= "want to maintain C"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
743. .7364
                                                                                                                                                                                                                                                                                                                                                                     Stone DM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        568 AAGGAAACACGGACACCCAA 549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 AAGGAAACACGGACACCCAA 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Page 12; 14pp; English.
Human poliovirus 3; strain Leon
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RNA virus; error reduction; ss

Poliovirus

\*tag=

2493

mutation

(first entry)

25-MAR-2003 · (revised)

AA022965;

14-JUL-1992

91WO-US005890.

20-AUG-1991;

WO9203538-A. 05-MAR-1992,

AAQ22965 standard; cDNA; 7432

AAQ22965/c RESULT 83

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AAX26152
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Plasmid pVR106 was produced by combining plasmids pVR104 and pVR105. It contains a full-length cDNA copy of the poliovirus genome. E.coli HB101 contg. this plasmid has been registered as ATCC 31844. The full-length poliovirus cDNA molecule is itself infectious and can be introduced into cells and these cultured to produce RNA virus. Alternatively, the infectious cDNA can be treated with mutagens and the altered material used to infect cells so that attenuated virual RNA is prod. and this used to make vaccines. For antibody prodn., cDNA capable of directing antigen prodn. is selected and isolated and incorporated into cells which are fined.) (Updated on 27-NAA antigen. (Updated on 25-NAR-2003 to correct PA field.) (Updated on 27-NAG-2003 to correct CDN3 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                       Prodn. of CDNA representing viral RNA sequences - by transcription,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 7440 BP; 2205 A; 1734 C; 1716 G; 1785 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 20; DB 1; Length 7440; 100.0%; Pred. No. 13; ive 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                insertion into vector and host cell transformation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                Example; Table 1, pages 25-31; 50pp; English
                                                                                                                                                                                                                                                                                                                                                          (MASI ) MASSACHUSETTS INST TECHNOLOGY.
ocation/Qualifiers
                                                                                                                                                                                                                                                               product= "4 (p63)"
                                                         1766. .2479
/*tag= c
/product= "VP3"
                                                   product= "VP2"
                                                                                                      product= "VP1"
                                                                                                                                                                                                                                      product= "VPg"
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81US-00320525
                                                                                     480. .3385
*tag= d
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*tag= e
                                                                                                                                                                 124. .5110
                                                                                                                                                                                          111. .5371
                                                                                                                                                                                                                      372. .5986
                                                                                                                                                                                                                                               987. .7375
                                                                                                                                                                                                                                                                                                                                                                           Baltimore D, Racaniello VR;
                                                                                                                                                                         /product= ".
                  product= "
                                   50. .1765
                                            tag= b
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                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1982-95059E/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                     P-PSDB; AAP20037.
                                                                                                                                                                                                                                                                                                                  20-APR-1981;
                                                                                                                                                                                                                                                                                                                                 20-APR-1981;
12-NOV-1981;
                                                                                                                                                                                                                                                                                WO8203632-A.
                                                                                                                                                                                                                                                                                                28-OCT-1982
 Key
                                   CDS
                                                            CDS
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The invention relates to a replication-competent recombinant Sabin type I poliovirus vector encoding a multiple cloning site and 3C-protease cleavage site between the two end N-terminal residues. This comprises a vector containing an exogenous vaccine gene at the multiple cloning site. A method of production of both vectors is also provided. The recombinant vectors are useful for developing various mucosal vaccines against a number of infectious diseases, including human immunodeficiency virus type I (HIV-I) (which causes acquired immunodeficiency syndrome (AIDS)), small pox, poliomyelitis and Hepatitis C. The poliovirus-mediated mucosal vaccine vectors overcome the disadvantages exhibited by Mahoney vectors by being safe to humans, replicable (having equal replication ability to that of the wild type) vectors, where the introduced vaccine genes are
                                                                                                                                                                                                                                                                                                                               Replication-competent; Sabin type 1 poliovirus vector; cloning site; 3G-protease cleavage site; mucosal vaccine; infectious disease; AIDS; human immunodeficiency virus type 1; HIV-1; small pox; poliomyelitis; Hepatitis C; acquired immunodeficiency syndrome; Mahoney vector; viral;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New replication-competent recombinant Sabin type 1 poliovirus vector useful for developing mucosal vaccines against HIV-type 1, small pox, poliomyelitis and hepatitis C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 7441 BP; 2210 A; 1730 C; 1715 G; 1786 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             stably maintained during viral passages
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Page 51-55; 64pp; English.
                                                                                                                                                                                                                                                                 DNA sequence of human poliovirus 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             565 AAGGAAACACGGACACCCAA 546
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                                                                    BP.
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                                                                    AAX26152 standard; DNA; 7441
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Best Local Similarity 100.0%;
Matches 20; Conservative C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (ALTW-) ALTWELL BIOTECH INC.
                                                                                                                                                                                                   21-MAY-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1999-167434/14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Jung HR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        poliovirus; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       07-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      07-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO9907859-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18-FEB-1999.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Poliovirus.
                                                                                                                                  AAX26152;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACC43138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bae YS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 86
ACC43138/c
ID ACC431
XX
AC ACC431
RESULT 85
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20; Conservative

Matches

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Gaps

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Gene expression vector; beta-galactosidase; luciferase; pGFPstopneoSECIS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention relates to a new bicistronic retroviral vector. These are used for (over) expression of proteins, suppressing expression of fono-) viral RNA and/or proteins by the antiseans technique, e.g. to suppress a dominant-negative phenotype, also infectious viral particles that contain the vectors, in gene therapy, particularly for control of guest versus host disease, especially where haematopoietic cells are transduced with the vector or where T cells are transduced with the vector or where T cells are transduced, for adoptive immunotherapy, but also for treating severe combined immune deficiency syndrome and for expression cloning of genes. The present sequence is a vector sequence shown in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bicistronic retroviral vector, useful in gene therapy, particularly of graft versus host disease, contains components of both murine embryonic stem cell and myeloproliferative sarcoma viruses.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 7925 BP; 1714 A; 2242 C; 2135 G; 1834 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleotide sequence of gene expression vector pGFPstopneoSECIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 20; DB 12; Length 7925; 100.0%; Pred. No. 13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hannemann J,
                                                                                                                                                                                                                                standard_name= "3'-LTR"
                                                                                                                                                                                                                                                                                                                                                                                                                                       (CELL-) CELLTECH GMBH BIOTECHNOLOGIE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 66-68; 91pp; German.
                                          "HSV-TK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3273 AAGGAAACACGGACACCCAA 3254
                                                                               /*tag= d
/standard_name= ".
3383. .4183
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                                                                                                                                                                    "neo"
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                                                                                                                                                                                                                                                                                                                                                        09-DEC-2002; 2002EP-00027555
                                                                                                                                                                                                                                                                                                                                                                                              09-DEC-2002; 2002EP-00027555
        .2700
                                                                  .3335
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gindullis F,
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                                                                                                                                                                      product=
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Les 20; Conservative
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                             *tag=
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                                                                                                                                                                                                                                                                           EP1428886-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACC43139;
                                                                  misc_RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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                                                                                                                              CDS
      SOS
                                                                                                                                                                                       LTR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The specification describes a recombinant gene expression vector, which comprises a promoter sequence; a gene of interest encoding betagalactosidaes, a TGA translational stop signal, and translationally linked to the gene of interest a selectable marker gene encoding broducing a host cell clone expression vector is useful for also useful for the selection of transformed host cells that express a sene of interest. The vector is also useful for the selection of transformed host cells that express a gene of interest. The present sequence represents pGFPetcopneo. It was used during construction of vectors of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                      New recombinant gene expression vector, useful for producing a host cell clone highly expressing a gene of interest, comprises a promoter sequence, gene of interest, translational stop signal and a selectable
                                                                          Gene expression vector; beta-galactosidase; luciferase; pGFPstopneo; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           immunosuppressive; gene therapy; vector; bicistronic retroviral vector; severe combined immune deficiency syndrome; protein expression; antisense; ds; gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 7873 BP; 1939 A; 2060 C; 2053 G; 1821 T; 0 U; 0 Other;
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                                        Nucleotide sequence of gene expression vector pGFPstopneo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel bicistronic retroviral vector related vector #4.
                                                                                                                                                                                                                                                                                                                                                                         Steinhilber W;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
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/standard name= "5'-LTR"
/*+...
                                                                                                                                                                                                                                                                                                                                                                         Schaefer KP,
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                                                                                                                                                                                                                                             31-JUL-2002; 2002WO-EP008520.
                                                                                                                                                                                                                                                                                      02-AUG-2001; 2001EP-00118632.
(first entry)
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nes 20; Conservative
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                                                                                                                                                                                                                                                                                                                                (ALTA-) ALTANA PHARMA AG.
                                                                                                                                                                                                                                                                                                                                                                       Hauser H, Mueller PP,
                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2003-268203/26.
                                                                                                                                                                WO2003014361-A1
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Unidentified.
17-JUN-2003
                                                                                                                                                                                                         20-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    marker gene.
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                                                                                                                       Synthetic:
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Matches
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Strathmann

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Gaps

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Indels

ADP74702/ RESULT

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number=
                                      number=
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Hauser H, Mielke C;
                                                                                                                                                                                            *tag=
                                                                                                                                                                                                                                                      *tag=
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                                                                                                                                                                                                                                                                                                            *tag=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
Matches 20; Conserv
                                                                                                                                                                                                                                                                                                                                                misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    polyA_signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO9811241-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            02-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16-SEP-1996;
30-SEP-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19-MAR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
intron
                                                      intron
                                                                                                                                                                      5' UTR
                                                                                                              505
                                                                                                                                                                                                                                RBS
                                                                                                                                                                                                                                                                                        CDS
                                                                                                                                                                                                                                                                                                                                                                                                                            SDS
g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ó,
                                                                                                                                                                                                                                                                                                                                            The specification describes a recombinant gene expression vector, which comprises a promoter sequence; a gene of interest encoding betagalactosidase; a TGA translational stop signal; and translationally linked to the gene of interest a selectable marker gene encoding broducing a host cell clone expression vector is useful for producing a host cell clone expressing a gene of interest. The vector is also useful for the selection of transformed host cells that express a gene of interest. The present sequence represents pGFPstopneoSECIS. It was used during construction of vectors of the invention
                                                                                                                                                                                                          New recombinant gene expression vector, useful for producing a host cell clone highly expressing a gene of interest, comprises a promoter sequence, gene of interest, translational stop signal and a selectable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        *tag= a
'note= "CMV promoter with an upstream MPSV enhancer"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PMCLDHAP tricistronic vector for the expression of hmAb45-TNF alpha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Circular; antibody-cytokine fusion protein; tricistronic vector; TNF alpha; IL-2; IRES; internal ribosome entry site; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Light chain hmAb425, variable region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 7943 BP; 1958 A; 2074 C; 2074 G; 1837 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1107. .1115
/*tag= f
/note= "Rest of the leader sequence"
                                                                                                                                Steinhilber W;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      *tag= c
note= "Partial leader sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                *tag= d
note= "5'UTR from poliovirus"
                                                                                                                                  Schaefer KP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
1. .904
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 89
AAV18096 standard; DNA; 8298 BP.
XX
AC AAV18096;
XX
DT 04-AUG-1998 (first entry)
XX
Circular; antibody-cytokine fusion
XX
XX
Synthetic.
XX
FH
Key
I. .904
FT
Promoter
Atag= a
FT
Intron
Atag= b
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Intron
Atag= b
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Intron
Atag= c
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Intron
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                                                                                                                                                                                                                                                                                                          Example 4; Fig 13; 52pp; English
                31-JUL-2002; 2002WO-EP008520.
                                                      02-AUG-2001; 2001EP-00118632
                                                                                                                                Hauser H, Mueller PP,
                                                                                            (ALTA-) ALTANA PHARMA
                                                                                                                                                                      WPI; 2003-268203/26.
                                                                                                                                                                                                                                                                      marker gene
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                                                                                                                                                                                                                                                                                                                                     note= "Poliovirus derived internal ribosome entry site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence represents a new pMCLDHAP tricistronic vector for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Welge T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             e.9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "Comprises of a 5' UTR from poliovirus, an
internal ribosome entry site and intron 4"
5280. .5876
                                                                                                                                                      product= "Light chain hmAb425, constant region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 8298 BP; 1974 A; 2364 C; 2134 G; 1826 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                             'note= "Heavy chain hmAb425 fused to TNF alpha"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Oligo:cistronic expression vector - useful for production of, MAb425/TNF-~a or MAb425/IL-2 antibody fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 20; DB 2; Length 8298; 100.0%; Pred. No. 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rieke E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'product= "Puromycin acetyl transferase"
note= "Selection marker"
5929. .6181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P-PSDB; AAW48647, AAW48648, AAW48649, AAW48650, AAW48651
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                                                                                                                                                                                                                                              note= "5' UTR from poliovirus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /standard name= "SV40 PolyA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bruemmer W,
                               g
r= Intron 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  97WO-EP004765.
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.1595
                                                                                                                                                                               914. .2028
                                                                                                                                                                                                                                                                             .2159
                                                                                          596. .1913
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The invention relates to a retroviral vector genome (G1) comprising two or more NOIs (nucleotide sites of interest), operably linked by one or more Internal Ribosome Entry Site(s) (IRES). Also included are a vector system (S1) comprising (G1), production (M1) of a lentiviral particle, a viral particle (P1) produced by (M1) or by (S1), a pharmaceutical composition comprising (G1), (S1) or (P1), a bicistronic cassette comprising a nucleotide sequence which encodes (T-cyclohydrolase 1 operably linked by one or more IRES(s); or D) Aromatic Amino Acid Dopa Decarboxylase and a nucleotide sequence which encodes Vesicular Monoamine Transporter 2 operably linked by one or more IRES(s); a tricistronic cassette comprising a nucleotide sequence which encodes tyrosine hydroxylase, a nucleotide sequence that encodes GTP-cyclohydrolase 1 and conditions and a nucleotide sequence that encodes GTP-cyclohydrolase 1 and cassette comprising a nucleotide sequence that encodes GTP-cyclohydrolase 1 and conditions and a nucleotide sequence that encodes GTP-cyclohydrolase 1 and conditions and a nucleotide sequence which encodes GTP-cyclohydrolase 1 and conditions and a nucleotide sequence which encodes GTP-cyclohydrolase 1 and conditions and a nucleotide sequence which encodes GTP-cyclohydrolase 1 and conditions and a nucleotide sequence which encodes GTP-cyclohydrolase 1 and conditions and a nucleotide sequence which encodes GTP-cyclohydrolase 1 and conditions and a nucleotide sequence which encodes GTP-cyclohydrolase 1 and conditions and a nucleotide sequence which encodes GTP-cyclohydrolase 1 and conditions and a nucleotide sequence which encodes GTP-cyclohydrolase 1 and conditions and a nucleotide sequence which encodes GTP-cyclohydrolase 1 and conditions and a nucleotide sequence which encodes GTP-cyclohydrolase 1 and conditions and a nucleotide sequence which encodes GTP-cyclohydrolase 1 and conditions and a nucleotide sequence which encodes GTP-cyclohydrolase 1 and conditions and conditions and conditions and conditions and condi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .nvention, pONY8-BIC, comprising elements of the BIAV (Equine infectious
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cyclic; EIAV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Parkinson's disease; gene therapy; retroviral vector; ds; cyclic; EIAN neuroprotective; antiparkinsonian; NOI; IRES; lentiviral particle; nucleotide site of interest; Internal Ribosome Entry Site; pONY8-BIC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rohll J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            tyrosine hydroxylase, GTP-cyclohydrolase 1; bicistronic cassette;
Aromatic Amino Acid Dopa Decarboxylase; tricistronic cassette;
Vesicular Monoamine Transporter 2; neurodegenerative disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       anaemia virus) genome, human cytomegalovirus sequences, a plasmid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EIAV based retroviral vector pONY8-BIC.
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                                                       ABK86535 standard; DNA; 10448 BP
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                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                 (revised)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Escherichia coli
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                                                                                                                                                                                                                                                                                     07-AUG-2003
30-AUG-2002
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                                                                                                                                                                      ABK86535;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (OXFO-)
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ABK86535/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Viral vector that expresses single-chain interleukin-12 and costimulator, useful for treatment of tumors, viral infections, e.g. human immunodeficiency virus, and prion diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention relates to a viral vector that includes a nucleic acid encoding a single-chain interleukin-12 (IL-12) and a co-stimulatory protein. Viral vectors and virus particles derived from them are useful for treatment of tumours, infectious diseases (e.g. HIV, hepatitis A, B or C, cytomegalovirus or human papilloma virus), or prion diseases. The present sequence is a viral vector shuttle sequence used in the
                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                         cytostatic; virucide; anti-HIV; hepatotropic; neuroprotective; immunostimulant; expression cassette; viral vector; interleukin-12; co-stimulatory protein; cancer; infection; ds; gene.
 the bicistronic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Other;
                                           Sequence 10448 BP; 2780 A; 2431 C; 2611 G; 2626 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 20; DB 12; Length 10633; Pred. No. 14; Mismatches 0; Indels 0;
                                                                        20; DB 6; Length 10448;
No. 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 10633 BP; 2627 A; 2749 C; 2779 G; 2427 T; 0 U; 51
                                                                                                     0; Indels
backbone, a green fluorescent protein sequence and the cassette. (Updated on 07-AUG-2003 to correct OS field.)
                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                             Viral vector shuttle (CMV)IL12(IRES)4-1BBL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (UYHA-) UNIV HAMBURG-EPPENDORF KLINIKUM.
                                                                                         Pred. No
                                                                        100.0%; Score
100.0%; Pred.
                                                                                                                                                  3244 AAGGAAACACGGACACCCAA 3225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Fig 25; 129pp; German
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         exemplification of the invention.
                                                                                                                                   1 AAGGAAACACGGACACCCAA 20
                                                                                                                                                                                                                                     AD007660 standard; DNA; 10633 BP.
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100.0%;
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                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similaricy
nes 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Schnieders F;
                                                                                                     20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2004-357221/33.
                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO2004035799-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic.
Unidentified.
                                                                                                                                                                                                                                                                                                15-JUL-2004
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                                                                                                                                                                                                                                                                   AD007660;
                                                                        Query Match
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                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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                                                                                                                                                                                                           RESULT
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46

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Gaps

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0; Indels

Mismatches

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6; Length 11058;

DB 14;

Score 20; Pred. No. 1

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WO200229065-A2
                                    Kingsman AJ,
   07-AUG-2003
30-AUG-2002
                           11-APR-2002
                      Synthetic
 ABK86536;
                                        novel
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Chimeric; Hepatitis C Virus; HCV; poliovirus; liver cirrhosis;
NS3 protease gene; NSSA/5B; hepatocellular carcinoma; anti-HCV drug; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Recombinant gene encoding hepatitis C surrogate virus - comprises picornavirus and hepatitis C virus protease NS3 genes and hepatitis C virus protease NS3 target sites, useful for drug screening.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chimeric protease NS3/poliovirus gene NS3 delta-C-PV1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         & TECHNOLOGY.
                                                                                                                                                             3813 AAGGAACACGGACACCCAA 3794
                                                                                                                              1 AAGGAAACACGGACACCCAA 20
                                                                                                                                                                                                                                                                                           AAV12373/c
ID AAV12373 standard; DNA; 11326
                      100.0%;
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Query Match
Best Local Similarity 100.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (GLDS ) LG CHEM CO LTD. (UYPO-) UNIV POHANG SCI
                                                                                                                                                                                                                                                                                                                                                                                                                        (revised)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hahm BS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hepatitis C virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28-JUN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25-JUN-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                        17-OCT-2003
03-JUL-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       iovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   08-JAN-1998
                                                                                                                                                                                                                                                                                                                                                                         AAV12373;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chimeric.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Jang
                                                                                                                                                                                                                                                                   RESULT 93
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to a retroviral vector genome (G1) comprising two or more NOIs (nucleotide sites of interest), operably linked by one or more Internal Ribosome Entry Site(s) (IRES). Also included are a vector system (S1) comprising (G1), produced by (M1) of a lantiviral particle, a composition comprising (G1), produced by (M1) or by (S1), a pharmaceutical comprising a nucleotide sequence which encodes 1 tyrosine hydroxylase and a nucleotide sequence which encodes 1 tyrosine hydroxylase comprising a nucleotide sequence which encodes Vesicular Monoamine CC ansporter 2 operably linked by one or more IRES(s), a tricistronic cassette comprising a nucleotide sequence which encodes tyrosine C ansporter 2 operably linked by one or more IRES(s), a tricistronic cassette comprising a nucleotide sequence which encodes tyrosine C Transporter 2 operably linked by one or more IRES(s), a tricistronic cassette comprising a nucleotide sequence which encodes (TP-cyclohydrolase 1 and a nucleotide sequence that encodes GTP-cyclohydrolase 1 and a nucleotide sequence which encodes Mromatic Amino Acid Dopa pertopy and the viral pertopy and the viral particle (P1) can all be used to treat and/or prevent (by gene therapy) a couract of special part of the vector system (S1), and the viral particle (P1) can all be used to treat and/or prevent (by gene therapy) and also in the manufacture of a pharmaceutical composition to treat the above mentioned disease, respecially Parkinson's disease in a subject, and also in the manufacture of a pharmaceutical composition decomposition to treat the above mentioned disease. Treatment with vectors capable of delivering C e.g., Tyrosine hydroxylase, GTP-cyclohydrolase 1, Aromatic Amino Acid C bopa Decarboxylase and Vesicular Monoamine Transporter 2, are useful for that has targed sof treatment for sufference of paramaceutical capable of delayers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    they do not respond significantly to L-dopa treatment by prior art methodologies. The present sequence is retroviral vector of the invention, pONYB-TRIC comprising elements of the BIAV (Equine infectious banemia virus) genome, human cytomegalovirus sequences, a plasmid backbone, a green fluorescent protein sequence and the tricistronic cassette. (Updated on 07-AUG-2003 to correct OS field.)
                                                                                                                                                                                                                                  Parkinson's disease; gene therapy; retroviral vector; ds; cyclic; EIAV; neuroprotective; antiparkinsonian; NOI; IRES; lentiviral particle; nucleotide site of interest; Internal Ribosome Entry Site; DONY8-TRIC; tyrosine hydroxylase; GTP-cyclohydrolase 1; bicistronic cassette; Aromatic Amino Acid Dopa Decarboxylase; tricistronic cassette; Vesicular Monoamine Transporter 2; neurodegenerative disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    retroviral vector genome is useful in the treatment
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mazarakis ND, Martin-Rendon E,
                                                                                                                                                                                   EIAV based retroviral vector pONY8-TRIC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 8; Page 70-72; 106pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (OXFO-) OXFORD BIOMEDICA UK LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                          Equine infectious anemia virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           06-OCT-2000; 2000GB-00024550.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      05-OCT-2001; 2001WO-GB004433.
                                                                                                                                 (first entry)
                                                                                                   (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                Human cytomegalovirus.
Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2002-507885/54.
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Homo sapiens.
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The present chimeric sequence comprises of a Hepatitis C Virus (HCV)

protease NS3 gene and its target site NS5A/5B gene inserted into the open
creading frame of the poliovirus gene. HCV is the major etiologic agent of
non-A, non-B hepatitis, and has been implicated in liver cirrhosis and
hepatocellular carcinoma. The invention provides a hepatitis C surrogate
virus comprising of the recombinant gene described. Upon expression, the
HCV NS3 protease would cleave its target site to become independent of
the poliovirus polyprotein. HCV NS3 protease contained within the
surrogate is a good therapeutic target molecule for the development of
cuti-HCV drugs, since its activity is considered essential for viral
proliferation. The surrogate virus is claimed to be useful than the
existing in vitro systems for HCV culture for screening anti-HCV drugs
cand testing for their efficacy. It is also considered to be useful for
studying HCV genes in viral replication. (Updated on 17-OCT-2003 to
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Claim 1; Fig 6A-6E; 36pp; English.
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es 20; Conserv
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Matches
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Sequence 11058 BP; 2875 A; 2647 C; 2813 G; 2723 T; 0 U; 0 Other;

AD007659;

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Viral vector that expresses single-chain interleukin-12 and costimulator, useful for treatment of tumors, viral infections, e.g. human immunodeficiency virus, and prion diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention relates to a viral vector that includes a nucleic acid encoding a single-chain interleukin-12 (IL-12) and a co-stimulatory protein. Viral vectors and virus particles derived from them are useful for treatment of tumours, infectious diseases (e.g. HIV, hepatitis A, B or C, cytomegalovirus or human papilloma virus), or prion diseases. The present sequence is a viral vector used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    expression; gene polymorphism; cross-species hybridisation; probe;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Collection of at least four nucleic acid probes for analysis of gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Seguence 38246 BP; 8959 A; 10813 C; 10384 G; 8043 T; 0 U; 47 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 20; DB 12; Length 38246;
Pred. No. 15;
; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Picornaviridae DNA 5'-untranslated region specific probe.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Fig 27; 129pp; German
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                                                                                                                                     10-OCT-2003; 2003WO-EP011252.
                                                                                                                                                                                  11-OCT-2002; 2002DE-01048141
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100.
Matches 20, Conservative
                                                                                                                                                                                                                                                                             Schnieders F;
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                                                                                                                                                                                                                                                                                                                        WPI; 2004-357221/33.
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(HSIU/) HSIUNG C A.
(LINC/) LIN C.
                                             WO2004035799-A2.
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Unidentified.
                                                                                          29-APR-2004
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                                                                                                                                                                                                                                                                           Waehler R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADK66744/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Viral vector that expresses single-chain interleukin-12 and costimulator, useful for treatment of tumors, viral infections, e.g. human immunodeficiency virus, and prion diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention relates to a viral vector that includes a nucleic acid encoding a single-chain interleukin-12 (IL-12) and a co-stimulatory protein. Viral vectors and virus particles derived from them are useful for treatment of tumours, infectious diseases (e.g. HIV, hepatitis A, B or C, cytomegalovirus or human papilloma virus), or prion diseases. The present sequence is a viral vector shuttle sequence used in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                vector; interleukin-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 11746 BP; 2920 A; 3037 C; 3055 G; 2683 T; 0 U; 51 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                    cytostatic; virucide; anti-HIV; hepatotropic; neuroprotective; immunostimulant; expression cassette; viral vector; interleuki co-stimulatory protein; cancer; infection; ds; gene.
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                                                                                                                                                                                                                           Viral vector shuttle (CMV) IL12 (IRES) 4-1BBL (IRES) IL-2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Fig 24; 129pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            exemplification of the invention.
                                                                                     AD007659 standard; DNA; 11746 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AD007662 standard; DNA; 38246 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11-OCT-2002; 2002DE-01048141
                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Schnieders F;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2004-357221/33.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Viral vector pAd-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                   WO2004035799-A2
                                                                                                                                                                                                                                                                                                                                                              Synthetic.
Unidentified.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20;
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Synthetic

AD007662;

SXXXXXXXXXXXXXXX

RESULT 95

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Query Match

Matches

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Gaps

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                                                                                                                  The present invention relates to a collection of at least four nucleic acid probes, each including a segment, the entirety of which hybridises under low stringency conditions to at least a first gene of first species and a second gene of second species, where the hybridising probes correspond to different genes of the two species and the genes are orthologous to each other. The invention is useful for analysis of gene expression and of gene polymorphisms. The probes are designed for cross-species hybridiaation, e.g. by identification of conserved segments among orthologous genes. The present sequence is Picornaviridae DNA 5'-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Trans-species nucleic acid probe - for a probe collection having at least four nucleic acid probes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to a collection of at least four nucleic acid probes comprising a segment able to hybridize to orthologous genes from at least two different species. In the embodiments of the invention, the probe segment is at least 60% identical to orthologous genes from two different species. The present sequence represents a degenerate probe used to detect 5' untranslated region (5'UTR) sequences from viruses of the Picornaviridae family.
expression and of gene polymorphisms, comprises each probe including segment and entirety of which hybridizes under low stringency conditions to genes of two species.
                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                 DB 12; Length 62;
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                                                                                                                                                                                                                                                                                                                              Sequence 62 BP; 9 A; 11 C; 15 G; 20 T; 0 U; 7 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 62 BP; 9 A; 11 C; 15 G; 20 T; 0 U; 7 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Picornaviridae 5'UTR degenerate probe, SEQ ID NO:5.
                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA detection; hybridization; 5'-UTR; probe; 88
                                                                                                                                                                                                                                                                                                                                                                                95.0%; Pred. No. 15;
                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example; SEQ ID NO 5; 46pp; Chinese.
                                                                                   Example; SEQ ID NO 5; 11pp; English.
                                                                                                                                                                                                                                                                                             exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                   1 AAGGAAACACGGACACCCAA 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                           57 AAKGAAACACGGACACCCAA 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AEC07516 standard; DNA; 62 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-FEB-2002; 2002US-00357541.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14-FEB-2003; 2003TW-00103058
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (NAHE-) NAT HEALTH RES INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lin J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 95.0
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Shiung J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2005-579874/59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Picornaviridae
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Juang J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AEC07516;
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DB 14; Length 62;

100.0%; Score 20;

Query Match

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                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention describes the application of nucleotide primer to detecting enterovirus. The detection method and the reagent kit are disclosed. This sequence represents an enterovirus detection method associated primer
                                                                                                                                                                                                                                                                                                                                                                                           Process, primer and probe for detecting and discriminating enterovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       p3 probe used to detect enterovirus type 71 (EV71) in a sample.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 20; DB 8; Length 28;
Pred. No. 22;
1; Mismatches 0; Indels
           Indels
                                                                                                                                                                          Enterovirus detection method associated primer #11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 28 BP; 2 A; 4 C; 6 G; 15 T; 0 U; 1 Other;
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                                                                                                                                                                                                                                                                                                                             (JING-) JINGYU BIOLOGIC SCI TECHNOLOGY IND CO LT.
 d. No. 15;
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Detection; enterovirus type 71; probe; ss
  Pred
                                                                                                                                                                                              Enterovirus detection; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 AAGGAAACACGGACACCCAA 20
                                1 AAGGAAACACGGACACCCAA 20
                                                   57 AAKGAAACACGGACACCCAA 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24 AADGAAACACGGACACCCAA 5
           1;
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| Similarity 95.0%;
19; Conservative
                                                                                                         ACD26711 standard; DNA; 28
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                                                                                                                                                                                                                                                                                                                                                  Zeng Y;
                                                                                                                                                                                                                                                                                                                                                                       WPI; 2003-230558/23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
les 19; Conserv
                                                                                                                                                                                                                                                                                                                                                  Bai Q,
                                                                                                                                                   11-SEP-2003
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                                                                                                                                                                                                                    Enterovirus
                                                                                                                                                                                                                                       CN1366066-A
                                                                                                                                                                                                                                                              28-AUG-2002
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 Local
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 Best Loc
Matches
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us-10-829-474-2.rng

The invention provides a method and a kit for detecting and differentiating an enterovirus type 71 (BV71) in a sample. The method differentiating an enterovirus type 71 (BV71) in a sample. The method form an amplificating nucleic acids in the sample with a pair of primers to form an amplification product; contacting the amplification product with at least one synthetic nucleotide sequence fixed on a solid substrate and detecting hybridisation. The present sequence is a probe used to detect New kit comprising a pair of oligonucleotide primers for nucleic acid amplification, useful in detecting and differentiating an enterovirus in detecting hybridisation. The present sequence is a probe and differentiate enterovirus type 71 (EV71) in a sample. Sequence 28 BP; 2 A; 4 C; 6 G; 15 T; 0 U; 1 Other; Wang Claim 1; SEQ ID NO 11; 14pp; English. Bair C, Tseng Y, Wang Y, (CHIP-) CHIP BIOTECHNOLOGY INC 28-NOV-2000; 2000US-00724678. 28-NOV-2000; 2000US-00724678. WPI; 2004-793563/78. sample. Lee K, 

0; Indels Pred. No. 22; 1; Mismatches 1 AAGGAAACACGGACACCCAA 20 24 AADGAAACACGGACACCCAA 5 95.0%; 19; Conservative Local Similarity Matches 셤 ò

Gaps

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DB 13; Length 28;

100.0%; Score 20;

Query Match

ADW75017 standard; DNA; 70 BP ADW75017; ADW75017/ 

Human rhinovirus probe PBRh 00006. (first entry) 07-APR-2005

respiratory disease; Chlamydia pneumoniae infection;
SARS coronavirus infection; treponema pallidum infection; sialodenitis;
rubella virus infection; rhinovirus infection;
respiratory syncytial virus infection; influenza virus infection;
parainfluenza virus infection; mycoplasma infection;
measles virus infection; HIV infection; HIVI infection;
hepatitis A virus infection; hepatitis B virus infection;
hepatitis E virus infection; hepatitis G virus infection; probe; 88; blochip; DNA chip; microorganism detection; diagnosis; adenovirus infection; coronavirus infection; herpesvirus infection

Human rhinovirus sp.

WO2005005658-A1.

20-JAN-2005.

14-JUL-2003; 2003WO-CN000561

14-JUL-2003; 2003WO-CN000561.

CAPITAL BIOCHIP CO LTD UNIV QINGHUA. (UYQI)

Tao S, Cheng J;

This invention describes a novel chip used to detect a coronavirus causing the severe actue respiratory syndrome (SARS-CoV) and a non-SARS-COV infectious organism. The chip comprises an oligonucleotide probe complementary to a nucleotide sequence of SARS-COV or non-SARS-COV coronary and a non-SARS-COV or infectious organism. The chip comprises an oligonucleotide probe complementary to a nucleotide sequence of SARS-COV or non-SARS-COV or non-sequence is a gene encoding the spike glycoprocein. the small envelope containing SARS-COV a non-SARS-COV infectious organism. The detection inmobilization reaction when a sample containing or subjected of containing SARS-COV a non-SARS-COV infectious organism. The detection infellodes multiplex PCR using primers which amplify nucleotide equences from an influenza A and B virus, a human metapneumovirus, human containing sample containing sample ontaining sample or the SARS-COV is detected of containing dense of the SARS-COV, a positive hybridization signal using the negative control probe. Detecting a positive hybridization signal using the negative control probe. Detecting a positive hybridization signal using the negative control probe. Detecting sample of the SARS-COV indicates mutation of signal using the spike glycoprotein gene of the SARS-COV indicates mutation of signal using the positive control probe. Detecting sample signal using the spike glycoprotein gene of the SARS-COV indicates mutation of signal using the spike glycoprotein gene of the SARS-COV indicates mutation of signal using the spike glycoprotein gene of the SARS-COV indicates mutation of signal using the spike glycoprotein gene of the SARS-COV indicate is infected by SARS-COV and/or a non-SARS-COV infectious organism causing SARS-like symptoms. This sequence represents a probe used in the method coronavirus, canine coronavirus, feline coronavirus, porcine epidemic diarrhea virus, porcine transmissible gastroenteritis virus, bovine coronavirus, feline infectious peritonitis virus, rat coronavirus, neonatal calf diarrhea coronavirus, porcine hemagglutinating encephalomyelitis virus, puffinosis virus, turkey coronavirus or a sialodacryoadenitis virus of rat. The methods and compositions of the invention are useful in amplifying and detecting SARS-CoV nucleotide sequences, in particular for diagnosing early-stage SARS patients (infected less than one to three days) and determining whether a subject New chip for assaying for a coronavirus causing the severe acute respiratory syndrome (SARS-CoV) and a non-SARS-CoV infectious organism comprising a support and oligonucleotide probes. nfected less than one to three days) and determining whe infected by SARS-CoV and/or a non-SARS-CoV infectious Disclosure; Page 34; 122pp; English of the invention. 

ö 95.0%; Score 19; DB 14; Length 70; 100.0%; Pred. No. 29; Indels ö 100.0%; Prec. ... 2 AGGAACACGGACACCCAA 20 34 AGGAAACACGGACACCCAA Query Match Best Local Similarity 100.0 Matches ·19, Conservative 8 셤

Sequence 70 BP; 11 A; 12 C; 20 G; 27 T; 0 U; 0 Other;

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Gaps

9, 2006, 00:30:11 completed: March Job time : 214.388 secs Search

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CN835108 AGENCOURT CW118544 MARC 1010 CW117765 MARC 1009 CK412195 AUF IDHAK	BM415978 OP21060 M CG745203 P038-1-B1	CK027487 AGENCOURT CZ679560 OM Ba023 BZ020345 OchO4a08. BH693975 BOMT227TP	CW176116 104 588 1 CD290195 StrPU538. CD319193 StrPU538.	DN493639 G079P41.5 CW585488 OA_ABa011 AI61850 zewD0061.	BP813540 BP813540 BP664023 BP664023 CA730096 wiplc.pk0	BU237703 603410683 AG224508 Lotus cor	BQ803856 WHE2842 H CA728920 wdilc.pk0	CW445890 Isbb001f1 BU229997 603947773 CA013161 HT07J07r CF352554 lac30c03.	CA637743 wreln.pk0 BG727965 £p08e03.x AQ293334 HS 2266 BD6231015 BD6231015	DE001557 Branchios CL773304 OR BB2008 CG099060 PHTH.20TD	CN20608 FOILD CN206088 TOF6515 G BU99224 HD09102r	CD893867 G118.124L CG046335 PUIFW42TB BZ274036 CH230-403	CX682423 ydf10h05. BU476293 603471630 BZ510687 BOMQH50TF AG311675 Mus muscu	AG514370 Mus muscu AG442384 Mus muscu DT057597 AGENCOURT	DT060396 AGENCOURT AG429016 Mus muscu	AQ740823 HS 5508 A DT060112 AGENCOURT	CB24/499 UL-M-F10- DT057062 AGENCOURT CV944482 PU014G10	BF254545 HVSME£000 CD303542 AGENCOURT	CZ511376 GMW2-49L8 CZ517024 GMW2-49L8	CA789059 AGENCOURT BF029135 601764643	BE881640 601490060 BISS1640 601490060	BU911794 AGENCOURT BU911794 AGENCOURT BG335613 602404233	BF532081 602073196 CL111503 ISB1-55G5	EL337949 602035776 CL049473 CH216-69P CC276125 CH261-128
17.4 87.0 848 17.4 87.0 891 17.4 87.0 905 17.4 87.0 961	27 17.4 87.0 963 3 28 17.4 87.0 1121 10	17.4 87.0 1134 7 17 85.0 683 10 17 85.0 712 9 17 85.0 751 9	33 16.8 84.0 108 10 34 16.8 84.0 209 6 35 16.8 84.0 210 6	16.8 84.0 351 8 16.8 84.0 363 10 16.8 84.0 370 1	39 16.8 84.0 391 3 40 16.8 84.0 397 3 41 16.8 84.0 412 6	16.8 84.0 427 5 16.8 84.0 444 10	16.8 84.0 475 5 16.8 84.0 484 6	4/ 16.8 84.0 485 10 48 16.8 84.0 514 5 49 16.8 84.0 519 5 50 16.8 84.0 525 6	16.8 84.0 544 6 16.8 84.0 546 2 16.8 84.0 559 9	16.8 84.0 607 11 16.8 84.0 608 10 16.8 84.0 628 10	58 16.8 84.0 632 7 59 16.8 84.0 637 5 60 16 8 84.0 637 5	61 16.8 84.0 656 62 16.8 84.0 661 10 666 9	64 16.8 84.0 673 8 CX682423 C 65 16.8 84.0 678 5 BM476293 66 16.8 84.0 683 9 BZ510687 C 67 16.8 84.0 686 10 AG311675	16.8 84.0 709 10 16.8 84.0 715 10 16.8 84.0 729 8	71 16.8 84.0 735 8 72 16.8 84.0 737 10 73 10	16.8 84.0 756 9 16.8 84.0 763 8	77 16.8 84.0 794 8 78 16.8 84.0 822 8	79 16.8 84.0 829 2 80 16.8 84.0 872 6	16.8 84.0 908 10 16.8 84.0 908 10 16.8 84.0 916 10	84 16.8 84.0 918 6 85 16.8 84.0 919 2	16.8 84.0 935 2 16.8 84.0 935 2	89 16.8 84.0 953 5 90 16.8 84.0 959 2	16.8 84.0 1031 2 16.8 84.0 1032 10	16.8 84.0 10/1 2 16.8 84.0 1097 10 16.8 84.0 1123 9
GenCore version 5.1.7 Copyright (c) 1993 - 2006 Biocceleration Ltd.	OM nucleic - nucleic search, using sw model	Run on: March 9, 2006, 00:12:30 ; Search time 1570.68 Seconds (without alignments) 595.756 Million cell updates/sec	US-10-829-474-2 BCOIE: 20	TY_NUC	Gapop 10.0 , Gapext 1.0 Searched: 41078325 seqs, 23393541228 residues	Total number of hits satisfying chosen parameters: 82156650	Minimum DB seq length: 0 Maximum DB seq length: 2000000000	Post-processing: Minimum Match 0% Maximum Match 100% Listing first 500 summaries	EST:* : gb_est1:* : qb_est2:*	3: 9b_est3:* 4: 9b_htc:* 5: 9b est4:*		0	Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.	de ·	Result No. Score Match Length DB ID  No. Score Match Length DB ID	1 19 95 2 18.4 92	18.4 92.0 962 11 CNSO3BCU AL2363	18.4 92.0 1042 3 BQ056756 BQ056756 18.4 92.0 1230 2 BG752980 BG75298 18 90 924 3 BW356243	9 17.4 87.0 520 9 AZ078930 AZ07893	11 17.4 87.0 682 10 CW718506 CW7185.12 17.4 87.0 689 10 CW682736 CW682731 17.4 87.0 689 10 CW682736 CW682736 CW708162	17.4 87.0 750 7 CP998205 CP647951	17.4 87.0 770 11 CNSO3817 AL222036 17.4 87.0 785 7 CV480587 CV480587 3	.4 87.0 794 2 BG985751 BG985751 .4 87.0 794 7 CV486670 CV486670 CV486670 CV486670 CV48670 CV48	17.4 87.0 819 10

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5.4 77.0 242 1 BB019730 5.4 77.0 244 2 BB443255 5.4 77.0 245 2 BB443255 5.4 77.0 249 1 BB045234 5.4 77.0 262 2 BB403471 5.4 77.0 262 2 BB403471 5.4 77.0 272 1 BB15553 5.4 77.0 272 1 BB15685 5.4 77.0 273 1 BB15685 5.4 77.0 276 2 BB32965 5.4 77.0 276 2 BB32969 5.4 77.0 276 2 BB25692 5.4 77.0 285 2 BB32693 5.4 77.0 287 1 BB036692 5.4 77.0 289 1 BB052897 5.4 77.0 289 1 BB052897 5.4 77.0 299 2 BB326897 5.4 77.0 299 1 BB0569297 5.4 77.0 299 1 BB0569297 5.4 77.0 299 2 BB326663 5.4 77.0 299 1 BB071614 5.4 77.0 310 2 BB326769 5.4 77.0 310 3 BB326769 5.4 77.0 311 3 BM496945 5.4 77.0 319 1 BB071614 5.4 77.0 319 1 BB071614 5.4 77.0 319 1 BB071619 5.4 77.0 325 1 BB33670 5.4 77.0 319 1 BB071619 5.4 77.0 326 1 BB33670 5.4 77.0 319 1 BB071619 5.4 77.0 326 1 BB33670 5.4 77.0 319 1 BB071619 5.4 77.0 310 2 BB071619 5.4 77.0 2 20.0 2000 5.5 20.0 2000 5.5 20.0 2000 5.5 20.0 2000 5.5 20.0 2000 5.5 20.0 2000 5.5 20.0 2000 5.5 20.0 2000 5.5 20.0 2000 5.5 20.0 2000 5.5 20.0 2000 5.5 20.0 2000 5.5 20.0 2000 5.5 20.0 2000 5.5 20.0 2000 5.5 2000 5.5 2000 5.5 2000 5.5 2000 5.5 2000 5.5 2000 5.5 200	weill, Brottier, P. in, J. P., Weill, D., Brottier, P. in, J. P., Weissenbach, J. and racted cDNA library from tile incomment of the control
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510 AAGGAAACACGGAAACCCAA 491
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HTC; cDNA; full-length;
Tetraodon nigroviridis
Tetraodon nigroviridis
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CNSOFP9W/c
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5', mRNA sequence.
CK751666
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Site_2: Xhol; This is a directionally cloned,
non-normalized library. This library has been generated by
the Floral Genome Project (FGP). The Floral Genome Project
is funded by NSF's Plant Genome Research Program
(DBI-0115684). More information about the project can be
obtained at http://fgp.bio.psu.edu"
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208 Mueller Laboratory, Department of Biology, ATTN Rm212, Penn
State University, University Park, PA 16802, USA
Tel: 814 863 6413
Fax: 814 865 9131
Email: cwd3@psu.edu or jhl10@psu.edu
The sequence provided is trimmed of vector and low quality regions.
The sequence and original trace file are available from the Plant
Genome Network website (http://pgn.cornell.edu)
Plate: atr02-9ms1 row: b column: 08
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Spermatophyta, Magnoliophyta, basal Magnoliophyta, Amborellales,
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/clone="BNOAA100ZB08"
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dePamphilis, C., Carlson, J., Ma, H., Soltis, D., Soltis, P.,
Oppenheimer, D., Frohlich, M., Doyle, J., Tanksley, S., Webb, M.,
Leebens, Mack, J., Landherr, L., Ilut, D. and Wall, K.
Generation of ESTs from early female flower buds of Amborella
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                                                                                                                                                    95.0%; Score 19; DB 1; Length 603; 100.0%; Pred. No. 2.6e+02; ive 0; Mismatches 0; Indels
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Unpublished (2003)
Contect: Claude dePamphilis or James Leebens-Mack
Mueller Laboratory
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/tissue_type="female flower buds"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Amborella trichopoda"
                                                                                                /note="subtracted cDNA library"
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/lab_host="SOLR"
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Jaillon, O., Aury, J.M., Brunet, F., Petit, J.L., Stange-Thomann, N., Maucell, E., Bouneau, L., Fischer, C., Ozouf-Costaz, C., Bernot, A., Nicad, S., Jaffe, D., Fisher, S., Lutfalla, G., Dossat, C., Squrens, B., Dasfley, C., Salanoubat, M., Levy, M., Boudet, N., Castellano, S., Anthouard, V., Jubin, C., Castelli, V., Katinka, M., Vacherie, B., Biemont, C., Skalli, Z., Cattolico, L., Poulain, J., De Berardinis, V., Cruaud, C., Dupratt, S., Brottler, P., Coutanceau, J.P., Gouzy, J., Parra, G., Lardier, G., Chapple, C., McKernan, K.J., McEwan, P., Bosak, S., Kellis, M., Volff, J.N., Guigo, R., Zody, M.C., Robinson-Rechari, M., Lauder, G., Chachter, V., Quetier, F., Saurin, W., Scarpelli, C., Wincker, P., Lander, E.S., Weissenbach, J. and Roest Crollius, H.
Genome duplication in the teleost fish Tetraodon nigroviridis reveals the early vertebrate proto-karyotype
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                                                                                                   CR682120.2 GI:56281159
HTC; cDNA; full-length; full-length cDNA; Tetraodon nigroviridis.
Tetraodon nigroviridis
Tetraodon nigroviridis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthomorpha; Acanthomorpha; Acanthomorpha; Acanthomorpha; Tetraodontidea; Tetraodontiformes;
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95.0%; Pred. No. 5.2e+02;
iive 0; Mismatches 1;
CNSOFP9W 845 bp mRNA Tetraodon nigroviridis full-length cDNA.
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Janes Carollius, H.
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sctinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetradontoidea; Tetraodontidae; Tetraodon.
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetradontoidea; Tetraodontidae; Tetraodon.
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Submitted (24-NOV-2004) Genoscope - Centre National de Sequencage
La rue Gaston Cremieux, CP 5706 - 91057 BYRX cedex - FRANCE
(E-mail : seqrefégenoscope.cns.fr - Web : www.genoscope.cns.fr)
On Dec 3, 2004 this sequence version replaced gi:51187879.
The sequences are based on single pass reads.
More information available at
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Estimate of human gene number provided by genome-wide analysis using Tetraodon nigroviridis DNA sequence
Nat. Genet. 25 (2), 235-238 (2000)
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95.0%; Pred. No. 5.2e+02;
live 0; Mismatches 1
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Location/Qualifiers
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Tetraodon nigroviridis
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Submitted (12-APR-2000) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
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Roest Crollius, H., Jaillon, O., Dasilva, C., Ozouf-Costaz, C., Fizames, C., Fischer, C., Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and Weissenbach, J. Characterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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Tissue Procurement: Lou Staudt
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.B. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.B. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2054 row: g column: 09
High quality sequence stop: 587.
Location/Qualifiers
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1 (bases 1 to 1042)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)

Contact: Robert Strausberg, Ph.D.
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/organism="Tetraodon nigroviridis"
/mol Lype="genomic DNA"
/mol Lype="genomic DNA"
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/clone="lb="G"
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/clone="IMAGE:5809184"
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Pred. No. 5.3e+02;
0; Mismatches 1;
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Best Local Similarity 95.0%;
Matches 19; Conservative
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arboreum cDNA clone GA_Ea0018E15r, mRNA sequence.
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Wing,R.A., Frisch,D., Yu,Y., Main,D., Rambo,T., Simmons,J.,
Henry,D., Wood,T.C., Leslie,A. and Wilkins,T.A.
An integrated analysis of the genetics, development, and evolution
of the cotton fiber
Unpublished (2000)
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Stainopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
1 (bases 1 to 458)
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ZF001-P00027-DPB-F-D E08 GISZF001 Danio rerio cDNA clone
IMAGE:6901841 5' simīlar to (NM_002231) kangai 1, mRNA sequence.
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/note="Vector: pBK-CMV; Site_l: EcoRI; Site_2: XhoI"
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100.0%; Pred. No. 8.2e+02;
ive 0; Mismatches 0;
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Clembon University
100 Jordan Hall, Clemson, SC 29634, USA
Trel: 864 656 7288
Fax: 864 656 4293
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/organism="Gossypium arboreum"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: rwing@clemson.edu
Total High Quality bases = 150
Seg primer: TAATACGACTCACTATAGGG
High quality sequence start: 4
High quality sequence etcp: 900.
Location/Qualifiers
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             /mol_type="mRNA"
/strain="AKA"
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BM359242.1 GI:18099988
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//ub_xref="taxon:9606"
/db_xref="taxon:9606"
/dlone=TMAGE:4876160"
/tissue_type="normal pigmented retinal epithelium"
/tissue_type="normal pigmented retinal epithelium"
/tissue_type="normal pigmented retinal epithelium"
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/clone lib="NIH MGC 43"
/note="Organ: eye; "dector: pOTB7; Site 1: XhoI; Site 2:
/note="Organ: eye; "dector: pOTB7; Site 1: XhoI; Site 2:
/note="Organ: eye; "dector: pOTB7; Site 1: XhoI; Site 2:
/note="Organ: eye; "dector: poTB7; Site 1: XhoI; Site 2:
/note="Organ: eye; "dector: poTB7; Site 1: XhoI; Site 2:
/note="Organ: eye; "dector: poTB7; Site 1: XhoI; Site 2:
/note="Organ: eye; "dector: poTB7; Site 1: XhoI; Site 2:
/note="Organ: eye; "dector: poTB7; "dectionally constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of Garald M. Rubin (University of Garald M. Rubin: University of Garald M. Rubin: (University of Garald M. Rubin:
/clone_lib="NIH MGC_99"
/note="Organ: lymph, Vector; pOTB7; Site_1: XhoI; Site_2:
ENCRI; CNDA made by Oligo-dr priming. Directionally cloned
into EncRIXhol sites using the following 5' adaptor:
GGCACGAG(G). Size-selected >500bp for average insert size
I.8kb. Library constructed by Ling Hong in the laboratory
of Gerald M. Rubin (University of California, Berkeley)
using ZAP-CDNA synthesis kt (Stratagene) and Superscript
II.RT (Life Technologies). Note: this is a NIH_MGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BG752980 1230 bp mRNA linear BST 15-MAY-2001 602732438F1 NIH_MGC_43 Homo sapiens cDNA clone IMAGE:4876160 5',
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S NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs.remail.nih.gov
Tissue Procurement: ArCC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Preparation: Ling Hong/Rubin niformation can be home through the I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MCC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Rolumn: 09
High quality sequence start: 23
High quality sequence stop: 98.

1. 1230
Location/Qualifiers
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Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
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Homo sapiens
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/lab host="DHIOB"
/clone lib="RPCI-23"
/note="Corgan: Kidney/Brain; Vector: pBACe3.6; Site_1:
/note="Corgan: Kidney/Brain; Vector: pBACe3.6; Site_1:
ECORI; Site_2: ECORI; Female C57BL/6J mouse kidney and/or brain genomic DNA was isolated and partially digested with a combination of EcoRI and ECORI methylase. Size selected DNA was cloned into the pBACe3.6 vector at the ECORI sites. The ligation products were transformed into DH10B electrocompetent cells (BRL Life Technologies). "
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Single pass sequencing. Bases called with phred v0.020425.c and
trimmed with the aid of the trim_alt option. Vector identified with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pecora; Bovidae; Bovinae; Bos.
I (bases 1 to 682)
Smith, T.P.L., Stone, R.T., Keele, J.W., Snelling, W.M. and Harhay, G.P. SwP discovery in cattle based on low coverage sequencing of BAC
                                                                                                                                                                            Clones are derived from the mouse BAC library RPCI-23. For BAC library availability, please contact Pieter de Jong (pieterdebjong.med.buffalo.edu. Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm) or from Resea ch Genetics (info@resgen.com). BAC end page: http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html Plate: 410 row: F column: 20 Seq primer: T7 Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CW718506 682 bp DNA linear GSS 05-NOV-2004
MARC_1010385 CHORI-240-397C5 Bos taurus genomic clone 1C6, genomic
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Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          87.0%; Score 17.4; DB 9; Length 520; 94.7%; Pred. No. 1.5e+03; ive 0; Mismatches 1; Indels (
                     Department of Eukaryotic Genomics
The Institute for Genomic Research
7712 Medical Center Dr., Rockville, MD 20850, USA
771: 301 838 0200
Fax: 301 838 0208
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Fax: 402 762 4390
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Seg primer: GTAATACGACTCACTATAGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="taxcn:10090"
/clone="RPCI-23-410F20"
/sex="Female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /mol_type="genomic DNA"
/strain="C57BL/6J"
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Contact: Smith TPL
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                                                                                                                                                            Email: szhao@tigr.org
       Contact: Shaying Zhao
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Best Local Similarity 94.79
Matches 18; Conservative
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Unpublished (2004)
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CW718506/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /dlone lib="GISZF001"
//dlone lib="GISZF001"
//orde="Vector: pDNR-LIB; Site_1: Sfi A (GGCCATTACGGCC);
Site_2: Sfi B (GGCGCTCGGCC); Priming method: Sfi-(dT)30
Primed; Priming sequence: 5.ATTCTAGA GGCCGAGGCGCC
GACATG(T)30VN; Directionally cloned, 5. cloning site:
Sfi A site GGCCATTACGGCC; 5. linker/adaptor sequence:
5.AAGCAGTGCTATCAACGAGAGTGGCC; 3. cloning site: Sfi B
site GGCCCTCGGCC; 3. linker/adaptor sequence: same
as the priming sequence; Average insert size: Zkb; For
PCR insert analysis: Use M13 Forward and reverse primers;
Library Amplified Recombinants (inserts): 98%; Library
complexity: 5x106; Full-length construction (method):
SMART, a Clontech method; Library constructed by: S.
Mathavan, Chia-Lin Wei, and Yijun Ruan Genome Institute of
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Zhao,S., Nierman,W., Peldblyum,T., Malek,J., Shatsman,S., Akinret,B., Levins,M., Mcgann,S., Tsegaye,G., Geer,K., Krol,M., de Monge BAC End Sequences from Library RPCI-23 Unpublished (1999)
Other_GSSs: RPCI-23-410F20.TJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /tissue_type="Embryo"
/dev stage="7 Different embryonic Stages( From just
fertilized Embryos to 72 hours just hatched baby fish)"
/lab_host="DH10B"
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Mathavan, S., Wei, C., Thoreau, H., Chia, J.M. and Ruan, Y. Genome Institute of Singapore, Zebrafish EST Collection Unpublished (2003)
Contact: Ruan Y
Cloning and Sequencing
Genome Institute of Singapore
Genome Institute of Singapore
60 Biopolis Street, #02-01, Genome, Singapore 138672
Tel: +65 6478 8073
Email: ruanyj@gis.a-star.edu.sg
GIS Clone ID: ZP001-P00027-PP_J16
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BACKWARD: M13
Plate: ZF001-P00027-DPE-F-D
Seq primer: CCGCATAACTTGTATAGCA
High quality sequence stop: 458.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'organism="Danio rerio"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /mol_type="mRNA"
/db_xref="taxon:7955"
/clone="IMAGE:6901841"
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Gaps ò GSS 05-NOV-2004

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/clone lib="NHT ZGC 7"
/clone lib="NHT ZGC 7"
/clone lib="WHT ZGC 7"
/clone lib="WHT ZGC 7"

Bulk tissue was collected from a whole adult individual
from the Tuebingen strain. 1st strand cDNA was primed with
a Not I - oligo(dT) primer, double-stranded cDNA was
cloned into the Not I and EcoRV sites of pExpress-1.
Library was size-selected for >1 kb fragments and
normalized. A non-normalized version of this library is
also available (NIH ZGC 10). Library was constructed by
Open Biosystems (Huntsville, AL)"
                                                                                                                                 AGENCOURT_16626291 NIH_ZGC_7 Danio rerio cDNA clone IMAGE:7052495
5', mRNA sequence.
CK029165
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                                                                                                                                                                                                                                                                                                                      Danio rerio
banio rerio
Mukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
1 (bases 1 to 717)
Nat-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CDNA Library Preparation: Open Biosystems
CDNA Library Arrayed by: The I.M.A.G.B. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.B. Consortium/LLNL at:
http://mage.llnl.gov
Plate: LLAM14826 row: k column: 21
High quality sequence stop: 686.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          oupunished (1999)
Contact: Daniela S. Gerhard, Ph.D. Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 RM10A07 Betheada, MD 20892
Bmail: cgapbs r@mail.nih.gov
Tissue Procurement: Len Zon, Harvard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /tissue_type="whole body"
/lab_host="DH108"
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/organism="Danio rerio"
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/db_xref="taxon:7955"
/clone="IMAGE:7052495"
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         1 AAGGAAACACGGACACCCA 19
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                                                                                                                                                                                                                                                       CK028165.1 GI:38554089
                                                                                                                                                                                                                                                                                                   Danio rerio (zebrafish)
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AG479585.1 C
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AG479585/c
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OG_BBa0039K22 r OG_BBa Oryza glaberrima genomic clone OG_BBa0039K22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /tissue type="young leaves"
/lab_host="DH10B T1 phage resistant"
/clone lib="0G BBa"
/note="Vector: pAGIBAC1; Site_1: HindIII; Site_2: HindIII"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopaida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.

Ehrhartoideae; Oryzeae; Oryza.

I (bases 1 to 689)

Kim, H., VY., Wissotski, M., Byrne, M., Stum, D., Smart, D., Rao, K., Luo, M., Jetty, R., Kudrna, D., Muller, C., Hatfield, J., Soderlund, C. and Wing, R.
                                                                                                                                                                             /tissue_type="Blood"
/clone_lib="CHORI-240-397C5"
/note="Vector: pBLUESCRIPT SK-; Site_1: BamH1; Site_2: BamH1; BAC DNA was digested with Sau3A. Fragments Werr Sketted to 800-1200 bases and subcloned into pBLUESCRIPT SK-.
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                                                                                                                                                                                                                                                                                                                                                                  Length 682;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Rod A. Wing
Arizona Genomics Institute
University of Arizona
Tel: 520 626 9595
Fax: 520 621 1259
                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                         Query Match 87.0%; Score 17.4; DB 10; Best Local Similarity 94.7%; Pred. No. 1.5e+03; Matches 18; Conservative 0; Mismatches 1;
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BACKWARD: CAC TCA TTA GGC ACC CCA
Plate: 0039 row: K column: 22
Seg primer: CAC TCA TTA GGC ACC CCA
Class: BAC ends.
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db_xref="taxon:4538"
clone="OG_BBa0039K22"
                                                                                     /mol_type="genomic DNA"
/db_xref="taxon:9913"
                                                                   organism="Bos taurus"
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Oryza glaberrima
                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3', genomic survey sequence.
CW682736
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                                                                                                                                   /clone="1C6"
/sex="Male"
Class: BAC subclone.
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                                                . .682
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Gaps

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1. .750
/organism="Danio rerio"
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S Hattori, M., Toyoda, A., Noguchi, H., Kojima, T. and Sakaki, Y.

Direct Submission

Submitted (17-NOV-2003) Massahira Hattori, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);

1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa, 230-0045, Japan
(R-mall:hattoriegsc.riken.jp, URL:http://hgp.gsc.riken.go.jp/,
Tel:81-45-503-9111, Fax:81-45-503-9170)

Clones are derived from the mouse BAC library MSMg01. For BAC
library availability, please contect Kuniya Abe (abe@rtc.riken.jp).
Tsukuba Institute for Physical and Chemical Research (RIKEN) 3-1-1

Koyadai, Tsukuba, 305-0074 Japan

Phone: 81-298-36-9189, fax: 81-298-36-9199
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AGENCOURT 16393924 NIH_ZGC_7 Danio rerio cDNA clone IMAGE:7038534
5', mENA Fequence.
CF9998205
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                                                                                                                            Abe,K., Noguchi,H., Tagawa,K., Yuzuriha,M., Toyoda,A., Kojima,T., Ezawa,K., Saitou,N., Hattori,M., Sakaki,Y., Moriwaki,K. and Shiroishi,T.
Contribution of Asian mouse subspecies Mus musculus molossinus to genomic constitution of strain C57BL/6J, as defined by BAC-end sequence-SNP analysis
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1 (bases 1 to 750)

11 (bases 1 to 750)

12 (bases 1 to 750)

Nati-MCC http://mcc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)
                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
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Pred. No. 1.6e+03;
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/clone_lib="MSMg01 Mouse Male BAC Library"
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musculus molossinus (Japanese wild mouse) musculus molossinus
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                                                                                        Sciurognathi; Muridae; Murinae; Mus.
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/sub_species="molossinus"
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94.7%;
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Best Local Similarity 94.7
Matches 18; Conservative
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/mol type="mRNA"
// (db xref="taxon:7955"
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// (clone="INAGE:7038534"
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// (clone="lb="NHT ZGC_7"
// (note="Vector: pExpress]; Site_1: NotI; Site_2: EcoRV;
// (note="Vector: pExpress]
// (note="Vector: pExpr
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Tetraodon nigroviridis genome survey sequence PUC-Ori end of clone
004G16 of library G from Tetraodon nigroviridis, genomic survey
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AL232036.1 GI:7891040
GSS; genome survey sequence.
Tetraodon nigroviridis
Tetraodon nigroviridis
Tetraodon nigroviridis
Tetraodon nigroviridis
Antaryota: Metacada; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Buteleostei; Acanthomorpha; Acanthomorpha; Acanthomorpha; Acanthomorpha; Tetraodontiformes;
Tetradontoidea; Tetraodontidae; Tetraodon.
Contact: Daniela S. Gerhard, Ph.D.

Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rml0A07 Betheada, MD 20892
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Len Zon, Harvard
CDNA Library Preparation: Open Biosystems
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM1790 row: f column: 04
High quality sequence stop: 698.
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Nat. Genet. 25 (2), 235-238 (2000)
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Similarity 9
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                                                                          Submitted (12-APR-2000) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr The Sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
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AGENCOURT 33240879 NIH_ZGC_19 Danio rerio cDNA clone IMAGE:7452402
31, mRNA Fequence.
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Contact: Daniela S. Gerhard, Ph.D.

Office of Cancer Genomics
National Cancer Institute / NIH

Bldg. 31 Rm10A07 Bethesda, MD 20892

Email: Gapbs.remail.nih.gov
Tissue Procurement: William S. Talbot, Stanford University
CDNA Library Preparation: Dr. Sundo Sugno
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAMIS709 row: j column: 16
High quality sequence start: 8
High quality sequence statt: 8
High quality sequence statt: 8
High quality sequence statt: 6
Location/Qualifiers
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Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
1 (Dases 1 to 785)
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/lab_host="DH10B TonA"
/clone lib="NIH ZGC 19"
/note="Organ: mixed; Vector: pME188-FL3; Site_1: DraIII;
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National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                          /organism="Tetracdon nigroviridis"
/mol_type="genomic DNA"
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/clone="004G16"
/clone="1b="G"
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end : PUC-Ori"
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Pred. No. 1.6e+03;
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94.7%;
                      (bases 1 to 770)
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Best Local Similarity 94.7
Matches 18; Conservative
                                         Genoscope.
Direct Submission
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BG985751 13-JUN-2001 2867 NICHD_Zebrafish_normalized_I Danio rerio cDNA clone 2867, mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /dev stage="bud to 10 somite stage embryos"
/clone lib="NICHD Zebrafish normalized I"
/note="Vector: pBluescript KS+; Site 1: Not1; Site 2:
Sal1; RNA was reverse-transcribed to first strand cDNA
using SuperScriptII reverse-transcriptase and tagged
oligo-dT primer which contains several restriction sites
including a Not1 site:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gactagttctagatcgcgatcgcgaGCGGCCGCcttttttttttttt. Second
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1 (bases 1 to 794)

Kudoh,T., Tsang,M., Hukriede,N.A., Chen,X., Dedekian,M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Concact: Dawid IB
Laboratory of Molecular Genetics
National Institute of Child Health and Human Development, NIH
Bldg.6B, Room 413, 9000 Rockville Pike, Bethesda, MD 20892 USA
Tel: 301 496 4448
                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
DraIII; 1st strand cDNA was primed with an
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Genome Res. 11 (12), 1979-1987 (2001)
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/db_xref="taxon:7955"
/clone="2867"
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94.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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SOURCE

REFERENCE AUTHORS TITLE JOURNAL COMMENT

ACCESSION VERSION KEYWORDS

CV486670/c DEFINITION

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EMERATYOETS CHORDERS Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.

Cypriniformes; Cyprinidae; Danio.

I (bases 1 to 798)

NH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

National Institute of Health, Mammalian Gene Collection (MGC)

Office of Cancer Genomics

National Cancer Institute / NIH

Bud; 31 RANJOAD7 Betheeda, MD 20892

Email: cgapbs-rômail.nih.gov

Tissue Procurement: Len Zon, Harvard

CDNA Library Preparation: Open Biosystems

CDNA Library Arrayed by: The I M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Llocation/Qualifiers

STANDARS CONSORTIUM (LINL)

High quality sequence stop: 720.

High quality sequence stop: 720.
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/clone lib="NIH ZGC 7"
/note="Vector: pExpress1; Site_1: NotI; Site_2: EccRV;
Inote="Wector: pExpress1; Site_1: NotI; Site_2: EccRV;
Bulk tissue was collected from a whole adult individual
from the Tuebingen strain. 1st strand cDNA was primed with
a Not I - oligo(dT) primer, double-stranded cDNA was
cloned into the Not I and EccRV sites of pExpress-1.
Library was size-selected for >1 kb fragments and
normalized. A non-normalized version of this library is
also available (NIH ZGC 10). Library was constructed by
Open Biosystems (Huntsville, AL)"
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AGENCOURT_32003381 NIH_ZGC_17 Danio rerio cDNA clone IMAGE:7416843
S', mRNA Sequence.
CV126404
                                                                                  CK026895 198 bp mRNA linear EST 26-NOV-2003
AGENCOURT_16619433 NIH_ZGC_7 Danio rerio cDNA clone IMAGE:7054646
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Danio rerio
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /mol_type="mRNA"
/db_xref="taxon.7955"
/clone="IMAGE:7054646"
/tissue_type="whole body"
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Danio rerio"
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Matches 18; Conserva
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                                        RESULT 20
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AGENCOURT_33240863 NIH_ZGC_19 Danio rerio cDNA clone IMAGE:7452401
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NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Daniela S. Gerhard, Ph.D.
Contact: Daniela S. Gerhard, Ph.D.
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 RanloAo7 Berheada, MD 20892
Email: cgapbs-remail.nih.gov
Tissue Procurement: William S. Talbot, Stanford University
cDNA Library Preparation: Dr. Sund. Sugano
cDNA Library Preparation: Dr. Sund. Sugano
cDNA Library Preparation: McC. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MCC.clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM15709 row: j column: 15
High quality sequence start: 6
Incation/Qualifiers
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                 Length 794;
                                                              1; Indels
               Score 17.4; DB 2;
Pred. No. 1.6e+03;
0; Mismatches 1;
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Danio rerio
               87.0%;
94.7%;
Query Match
Best Local Similarity 94.77
Marches 18; Conservative
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/clone="IMAGE:7289204"
      Smith TPL
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         Contact:
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1 (bases 1 to 819)
Smith,T.P.L., Stone,R.T., Keele,J.W., Snelling,W.M. and Harhay,G.P. SNP discovery in cattle based on low coverage sequencing of BAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone="IMAGE:7416843"
/tissue_type="Dissected hearts form 100 Zebrafish samples were pooled"
/lab host="DH108 TonA"
/clone_lib="NHH ZGC_17"
/note="Organ: heart; Vector: pME18S-FL3; Site_1: DraIII; Site_2: DraIII; lst strand cDNA was primed with an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     [GGGGCTGAAGACGGCCTATGTTTTTTTTTTTTTT];
double-stranded cDNA was ligated to a DrallI adaptor
[GGCUNACUGG], digested and directionally cloned into
distinct DrallI sites of the pME18S-FL3. Library was size
selected for 1.0 kb, with a average insert size of ~1.2kb.
Library constructed by Yutaka Suzuki (University of Tokyo
Institute of Medical Science). Custom primers recommended
for sequencing: 5' end primer 5'-GGATGTTGCCTTAACTTCTA-3'
and 3' end primer 5'-CGACTGCAGCTCGAGCAA-3'. Note: This
is a Zebrafish Gene Collection (ZGC) library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GSS 05-NOV-2004
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MARC_1009233 CHORI-240-397C5 Bos taurus genomic clone 1C6, genomic
Survey sequence.
CW117728
                                                                                                   Contact: Daniela 1239, Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 RmloAOV Bethesda, MD 20892
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Will Talbot
CDNA Library Arrayed by: The I.M.A.G.B. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information and bettp://image.llnl.gov
Rttp://image.llnl.gov
Rians. Consortium/LLNL at:
High quality sequence start: 16
High quality sequence start: 16
High quality sequence stop: 728.
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(LLNL)
                                         NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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Cypriniformes; Cyprinidae; Danio. (bases 1 to 800)
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'db_xref="taxon:7955"
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Other_GSSs: MARC_1010385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 AAGGAAACACGGACACCCA 19
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Best Local Similarity 94.7%;
Matches 18; Conservative
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CW717728
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Rukaryota; Meopterygii; Teleostei; Ostariophysi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cyptiniformes; Cyprinidae; Danio.

I (bases 1 to 848)
S NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)
L Unpublished (1999)
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg: 31 Rm10A07 Bethesda, ND 20892
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: John Ngai, Univ of CA, Berkeley
                                                                                                   Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called with phred v0.020425.c and
trimmed with the aid of the trim_alt option. Vector identified with
cross match v0.990329.
Seq primer: AATTAACCCTCACTAAAGGG
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5', mRNA Sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                             /tissue_type="Blood"
/clone_lib="CHORL-240-197C5"
/note="Vector: pBLUBSCRIPT SK-; Site_l: BamHI; Site_2:
BamHI; BAC DNA was digested with Sau3A. Fragments were
sized to 800-1200 bases and subcloned into pBLUBSCRIPT
SK-.
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Plate: LLAM15301 row: f column: 18
High quality sequence start: 21
High quality sequence stop: 656.
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USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
TE1: 402 762 4366
Fax: 402 762 4390
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Pred. No. 1.6e+03;
0; Mismatches 1;
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/db_xref="taxon:9913"
/clone="1C6"
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                                                                                                                                                                                                                                                                                                                                 /organism="Bos taurus"
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Best Local Similarity 94.7
Matches 18; Conservative
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/sex="Male"
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                                                                          Bos taurus (cow)
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Matches 18; Conserv
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CK412195/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called with phred v0.020425.c and
trimmed with the aid of the trim_alt option. Vector identified with
cross_match v0.990329.
Seq primer: GTAATACGACTCACTATAGGG
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1 (bases 1 to 891)
Smith, T.P.L., Stone, R.T., Keele, J.W., Snelling, W.M. and Harhay, G.P. SNP discovery in cattle based on low coverage sequencing of BAC
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                                                                                                                                                                                                                                                                                                          GSS 05-NOV-2004
                                                                                                                                                                                                                                                                                                        CW718544 891 bp DNA linear GSS 05-NOV-2004
MARC_1010456 CHORI-240-397C5 Bos taurus genomic clone 1F5, genomic
Surrey sequence.
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/clone_lib="CHORL-240-397CS"
/note="Vector: pBLUESCRIPT SK-; Site_1: BamH1; Site_2:
|BamH1; BAC DNA was digested with Sau3A. Fragments were
sized to 800-1200 bases and subcloned into pBLUESCRIPT
SK-.
                                                                                                                                              Gaps
/lab_host="DH10B TonA"
/clone_lib="NIH_ZGC 4"
/note="Organ: brain/CNS; Vector: pME18S-FL3; Site_l:
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                                                                                                       Length 848;
                                                                                                                                            Indels
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PO Box 166, Clay Center, NE 68933-0166, USA
TEL: 402 762 4366
Fax: 402 762 4390
                                                                                                           DB 7;
                                                                                                         Query Match 87.0%; Score 17.4; DB 7; Best Local Similarity 94.7%; Pred. No. 1.6e+03; Matches 18; Conservative 0; Mismatches 1
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/db_xref="taxon:9913"
                                                     Dralli, Site 2: Dralli
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                                                                                                                                                                                                                 218 AAGGAAACACGGACACTCA 236
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (2004)
Other GSSs: MARC 1009304
Contact: Smith TPL
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CW718544/c
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Single pass sequencing. Bases called with phred v0.020425.c and trimmed with the aid of the trim_alt option. Vector identified with cross match v0.990329.
Seq primer: AATTAACCCTCACTAAAGGG Class: BAC subclone.
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Contact: Liu ZJ
The Fish Molecular Genetics and Biotechnology Laboratory, Department of Fisheries and Allied Aquacultures and Program of Cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CK412195

40F IpHdk 47 p20 Head kidney cDNA library Ictalurus punctatus cDNA 5' similar to Autosomal Highly Conserved Protein, mRNA sequence.
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Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Siluriformes;
Ictaluridae; Ictalurus.
                                                                                                                                                                                                                                              Smith, T.P.L., Stone, R.T., Keele, J.W., Snelling, W.M. and Harhay, G.P. SNP discovery in cattle based on low coverage sequencing of BAC
                                                                                                                Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
Pecora; Bovidae; Bovinae; Bos.
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/clone_lib="CHORI-240-397C5"
/note="Vector: pBLUESCRIPT SK-; Site_l: BamHI; Site_2:
BamHI; BAC DNA was digested with Sau3A. Fragments were
sized to 800-1200 bases and subcloned into pBLUESCRIPT
SK-.
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PO Box 166, Clay Center, NE 68933-0166, USA
TTE1: 402 762 48390
Fax: 402 762 4390
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94.7%; Pred. No. 1.6e+03;
iive 0; Mismatches 1;
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Ictalurus punctatus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /mol_type="genomic DNA"
/db_xref="taxon:9913"
/clone="1F5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: smith@email.marc.usda.gov
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                                                                                                                                                                                                                                                                                                                                        Unpublished (2004)
Other GSSs: MARC 1010456
Contact: Smith TPL
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CW717765.1 GI:55421475
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us-10-829-474-2.rst

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Unpublished (1999)
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Matches 18; Conserv
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                                                                                                                                       /organism="Ictalurus punctatus"
/mol type="mRNA"
/db Xref="taxon:7998"
/db Xref="taxon:7998"
/clone lib="flead kidney cDNA library"
/note="Organ: Head kidney; Vector: pSportl; Site_1: Notl; Site_2: Sall"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EST 28-JAN-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 (bases 1 to 963)
Mixed.J., Sosinski,B., Pokrzywa,R.M., Warry,A. and Opperman,C.
Mixed Stage EST's from Globodera pallida, the potato cyst nematode
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bukaryota, Metazoa, Nematoda, Chromadorea, Tylenchida, Tylenchina,
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                              203 Swingle Hall, Auburn University, Auburn, AL 36849, USA Tel: 334 844 4054
Fax: 334 844 9208
Email: zlu@acesag.auburn.edu
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                                                                                                                                                                                                                                                                                                87.0%; Score 17.4; DB 7; Length 961; 94.7%; Pred. No. 1.6e+03; ive 0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OP21060 Mixed Stage BST's from Globodera pallide nematode Globodera pallida cDNA, mRNA sequence.
BM415978
BM415978.1 GI:18382777
EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Opperman, C
Center for the Biology of Nematode Parasitism
NC State University; IACR-Rothamsted
Campus Box 7616; Raleigh, NC 27695, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Globodera pallida"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: warthogounity.ncsu.edu
GT11-9PCN F A05_GT11-9 F 033.ab1.
Location/Qualifiers
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/db_xref="taxon:36090"
                                                                                                     Seq primer: T7.
Location/Qualifiers
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and Molecular Biosciences
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                Auburn University
                                                                                                                                                                                                                                                                                                                                    18; Conservative
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Globodera pallida
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Fax: 919.515.9500
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Best Local Similarity
Matches 18; Conserv
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Best Local S
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Matches
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AUTHORS
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BM415978
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Srinivasan, J., Sinz, W., Jesse, T., Wiggers-Perebolte, L., Jansen, K., Buntjer, J., van der Meulen, M. and Sommer, R.J. An integrated physical and genetic map of the nematode Pristionchus
CG745203 1121 bp DNA linear GSS 24-OCT-2003
P038-1-B12.ya Ppa EcoRI BAC Library Pristionchus pacificus genomic,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AGENCOURT 16624073 NIH_ZGC_7 Danio rerio cDNA clone IMAGE:7053855 CK027487
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1 (bases 1 to 1134)
NIH-MGC http://mgc.nci.nih.gov/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db xref="taxon:54126"
/clone_lib="tpp EcoR! BAC Library"
/note="The library was generated by a partial digest
the genomic DNA with EcoR! and cloning into the BAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gapa
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Neodiplogasteridae; Pristionchus.
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CDNA Library Arrayed by: The I.M.A.G.B. Consortium (LLNL)
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Max-Planck-Institute for Developmental Biology
Spemanustr. 37-39, Tuebingen D-72076, Germany
Tal: 00497071601371
Fax: 00497071601498
Email: ralf.sommer@tuebingen.mpg.de
                                                                                                                                                                                                                                                                                                                                                                                                                   Genet. Genomics 269 (5), 715-722 (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Pristionchus pacificus"
/mol type="genomic DNA"
/strain="California"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    87.0%; Score 17.4; DB 10;
ilarity 94.7%; Pred. No. 1.6e+03;
Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Daniels S. Gerhard, Ph.D. Office of Cancer Genomics National Cancer Institute / NIH Bldg. 31 Rm10A07 Bethesda, MD 20892 Email: cgapbs r@mail.nih.gov Tissue Procurement: Len Zon, Harvard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Class: BAC ends.
Location/Qualifiers
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                                                      genomic survey sequence.
                                                                                                          CG745203.1 GI:37966129
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Pristionchus pacificus
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us-10-829-474-2.rst

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DNA linear GSS 19-FEB-2002 BOMIZ27TF BO_2_3 KB Brassica oleracea genomic clone BOMIZ27, genomic survey sequence.
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//clone lib="Wector: pOTw13; Whole genome shotgun library from Inote="Wector: pOTw13; Whole genome shotgun library from flowering buds. DNA was purified from a crude nuclear prep using Brassica oleracea TO1000DH3 buds provided by Thosmas Osborn at the University of Wisconsin. Genomic DNA was provided by Pablo Rabinowicz (CSHL) and the shotgun library prepared at Washington University Genome Sequencing Center.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Brassica oleracea
Brastycia, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicotyledons,
rosids, eurosids II, Brassicales, Brassicaceae, Brassica.
                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 (bases 1 to 712)
Delehaunty,K., Fewell,G., Fulton,L., McCombie,W.R., Miner,T.,
Nash,W., Rabinowicz,P.D. and Wilson,R.K.
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                                                                       Length 683;
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                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Whole genome shotgun reads from Brassica oleracea Unpublished (2002)
                                                                         Score 17; DB 10; I
Pred. No. 2.4e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genome Sequencing Center
Washington University School of Medicine
Email: submissions@watson.wustl.edu
Plate: oeh04 row: a column: 08
Seq primer: -21UPpOT forward
Class: shotgun

    .712
    /organism="Brassica oleracea"

                                                                     11 Score 17; DB 11 Score 17; DB 11 Score 17; DB 100.0%; Pred. No. 2.4 Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /mol_type="genomic DNA"
/db_xref="taxon:3712"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          High quality sequence start: 28
High quality sequence stop: 551.
Location/Qualifiers
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                                                                                                                                                                    3 GGAAACACGGACACCCA 19
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Brassica oleracea
       HindIII"
                                                                                        Local Similarity
les 17; Conserv
                                                                                                                                                                                                                                                                                                                                                                              sequence.
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                                                                         Query Match
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BH693975
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AUTHORS
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KEYWORDS
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                                                                                                                                                                                                                                                  /clone="INWGE:7053585"
/tissue_type="whole body"
/lab host="DH108"
/clone="InWESC7"
/clone="Vetcr: DEXPIRESS! Site_1: Not1; Site_2: ECORV;
/notoe="Vetcr: DEXPIRESS! Site_1: Not1; Site_2: ECORV;
/notoe="Vetcr: DEXPIRESS! Site_1: Not1; Site_2: ECORV;
/notoe="Vetcr: DEXPIRESS! Site_1: Site_1: Not1; Site_2: ECORV;
Bulk tissue was collected from a whole adult_individual
from the Tuebingen strain. Ist strand CDNA was primed with
a Not I - oligo(dT) primer, double-stranded cDNA was
cloned into the Not I and ECORV sites of pExpress-1.
Library was size-selected for >1 kb fragments and
normalized. A non-normalized version of this library is
also available (NIH ZGC 10). Library was constructed by
Open Biosystems (Huntsville, AL)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             683 bp DNA linear GSS 07-JUL-2005 OM Ba0237005.r OM Ba Oryza minuta genomic clone OM Ba0237005 3', CZ679560
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1 (Bases 1 to 683)
Kim, H., Collura, K., Wissotski, M., Byrne, M., Stum, D., Smart, D., Rao, K., Luo, M., Jetty, R., Kudrna, D., Muller, C., Soderlund, C. and
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.llnl.gov
Plate: LLAM14830 row: d column: 13
High quality sequence stop: 832.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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/mol_type="genomic DNA"
/mol_type="genomic DNA"
/mol_type="leaven: 63629"
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/lab_nost="leaves"
/lab_nost="DH10B"
/clone=lib="0M_Ba"
/note="Vector: pCUGIBAC1; Site_1: HindIII; Site_2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 1134;
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Forbes Building Room 303, Tucson, AZ 85721-0036, USA
TEL: 520 626 9595
Fax: 520 621 1259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Indels
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Pred. No. 1.6e+03;
0; Mismatches 1;
                                                                                                                                                                                       /organism="Danio rerio"
/mol_type="mRNA"
/db_xref="taxon:7955"
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Plate: 0237 row: O column: 05
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         87.0%;
94.7%;
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Best Local Similarity 94.7
Matches 18; Conservative
                                                                                                                                                                    . .1134
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Class: BAC ends.
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Oryza minuta
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JOURNAL
COMMENT
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CZ679560
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KEYWORDS
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DEFINITION
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SOURCE
ORGANISM
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                          FEATURES
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Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sorghum bicolor (sorghum)
Sorghum bicolor
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Varidiplantae, Streptophyta, Embryophyta,
Spermatophyta, Magnoliophyta, Lillopaida, Poales, Poaceae, PACCAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    L (Dases 1 to 108)
Bedell, J.A., Budiman, M.A., Nunberg, A., Citek, R.W., Robbins, D., Jones, J., Flick, E., Rohlfing, T., Fries, J., Bradford, K., McMenamy, J., Smith, M., Holeman, H., Roe, B.A., Wiley, G., Korf, I.F., Rabinowicz, P.D., Lakey, N., McCombie, W.R., Jeddeloh, J.A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                            1 (bases 1 to 751).

Ayele, M., Haas, B.J., Kumar, N., Mu, H., Xiao, Y., Van Aken, S., Utterback, T.R., Wortman, J.R., White, O.R. and Town, C.D. Whole genome shotgun sequencing of Brassica oleracea and its application to gene discovery and annotation in Arabidopsis Genome Res. 15 (4), 487-495 (2005)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone lib="BO_2_3 KB"
/note="Vector: pHoS1; Site_1: BstXI; 2-3 kb sheared
genomic DNA inserted into pHoS1 using BstXI linkers"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                       Email: cdtcwn@tigr.org
DNA is from a doubled haploid provided by Tom Osborn.
Seg primer: TF
Class: sheared ends.
                                                                                                                                                                                                                                                                               Medical Center Drive, Rockville, MD 20850, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            85.0%; Score 17; DB 9; Length 751; 100.0%; Pred. No. 2.4e+03; ive 0; Mismatches 0; Indels
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PLoS Biol. 3 (1), e13 (2005)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Bedell JA
Orion Genomics, LLC
4041 Forest Park Ave, St. Louis, MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'organism="Brassica oleracea"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tel: 314 615 6979

Fax: 314 615 5975

Fax: 314 615 5975

Fax: 314 615 5975

Fax: 318 615 617

Seq primer: 73 Reverse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /mol_type="genomic DNA"
/strain="TO1000DH3"
/db_xref="taxon:3712"
/clone="BOMIZ27"
                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
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                                                                                                                                                                                                               Other GSSs: BOMIZ27TR
Contact: Chris Town
                                                                                                                                                                                                                                                                                 9712 Medical Cente
Tel: 301-838-3523
Fax: 301-838-0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17; Conservative
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Best Local (
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JOURNAL
PUBMED
COMMENT
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CW176116
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KEYWORDS
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Email: pountka@molgen.mpg.de
The library was characterised by oligonucleotide fingerprinting
(ONF) to reduce sequencing redundancy. According to the ONF
procedure, clones that display the same hybridisation matrix with a
battery of 200 8mer oligonucleotides are grouped into clusters. One
clone per ONF cluster is selected for sequencing. The size of each
cluster is an indicator of the frequency of a transcript in the
analysed library. The cluster size as well as the coordinates of
the other clones assigned to the same ONF cluster as the clone from
which the above BST is generated is available at the sea urchin
project web site at: http://www.molgen.mpg.de/ag_seaurchin/ .cDNA
clones and filters are distributed via the Resource Center/Primary
Database of the German Human Genome Project (http://www.rzpd.de)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Strongylocentrotus purpuratus
Strongylocentrotus purpuratus
Strongylocentrotus purpuratus
Eukaryota; Metazoa; Echinodea; Echinoida;
Echinoidaa; Buechinodea; Echinoida;
Echinoidaa; Buechinoidae; Echinoida;
Strongylocentrotidae; Strongylocentrotus.

El (bases 1 to 209)
El (bases 1 to 209)
Strongylocentrotidae; Strongylocentrotus.

Reinhardt, R., Herwig, R., Panopoulou, G. and Lehrach, H.
Reinhardt, R., Herwig, R., Panopoulou, G. and Lehrach, H.
Genome Res. 13 (12), 2736-2746 (2003)
Genome Res. 13 (12), 2736-2746 (2003)
Lontact: Pourstka AJ
Laboract: Pourstka AJ
Laboract: Pourstka AJ
Laboract: Pourstka AJ
Laboract: AS, dept. Lehrach
Max-Planck-Institut fuer Molekulare Genetik
Ihnestri 63-73, D-14195 Berlin, Germany
Tel: +49 30 8413 1128
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                                                                                                                                                                                                                                                                                                                                                                                                    /note="Organ: leaf; Vector: pBCSK(-); Site_I: HincII; DNA prepared from purified nuclei was randomly sheared, end-repaired, size fractionated to enrich for the 0.5 to 5kb fraction, ligated into HincII-digested pBCSK(-) vector and electroporated into E. coli cells. This is a methylation filtered library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CD290195
StrPu538.003354 Sea urchin embryo 7hr cleavage stage CDNA library MPMGp538 Strongylocentrotus purpuratus CDNA clone
CALTP538J242;MPI_538_2J24 3', mRNA sequence.
                                                                                                                                                                                                                                       /db_xref="taxon:4558"
/clone="11158315"
/clone_lib="Sorghum methylation filtered library (LibID:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FORWARD: 5' CCCCAGGCTTTACACTTTATGCTTCCGGCTCG 3' (M13RSP) 5'-seq
BACKWARD: 5' GCTATTACGCCAGCTGGCGAAAGGGGGATGTG 3' (M13FSP) 3'-seq
Seq primer: 5' GCTATTACGCCAGCTGGCGAAAGGGGGATGTG 3' (M13FSP)
High quality sequence stop: 209.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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90.0%; Pred. No. 2.5e+03;
ive 0; Mismatches 2;
                                                                                                                       organism="Sorghum bicolor"
High quality sequence stop: 108.
Location/Qualifiers
                                                                                                                                                                 'mol_type="genomic DNA"
'cultivar="ATx623"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     81 AAGGAGACACGACAACCAA 100
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CD290195.1 GI:34741272
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Best Local Similarity 90.0
Matches 18; Conservative
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/note="Vector: pSport1; Site_1: Not1; Site_2: Sal1; Random primed and directionally cloned in pSport1 vector using a Not1 (5'-pGACTAGTTCTAGATGCGAGGGGCCGCC (7)15-3; and a Sal1 5'- TGGACCAGGGGTCGG-3' adapters (Gibco BRL)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EST 10-MAR-2005
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Populus tremula x Populus tremuloides
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids I; Malpighiales; Salicaceae; Saliceae; Populus.
1 (bases 1 to 351)
Sterky,F., Bhalerao,R.R., Unneberg,P., Segerman,B., Nilsson,P.,
Brunner,A.M., Charbonnel-Campaa,L., Lindvall,J.J., Tandre,K.,
Strauss,S.H., Sundberg,G., Gustafsson,P., Uhlen,M., Bhalerao,R.P.,
Nilsson,O., Sandberg,G., Karlsson,J., Lundeberg,J. and Jansson,S.
A Populus EST resource for plant functional genomics
Proc. Natl. Acad. Sci. U.S.A. 101 (38), 13951-13956 (2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             G079P41.5pR Populus tension wood cDNA library Populus tremula х
Populus tremuloides cDNA clone G079P41 5', mRNA sequence.
DN493639
                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Umea Plant Science Center, Department of Plant Physiology
Umea University
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DEFINITION OA_ABa0117123.r OA_ABa Oryza australiensis genomic clone
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/clone_lib="Populus tension wood cDNA library"
                                                                                                                                                                                                                                                                                                                84.0%; Score 16.8; DB 6; Length 210; 90.0%; Pred. No. 2.7e+03; ive 0; Mismatches 2; Indels C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 351;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
/clone="CALTp538J242;MPI_538_2J24"
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90.0%; Pred. No. 2.8e+03;
tive 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               901 87 Umea, Sweden
Tel: +46 90 786 5279
Fax: +46 90 786 6575
Email: bo.segerman@plantphys.umu.se.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       351 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /mol_type="mRNA"
/db_xref="taxon:47664"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  192 AAGGAAACCCAGACACCCAA 173
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone="G079P41"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Other ESTs: G079P41
Contact: Bo Segerman
                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 90.0
Matches 18; Conservative
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Local 51.
18;
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DN493639/c
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JOURNAL
PUBMED
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The library was characterised by oligonucleotide fingerprinting
(ONF) to reduce sequencing redundancy. According to the ONF
procedure, clones that display the same hybridisation matrix with a
battery of 200 Bmer oligonucleotides are grouped into clusters. One
clone per ONF cluster is selected for sequencing. The size of each
cluster is an indicator of the frequency of a transcript in the
analysed library. The cluster size as well as the coordinates of
the other clones assigned to the same ONF cluster as the clone from
which the above EST is generated is available at the sea urchin
project web site at: http://www.molgen.mpg.de/ag_seaurchin/. cDNA
clones and filters are distributed via the Resource Center/Primary
Database of the German Human Genome Project (http://www.rzpd.de)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Strongylocentrous properates
Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
Echinodea; Euchinodea; Echinodea;
Echinodea; Euchinodea; Echinodea;
Strongylocentrotidea; Strongylocentrotion;
S. poustka,A.,., Groth,D., Hennig,S., Thamm,S., Cameron,A., Beck,A.,
Reinhardt,R., Herwig,R., Panopoulou,G. and Lehrach,H.
Generation, annotation, evolutionary analysis, and database integration of 20,000 unique sea urchin EST clusters
Contact: Poustka AJ
laboraty 145, dept.Lehrach
Max-Planck-Institut fuer Molekulare Genetik
Ihnestr. 63-73, D-14195 Berlin, Germany
Tel: +49 30 8413 1128
Fax: +49 30 8413 1128
                                                                                                                                                                                                                                    /note="Vector: pSport1; Site_1: Not1; Site_2: Sal1; Random parimed and directionally cloned in pSport1 vector using a Not1 (5-pgAcTATTCTAGATCCGGAGGGGCGCCCC (7):2-3 and a Sal1 5'- TCGACCCACGCGTCG-3'adapters (Gibco BRL)"
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Strbubs8.000555 Sea urchin embryo hr cleavage stage cDNA library
MPMGp538 Strongylocentrotus purpuratus cDNA clone
CALTp538J242;MPI_538_2J24 5', mRNA sequence.
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Seq primer: 5'-CCGGTCCGGAATTCCCGGAT-3' pSport3/86
High quality sequence stop: 210.
                                                |db_xref="taxon:7668"
|clone="CALIPP380242; NPI 538 2024"
|clone="CALIPP380242; NPI 538 2024"
|close="taxon="whole embryo"
|dev_stage="embryonic 7hr"
|lab_host="s.coli, Xii blue"
|clone_lib="Sag urchin embryo 7hr cleavage stage CDNA
|ibrary MPMGp538"
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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0
                                                                                                                                                                                                                                                                                                                                                                                              84.0%; Score 16.8; DB 6; Length 209; 90.0%; Pred. No. 2.7e+03;
  organism="Strongylocentrotus purpuratus"

    .210
    /organism="Strongylocentrotus purpuratus"

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/db_xref="taxon:7668"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Strongylocentrotus purpuratus
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                             mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CD319193.1 GI:34791254
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CD319193/c
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193 AACGAAACACAGACACCCAA 174
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                                                                                                                                                                                                                                                                                                                                                    Express vector.
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90.0%;
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BP813540
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Best Local Similarity
Matches 18; Conserv
                                                                                                             source
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BP813540/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /tissue type="young leaves"
/lab host="DH10B T1 phage resistant"
/clone lib="OA_ABa"
/note="Vector: pAGIBAC1; Site_1: HindIII; Site_2: HindIII"
                                                                                Oryza australiensis
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Enthartoideae; Oryzeae; Oryza.

1 (bases 1 to 363)
Kim,H., Yu,Y., Stum,D., Yost,D., Rao,K., Luo,M., Jetty,R.,
Kudrna,D., Muller,C., Hatfield,J., Soderlund,C. and Wing,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2ewp0061.seq.F Zebrafish Embryonic Heart cDNA Library Danio rerio cDNA 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.

1 (bases 1 to 370)
Ton,C., Mably,J.D., Dempsey,A.A., Hwang,D.M., Fishman,M.C. and Liew,C.C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 363;
                                                                                                                                                                                                             OWAP Project
Unpublished (2004)
Contact: Rod A. Wing
Arizona Genomics Institute
University of Arizona
Forbes Building Room 303, Tucson, AZ 85721-0036, USA
Tal: 520 625 9595
Fax: 520 621 1259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             84.0%; Score 16.8; DB 10;
90.0%; Pred. No. 2.8e+03;
ive 0; Mismatches 2;
ABa0117123 3', genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Oryza australiensis"
/mol_trype="genomic DNA"
/db_xref="taxon:4532"
/clone="OA_ABa0117123"
                                                                                                                                                                                                                                                                                                                                                                                              FORWARD: TAA TAC GAC TCA CTA TAG GG
BACKWARD: CAC TCA TTA GGC ACC CCA
Flate: 0117 row: I column: 23
Seg primer: CAC TCA TTA GGC ACC CCA
Class: BAC ends.
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Harvard Medical School
75 Francis St. Boston, MA 02115,
Tel: 6177328915
                                                                                                                                                                                                                                                                                                                                                            Email: rwing@genome.arizona.edu
PCR PRimers
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                                 CW585488.1 GI:54477247
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                                                                     Oryza australiensis
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Best Local Similarity 90.0°
Matches 18; Conservative
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                                VERSION
KEYWORDS
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A1618550/c
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JOURNAL
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KEYWORDS
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Fax: 6179750995

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Email: mseki@rtc.riken.go.jp
An Arabidopsis full-length cDNA library was constructed essentially
as reported previously (Seki et al., 1998, 2002). This clone is in a
modified pBluescript vector.
Please visit our web site (http://pfgweb.gsc.riken.jp and
http://rarge.gsc.riken.jp) for further details.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BP813540 arril9 Arabidopsis thaliana cDNA clone RAFL12-06-L22 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Arabidopsis thaliana
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Mamooliophyta; eudicotyledons; core eudicotyledons;
rosida; eurosida II; Brassicales; Brassicaceae; Arabidopsis.

(bases 1 to 391)
Seki,M., Ishida,J., Kamiya,A., Satou,M., Nakajima,M., Akiyama,K.,
Iida,K., Enju,A., Sakurai,T., Arakawa,T., Carninci,P., Fukuda,S.,
Iida,J., Kawai,J., Sasaki,D., Shiraki,T., Hayashizaki,Y. and
                                                                                                                                                                                                                                                                                                                                      /dev_stage="embryonic day 3 post-fertilization"
/lab host="s.col; Xi.1-Bile mrF"
/lab host="s.col; Xi.1-Bile mrF"
/clone_lib="zebrafish Embryonic Heart cDNA Library"
/note="Organ: heart; Vector: Lambda ZAP Express; Site 1:
EcoR1; Site 2: XhoI; mRNA was purified from embryonic
zebrafish hearts (3 day post-fertilization). CDNA was
synthesized using a XhoI-Oligo dT adaptor-primer. EcoR1
adaptors were ligated, followed by digestion with XhoI,
Express vector. "
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 16.8; DB 1; Length 370;
Pred. No. 2.8e+03;
0; Mismatches 2; Indels
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/lab host="DH108"
/clone_lib="RAFL19"
Email: cliew@rics.bwh.harvard.edu
PCR PRimers
FORWARD: 5' GCCAAGCTCGAAATTAACCCTCACTAAAGGG 3'
BACKWARD: 5' CCAGTGAATTGTAAATGGCCTCACTATAGGGCG 3'
Seq primer: 5' GAAATTAACCCTCACTAAAGGG 3'
Location/Qualifiers
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Tel: 81-298-36-4359
Fax: 81-298-36-9060
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Plant Functional Genomics Research Group
RIKEN Genomic Sciences Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Arabidopsis thaliana (thale cress)
                                                                                                                                                                                                                                    /organism="Danio rerio"
/mol_type="mRNA"
/db_xref="taxon:7955"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   clone="RAFL22-06-L22"
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/db_xref="taxon:3702"
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/organism="Triticum aestivum"
/mol_type="mRNA"
/mol_type="mRNA"
/mol_type="taxon:4565"
/db_xref="taxon:4565"
/clone="wiplo."k002.e2"
/lab_hosf="bistils"
/clone_lib="wiplo"
/clone_lib="
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603410683F1 CSEQCHN24 Gallus gallus cDNA clone ChEST327e22 5', mRNA
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Gallus gallus

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Phasianinae; Gallus.

1 (bases 1 to 427)

Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E.,

Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.

A Comprehensive Collection of Chicken cDNAs

Curr. Biol. 12 (22), 1965-1969 (2002)
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, Spoideae, Triticeae, Tolan, M., Hainey, C., Yuan, Z., Maiao, G., Caraher, N. and Hanafey, M.K.
Dupont Wheat cDNA Sequence
Unpublished (2002)
Contact: Scott V. Tingey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Department of Biomolecular Sciences University of Manchester Institute of Science and Technology (UMIST)
                                                                                                                                                                                                                                                                                                              E. I. DuPont de Nemours and Company
1 Innovation Way, P.O. Box 6104, Newark, DE 19714-6104, USA
Tel: 302-631-2602
Fax: 302-631-2607
Email: Scott V. Tingey@USA.dupont.com
Seq primer: M13.
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/mol_type="mRNA"
/strain="White Leghorn, Hisex"
/db_xref="taxon:9031"
/clone="ChEG71272722"
/dev_stage="22"
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Fax: 01612360409
Email: Simon.Hubbard@umist.ac.uk.
Location/Qualifiers
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Best Local Similarity 90.0°
Matches 18; Conservative
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CA730096.1 GI:25452099
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/note="Site 1: BamH1; Site 2: Sall; Subtraction Library.
The sequence was obtained from samples subjected to
various stress and plant hormones-treated"
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reversed clone; Please visit our web site
(http://pfgweb.gsc.riken.go.jp/) for further details.
Location/Qualifiers
                                                                   84.0%; Score 16.8; DB 3; Length 391; 90.0%; Pred. No. 2.8e+03; ive 0; Mismatches 2; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Motoaki Seki
Plant Functional Genomics Research Group
RIKEN Genomic Sciences Center
3-1-1 Koyadai, Tukuba, Ibaraki 305-0074, Japan
Tel: 81-298-36-4359
Fax: 81-298-36-9060
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Arabidopsis thaliana
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/lab host="DH10B"
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Triticum aestivum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /mol_type="mRNA"
/db xref="taxon:3702"
                                                                                                                                                                                                                                           346 AAGGAAACACAGACAACCAA 327
                                                                                                                                                                                                      1 AAGGAAACACGGACACCCAA 20
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Matches 18; Conservative
                                                                                                                                         18; Conservative
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AUTHORS
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BP664023
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/lab host="DH10B"

Query Match

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RESULT 43 AG224508/c

DEFINITION

ACCESSION VERSION KEYWORDS SOURCE

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BP616001
BP616001 RAFL16 Arabidopsis thaliana CDNA clone RAFL16-18-B08 3',
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US Department of Agriculture, Agriculture Research Service, Pacific
                                                                                                                                                                                                                                                                                                                               Arabidopsis thaliana
Mkaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicotyledons,
rosids, eurosids II; Brassicales, Brassicaceae, Arabidopais.
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Triticum monococcum cDNA clone WHE2842_H02_004, mRNA sequence.
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Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Bukaryota, Viridiplantae, Liliopsida, Poales, Poaceae,
Booideae, Triticeae, Triticum.
1 (bases I to 475)
Anderson,O.D., Chao,S., Crossman,C., Dubcovsky,J., Echenique,V.,
Lazo,G.R., Pham,J., Rausch,C.J., Stamova,B., Wilson,C. and Woo,J.
The structure and function of the expressed portion of the wheat
genomes - Vernalized apex CDNA library from Triticum monococcum
Unpublished (2002)
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3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: 81-298-36-4359
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llarity 90.0%; Pred. No. 2.9e+03;
Conservative 0; Mismatches 2;
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/db_xref="taxon:3702"
/clone="RAFL16-18-B08"
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/clone_lib="RAFL16"
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BQ803856.1 GI:22018825
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                                                                                                                                                                    mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AG224508 444 bp DNA linear GSS 19-JUL-2003 Lotus corniculatus var. japonicus DNA, clone:LjB10118_r, genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (20-NOV-2002) Shusei Sato, Kazusa DNA Research Institute, The First Laboratory for Plant Gene Research; 2-6-7 Kazusa-kamatari, Kisarazu, Chiba 292-0818, Japan (E-mail:ssato@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/, Tel:81-438-52-3935(ex.2336), Fax:81-438-52-3934)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lotus corniculatus var. japonicus (Lotus japonicus)
Lotus corniculatus var. japonicus
Eukaryota, Viridiplantas Srreptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicotyledons,
rosids, eurosids I; Fabales, Fabaceae, Papilionoideae, Loteae,
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Pred. No. 2.9e+03;
); Mismatches 2; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Lotus corniculatus var. japonicus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           84.0%; Score 16.8; DB 5; Length 427; 90.0%; Pred. No. 2.9e+03; ive 0; Mismatches 2; Indels (
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/clone lib="genomic BAC library"
/note="VECTOR:pBeloBAC11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
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/strain="Miyakojima MG-20"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sato, S., Nakamura, Y. and Tabata, S.
Lotus japonicus BAC End sequences
bublished Only in Database (2002)
2 (bases 1 to 444)
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clone lib="CSEOCHN24"
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AG224508
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Matches 18; Conserv
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Query Match

Matches

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source

PEATURES

JOURNAL REFERENCE AUTHORS TITLE JOURNAL

REFERENCE AUTHORS

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'organism="Triticum aestivum"
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Best Local Similarity
Matches 18; Conserv
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CW445890/c
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Site_1: BcoRI; Site_2: XhoI; One-month old plants were
subjected to vernalization treatment by placing them in
the cold room at 6. under 15hr light/9hr dark condition.
Total RNA was prepared from apex tissue extracted from
plants with no cold treatment; and from plants with
2-week, 4-week cold treatment separately. Equal
amount of total RNA was pooled from all four samples, a
cDNA library was made using pooled polyA RNA and cDNA
clones were in vivo excised at the University of
California, Davis (V. Echenique, B. Stamova, J.
Dubcovsky). Plasmid DNA preparations and DNA sequencing
were performed in the OD Anderson lab (all other
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Triticum aestivum
Triticum aestivum
Triticum aestivum
Sukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; Lilliopsida; Poales; Poaceae;
Pooldeae; Triticeae; Triticum.

1 (bases 1 to 484)
1 (bases 1 to 484)
Mingey, S. V., Powell, W., Wolters, P., Dolan, M., Hainey, C., Yuan, Z.,
Miao, G., Caraher, N. and Hanafey, M.K.
Dupont Wheat cDNA Sequence
Unpublished (2002)
                                                                                                                                                                                                                                                                                                                                                                              /organism="Triticum monococcum"
/mol_type="mRNA"
/culfivar="Galls"
/culfivar="Galls"
/db_xref="taxon:4568"
/clone="WHE2842_H02_O04"
/tissue_type="Vernal_ized apex"
/dev_stage="Nom month old plants"
/dev_stage="Cone month old plants"
/db_host="E. coli XLOLR"
/clone_lib="Triticum monococcum vernalized apex cDNA
West Area, Western Regional Research Center 800 Buchanan Street, Albany, CA 94710, USA Tel: 5105555773
Fax: 5105595818
Fax: 5105595818
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E. I DuPont de Nemours and Company
I. InDovation Way, P.O. Box 6104, Newark, DE 19714-6104, USA
Tel: 302-631-2607
Fax: 302-631-2607
Email: Scott.V.Tingey@USA.dupont.com
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                                                                                                                                                                                                                                                                            Seq primer: SK primer.
Location/Qualifiers
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CA728920.1 GI:25450920
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
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/note="Organ: leaf; Vector: pBCSK(-); Site 1: HincII; DNA prepared from purified nuclei was randomly sheared, end-repaired, size fractionated to enrich for the 0.5 to 5 kb fraction, ligated into HincII-digested pBCSK(-) vector and electroporated into E. coli cells. This is a methylation filtered library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GSS 02-NOV-2004
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Sorghum.
1 (bases 1 to 485)
Bedell,J.A., Budiman,M.A., Nunberg,A., Citek,R.W., Robbins,D.,
Jones,J., Flick,E., Rohlfing,T., Fries,J., Bradford,K.,
McMenamy,J., Smith,M., Holeman,H., Roe,B.A, Wiley,G., Korf,I.F.,
Rabinowicz,P.D., Lakey,N., McCombie,W.R., Jeddeloh,J.A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     fsbb001f171e14f0 Sorghum methylation filtered library (LibID: 104) Sorghum bicolor genomic clone fsbb001f171e14, genomic survey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone_lib="Sorghum methylation filtered library (LibID:
                                                                                                                                                                                                                                                                        Site 1: EcoRI; Site 2:
Hi Line) developing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          84.0%; Score 16.8; DB 6; Length 484; ilarity 90.0%; Pred. No. 2.9e+03; Conservative 0; Mismatches 2; Indels C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Martienssen, R.A.
Sorghum genome sequencing by methylation filtration
PLoS Biol. 3 (1), e13 (2005)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
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Orion Genomics, LLC
4041 Forest Park Ave, St. Louis, MO 63108, USA
11-3 14 615 6975
Pax: 314 615 5975
/mol_type="mRNA"
/db_xref="taxon:4565"
/clone="wdilo.pk005.el0"
/tissue_type="inflorescence"
/lab_host="DH108"
/clone_lib="wdilc"
/hote="vector: pBluescript SK+; Si
/hote="vector: pBluescript SK+; Si
/hote="vector: pBluescript SK+; Si
/hote"vector: pBluescript SK+; Si
/hote="vector: pBluescript SK+; Si
/hote"vector: pBluescript SK+; Si
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Plate: fabb001f171 row: e column: 14
Seq primer: f Forward
Class: methylation filtered
High quality sequence stop: 485.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Sorghum bicolor"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db xref="taxon:4558"
/clone="fsbb001f171e14"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /mol_type="genomic DNA"
/cultivar="ATx623"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     485 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          219 AAGAAAACACGTACACCCAA 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 AAGGAACACGGACACCCAA 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sorghum bicolor (sorghum)
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us-10-829-474-2.rst

Matches

ORGANISM

REFERENCE AUTHORS TITLE JOURNAL PUBMED COMMENT

FEATURES

ACCESSION VERSION KEYWORDS SOURCE

DEFINITION

RESULT 48

g

BU229997

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/notes_vector: pBluescript SK+; Site 1: EcoRI (5'-end of CDNA); Site 2: XhoI (3'-end of CDNA); Due to a cloning artefact caused by the kit, in most cases the EcoRI site is NOT present, as well as the EcoRIadapter used for cloning. To excise the insert, restriction sites upstream EcoRI should be used (e.g. BamHI, SalI, PstI). NOTE: Also due to the cloning system used Blue/white selection for recombinats is not 100% reliable."
                                                                                                                                         Hordeum vulgare subsp. vulgare
Hordeum vulgare subsp. vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; Hordeum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 (bases 1 to 525)
Tidwell,R., Clifton,S., Marra,M., Hillier,L., Pape,D., Martin,J.,
Wylie,T., Theising,B., Bowers,Y., Gibbons,M., Ritter,E., Bennet,J.,
Ronko,I., Tsagareishvili,R., Belaygorod,L., Grow,A., Maguire,L.,
Waterston,R. and Wilson,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                        Shang, H., Potokina, E., Michalek, W., Weschke, W., Stein, N. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Stein Nis
Molecular Markers Group, Department Genbank
Molecular Markers Group, Department Genbank
Institute of Plant Genetics and Crop Plant Research (IPK)
Corrensstr. 3, 06466, Gatersleben, Germany
Tel: 039482-5522
Fax: 039482-5595
Fax: 039482-5595
Fax: 039482-5595
Fax: 039482-5595
Fax: 039482-5595
Seq Erimer: 7 row: J column: 7
Seq primer: Mi3rey.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CF352554 525 bp mRNA linear E0.
lac30c03.y1 SiEP Mus musculus cDNA 5', mRNA sequence.
CF352554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 16.8; DB 5; Length 519;
Pred. No. 2.9e+03;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1. .519
/organism="Hordeum vulgare subsp. vulgare"
/mol type="mRNA"
/cultivar="Barke"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone=HHT07J07"

tissue type="endosperm early"

telsue type="0-16 hours after imbibition"

lab host="XL10-Gold"

(clone_lib="HT"
                                                                                                                                                                                                                                                                                                                                                                                                                            Barley ESTs from germinating seeds Unpublished (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /sub_species="vulgare"
/db_xref="GABI:261687"
/db_xref="taxon:112509"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (house mouse)
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                                                                               CA013161.1 GI:24290505
          5-PRIME, mRNA sequence.
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Best Local Similarity 90.0°
Matches 18; Conservative
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                                                                                                                                             SOURCE
ORGANISM
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KEYWORDS
SOURCE
ORGANISM
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ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE
JOURNAL
COMMENT
                                           CCESSION
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KEYWORDS
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LOCUS
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// Jab host="12"
/ Jab host="1
                                                                                                                                                                                                                                                                                                                BU229997 514 bp mRNA linear EST 26-NOV-2002 603947773F1 CSEQCHN23 Gallus gallus clone ChEST903a19 5', mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CA013161 519 bp mRNA linear EST 23-OCT-2002 HT07J07r HT Hordeum vulgare subsp. vulgare cDNA clone HT07J07
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Bhasianinae; Gallus.

1 (bases 1 to 514)

Boardman, P. E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, B. Foogy, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J. A. Comprehensive Collection of Chicken cDNAs

Curr. Biol. 12 (22), 1965-1969 (2002)
       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Department of Biomolecular Sciences
University of Manchester Institute of Science and Technology
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84.0%; Score 16.8; DB 5; Length 514;

Best Local Similarity 90.0%; Pred. No. 2.9e+03;

Matches 18; Conservative 0; Mismatches 2; Indels (
   Indels
5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Gallus gallus"
/mol_type="mRNA"
/strain="White Leghorn, Hisex"
/db_xref="traxon:9031"
/clone="ChEST903a19"
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Box 88, Manchester, M60 1QD, UK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tel: 01612008930
Fax: 01612360409
Email: Simon.Hubbard@umist.ac.uk.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                  342 AAGGAAAACGGACACCAAA 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  344 AAGAAACCACGCACACCCAA 363
                                                                    1 AAGGAAACACGGACACCCAA 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 AAGGAAACACGGACACCCAA 20
                                                                                                                                                                                                                                                                                                                                                                                                                     BU229997
BU229997.1 GI:25470352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gallus gallus (chicken)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Simon Hubbard
18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gallus gallus
                                                                                                                                                                                                                                                                                                                                                                                        sequence.
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Gaps

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EST 20-AUG-2003

DEFINITION

RESULT 49

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ORIGIN

CA013161

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Contact: Stephen L. Johnson
Washington University School of Medicine
#444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: 2brafish@watson.wustl.edu
cDNA library Preparation: Leonard Ira Zon DNA Sequencing by:
Mabhington University Genome Sequencing Center Clone distribution:
Genome Systems, St. Louis, Missouri (web address:
www.genomesystems.com) (email contact: info@genomesystems.com) and
Research Genetics, Huntsville, Alabama (web address:
www.resgen.com) (email contact: info@resgen.com) and
RessourcenZentrumPrimarDatenbank, Berlin, Germany (web address:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     zebrafish identity (p-value greater than 1e-99) found to:
gi|2289384|gb|AA542449|AA542449 fa07all.sl Zebrafish ICRFzfls Danio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /tissue_type="kidney pooled from 300 wild type adults" /lab_host="%LOLR" /clone_lib="zebrafish gridded kidney" /note="Organ: kidney; Vector: pBK-CMV; Site_1: EcoRI; Site_2: *KhOI; Oligo dT cDNA library constructed from mRNA pooled from pooled kidney tissue from 300 adult zebrafish."
                                                                                                                                                                                                                                                                                                   EST 09-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cyprinidae; Danio.

1 (Dases 1 to 546)
1 (Dases 1 to 546)
2 (Jark, M., Johnson, S. L., Lehrach, H., Lee, R., Li, F., Marra, M., Eddy, S., Hillier, L., Kucaba, T., Martin, J., Beck, C., Mylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.
                                                                                                                                                                                                                                                                         fp08e03.x1 zebrafish gridded kidney Danio rerio cDNA clone IMAGE:4729037 3' similar to TR:095624 095624 CPLA2 INTERACTING PROTERIN; , mRNA sequence.
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                           Length 544;
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                                                                              2; Indels
                           Score 16.8; DB 6;
Pred. No. 2.9e+03;
                                                                           0; Mismatches
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High quality sequence stop: 353.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /mol_type="mRNA"
/db_xref="taxon:7955"
/clone="IMAGB:4729037"
                                                                                                                                                                         292 AATGAACCACGGACACCCAA 273
                                                                                                                              1 AAGGAAACACGGACACCCAA 20
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BG727965.1 GI:14013040
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                           84.0%;
90.0%;
                                                     Best Local Similarity 90.0
Matches 18; Conservative
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Best Local Similarity
Matches 18; Conservat
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BG727965/c
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                    Unpublished (2002)

Contact: Jeff Gordon and Mike Lovett

Contact: Jeff Gordon and Mike Lovett

Washington University School of Medicine
Library materials provided by: Stappenbeck Th.S. and Gordon J.I.

Library constructed by: Korshunova Y. and Lovett M. DNA sequencing

by: Washington University Genome Sequencing Center For information
on obtaining a clone please contact: Rose Tidwell

(tidwell@genetics.wustl.edu)
                                                                                                                                                                                                                                                                                                                                                                                                                     /tissue_type="small intestinal epithelial progenitors" | Alab host="OHEALpha Ultra Max cells (Invitrogen)" | Alab host="PHEALpha Ultra Max cells (Invitrogen)" | Alone | lib="SiBF" | Alone="Vector: pAMP1; The library was synthesized with modified SMART primers with dUTP at the end. After treatment with UDG the CDNA was cloned in pAMP1 vector by annealing."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   wreln.pk0002.c4 wreln Triticum aestivum cDNA clone wreln.pk0002.c4 with Triticum aestivum cDNA clone wreln.pk0002.c4 5' end, mRNA sequence.
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Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae;
Pooideae, Triticeae, Triticum.
1 (bases 1 to 544)
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/organism="Triticum aestivum"
/mol_type="mRNA"
/db_xref="texon:4565"
/clone="wreln.pk0002.c4"
/clone="wreln"
/clone lib="wreln"
/note="Vector: pBluescript SK+; Site_1: EcoRI; Site_2:
Xhol; Wheat (Triticum aestivum L.) root; normalized from wrel library"
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Mado,G., Caraher,N. and Hanafey,M.K.
DuPont Wheat CDNA Sequence
Unpublished (2002)
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Crop Genetics
E. I. DuPont de Nemours and Company
I. Innovation Way, P.O. Box 6104, Newark, DE 19714-6104, USA
Tel: 302-631-2607
Fax: 302-631-2607
Email: Scott.V.Tingey@USA.dupont.com
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 16.8; DB 6; Length 525;
Pred. No. 2.9e+03;
; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                              organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                Seq primer: -40RP from Gibco
High quality sequence stop: 525.
Location/Qualifiers
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Triticum aestivum
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CA637743/c
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Email: genome-reseggec.riken.jp, URL:http://genome.gsc.riken.jp/
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNs to
prepare full-length cDNs libraries for rapid discovery of new
genee. Genome Res. 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,N., Ohara,E.,
Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T.,
and Hayashizaki,Y.
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer. Genome Res.
10 (11), 1757-1771 (2000)
                                                                                                                                                                                                               Contact: Yoshhide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Hara, A., Hiramoto, K., Hori, F., Ishii, Y., Ito, M., Kawai, J., Kondo, M., Kouda, M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K., Ohno, M., Okazaki, Y., Okido, T., Salito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Tanaka, T., Toya, T., Muramatsu, M. and Hayashizaki, Y. Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara, Y. and Hayashizaki, Y.
Sugahara, Y. and Hayashizaki, Y.
Computer-based methods for the mouse full-length cDNA
computerine sequence clustering for construction of a
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
Kondo, S., Shinagawa, A., Saito, T., Kiyosawa, H., Yamanaka, I.,
Aizawa, K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           organism="Mus musculus"
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/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /mol_type="mRNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /sex="male"
                                                                                                                                                                                                                                                                                                                                                             Tel: 81-45-503-9222
Fax: 81-45-503-9216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            oblongata'
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1 (bases 1 to 559)
Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Mallace,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
                                                                                                                                                               AQ293334 15-DEC-1998 BNA linear GSS 15-DEC-1998 HS_2266_B2_E05_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2266 Col=10 Row=J, genomic survey
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Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Euarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Murinae, Mus.
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/note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in
E-Coli DH10B"
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Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
10449764
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University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
THE1: (206) 616-3818
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Sequence Tagged Connector
Plate: 2266 row: J column: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /mol_type="genomic_DNA"
/db_xref="taxon:9606"
/clone="Plate=2266 Col=10 Row=J"
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Location/Qualifiers
                      518 AAGGAAAGACGGCCACCCAA 499
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                                                                                                                                                                                                                                                                                                                                                          sapiens (human)
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lone\_lib="RIKEN full-length enriched, adult male medulla contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer  $\{5^\prime$ GAGAGAGAAGGATCCAAGAGCTCTTTTTTTTTTTTTVN 3'), cDNA was ij Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)
Please visit our web site (http://genome.gsc.riken.go.jp) for further details. /note="Site 1: Sal1; Site\_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory RIKEN Division of Experimental Animal Research in Rik tissue\_type="medulla oblongata"

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/organism="Zea mays"
/wol_type="genomic DNA"
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CG099060/c
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Submitted (31-MAR-2005) Asao Fujiyama, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suehiro-chou, Tsurumi-ku, Yokhoma, Kanagawa, 230-0045, Japan
(E-mail:afujiyam@gsc.riken.jp, URL:http://hgp.gsc.riken.jp/,
Tel:81-45-503-9111, Fax:81-45-503-9170)
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Oryza nivara
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
                                                                                                                                                                                         DE001557 607 bp DNA linear GSS 06-APR-201
Branchiostoma floridae DNA, clone: CH302-004F04.R, genomic survey
                                                                                                                                                                                                                                                                                           Branchiostoma floridae (Florida lancelet)
Branchiostoma floridae
Eukaryota, Metazoa, Chordata, Cephalochordata, Branchiostomidae,
                                     Gaps
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/clone_lib="CHORIO302 Amphioxus genomic BAC library"
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84.0%; Score 16.8; DB 2; Length 580; 90.0%; Pred. No. 2.9e+03; ive 0; Mismatches 2; Indels (
                                                                                                                                                                                                                                                                                                                                                                               Fujiyama,A., Toyoda,A., Hattori,M. and Sakaki,Y.
BAC end sequences of CHORI-302 Amphioxus Library
Published Only in Database (2005)
2 (bases 1 to 607)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1. .607
/organism="Branchiostoma floridae"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="common name:amphioxus"
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: ECORI
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                                                                                         396 AAGCAAACACGCACACAA 415
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                                                                     1 AAGGAAACACGGACACCCAA 20
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DE001557.1 GI:62243906
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                                 18; Conservative
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R.Site 2
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DE001557/c
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae, Andropogoneae; Zea.
1 (bases 1 to 628)
Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T.,
Resnick, A., Fraser, C.M., Yuan, Y., San Miguel, P., Ma, J. and
Bennetzen, J.
Ehrhartoideae; Oryzeae; Oryza.

8 1 (bases 1 to 608)

8 Kim, H., Yu, Y., Y., Stum, D., Yost, D., Rao, K., Luo, M., Jetty, R.,

8 Kim, H., Wuller, C., Hatfield, J., Soderlund, C. and Wing, R.

9 MAP Project (2004)

10 Unpublished (2004)

11 Contact: Rod A. Wing

Arizona Genomics Institute

9 University of Arizona

12 Forbes Building Room 303, Tucson, AZ 85721-0036, USA

12 1: 520 625 9595

8 Fax: 520 621 1259

8 Email: rwing@genome.arizona.edu
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                                                                                                                                                                                                                                                                                                                                                                                                  FORWARD: TAA TAC GAC TCA CTA TAG GG
BACKWARD: CAC TCA TTA GGC ACC CCA
Insert Length: 161 Std Brror: 0.00
Plate: 0086 row: D column: 16
Seg primer: CAC TCA TTA GGC ACC CCA
Class: BAC ends.
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Class: sheared ends.
Location/Qualifiers
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Unpublished (2003)
Other GSSs: PUIHL20TB
Contact: Cathy Whitelaw
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Fax: 301-838-0208
Email: whitelaw@tigr.org
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CG099060.1 GI:33981354
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84.0%;
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Best Local Similarity 90.0
Matches 18; Conservative
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Tortula ruralis
Tortula ruralis
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Bryophyta;
Buyaryota, Viridiplantae; Pottiales; Pottiaceae; Tortula.

1 (bases 1 to 632)
Oliver, M.J., Dowd, S.E., Zaragosa, J., Mauget, S.A. and Payton, P.R.
The rehydration transcriptome of the desiccation-tolerant bryophyte
Tortula ruralis: transcript classification and analysis
BMC Genomics 5 (1), 89 (2004)
                                                                                                                                                                                                                                                                                                    сигибовв 632 bp mRNA linear EST 30-APR-2004
Tor6515 Gametophyte rehydration Library Tortula ruralis cDNA, mRNA .
sequence.
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HD09102r HD Hordeum vulgare cDNA clone HD09102 5-PRIME, mRNA
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Sal1; Site_2: Not1"
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/notes="Vector: pCR4-TOPO; Site 1: EcoRI; 0.6-1.0 kb high
CoT selected genomic DNA library"
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                                                                                                                                 Length 628;
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                                                                                                                                                                 Indels
                                                                                                                             84.0%; Score 16.8; DB 10; 90.0%; Pred. No. 3e+03; iive 0; Mismatches 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3810 4th St, Lubbock, TX 79415, USA Tel: 806-749-5560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /mol_type="mRNA"
/db_xref="taxon:38588"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fax: 806-723-5272
Email: moliver@lbk.ars.usda.gov
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strain="B73"
                                                                                                                 Query Match
Best Local Similarity 90.09
"...hes 18; Conservative
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BU992244
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AUTHORS
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BU992244
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/clome_lib="HD"
/note="Vector: pBluescript SK+; Site_1: EcoRI (5'-end of cDNA); Site_2: XhoI (3'-end of cDNA); Due to a cloning artefact caused by the kit, in most cases the EcoRI site is NOT present, as well as the EcoRIadapter used for cloning. To excise the insert, restriction sites upstream EcoRI should be used (e.g. BamHI, SalI, PStI). NOTE: Also due to the cloning system used Blue/white selection for recombinats is not 100% reliable.Average insert size is 1 kb"
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Bukaryota; Magnoliophyta; Liliopsida; Poales; Poaceae;
Shrhatcoideae; Oryzae; Oryza.
1 (bases 1 to 643)
Kim,H., Yu,Y., Stum,D., Yost,D., Rao,K., Luo,M., Jetty,R.,
Kudrna,D., Muller,C., Hatfield,J., Soderlund,C. and Wing,R.
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Pooideae, Triticeae, Hordeum.
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Pred. No. 3e+03;
0; Mismatches 2; Indels C
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Arizona Genomics Institute
University of Arizona
Tebes Building Room 303, Tucson, AZ 85721-0036, USA
Tel: 520 626 9595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /tissue type="callus"
/dev_stage="callus (5-10 mm in diameter)"
/lab_host="XL10-Gold"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fax: 039482-5595
Email: stein@ipk-gatersleben.de
Insert Length: 637 Std Error: 0.00
Plate: 9 row: I column: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'organism="Hordeum vulgare"
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/cultivar="Golden Promise"
/db_xref="GABI:242352"
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/clone="HD09102"
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CG046335 661 bp DNA linear GSS 19-AUG-2003 PUIFW42TB ZM_0.6_1.0_KB Zea mays genomic clone ZMMBTa0574G11,
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CH230-403G9.TJ CHORI-230 Segment 2 Rattus norvegicus genomic clone
CH230-403G9, genomic survey sequence.
                                                                                                                                                                                                                                                                        Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Bermatophyta, Bermatophyta, Bermatophyta, Pagermatophyta, Pades, Pades, Padccae, PACCAD clade, Panicoldeae, Andropogoneae, Zea.

1 (bases 1 to 661)
Mittelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T., Resnick, A., Fraser, C.M., Yuan, Y., San Miguel, P., Ma, J. and Bennetzen, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="taxon:4577"
/clone="zmmBra0574611"
/clone_lib="zm_06_1.0 KB"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; 0.6-1.0 kb high
COT selected genomic DNA library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rattus norvegicus (Norway rat)
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Rattus.
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Shartsbeyn,A., Gebregeorgis,E., Overton,L., Russell,D., Chen,D.,
Riggs,F., de and Fraser,C.M.
Rat BAC End Sequences from Library CHORI-230 MboI segment
Unpublished (1999)
Other GSSs: CH230-403G9.TV
Contact: Shaying Zhao
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
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90.0%; Pred. No. 3e+03;
live 0; Mismatches 2;
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/strain="B73"
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/organism="Zea mays"
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125 AAGAAAACAAGGACACCCAA 144
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Unpublished (2003)
Other_GSSs: PUIFW42TD
Contact: Cathy Whitelaw
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fax: 301-838-0208
Email: whitelaw@tigr.org
                                                                                                                                                   genomic survey sequence.
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GSS.
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BZ274036.1 GI:23994788
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Class: sheared ends
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Best Local Similarity 90.03
Matches 18; Conservative
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CG046335/c
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BZ274036
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.organism="Oryza nivara"

/mol_type="genomic DNA"

/db_xref="caxon:4536"

/clone="OR_BBa0140P17"

/tissue_type="young leaves"

/lab_host="DH10B-T1 phage resistant"

/clone_lib="OR_BBa"

/note="Vector: pAGIBAC1; Site_1: HindIII; Site_2: HindIII"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CD893867 656 bp mRNA linear EST 14-JUL-2003 GI18.124L19F010828 G118 Triticum aestivum cDNA clone G118124L19,
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Triticum aestivum
Triticum aestivum
Sukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta; Liliopsida, Poales, Poaceae;
Pooldeae, Triticeae, Triticum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This sequence has been generated in the framework of the french plant genomics programme 'Genoplante' (http://www.genoplante.com and http://genoplante.info.infobiogen.fr).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Genoplante, a major partnership french program in plant genomics Unpublished (2003)
Contact: Genoplante
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pollination)"
/clone_lib="G118"
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Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
                                                    FORWARD: TAA TAC GAC TCA CTA TAG GG
BACKWARD: CAC TCA TTA GGC ACC CCA
Insert Length: 161 Std Brror: 0.00
Plate: 0140 row: P column: 17
Seg primer: TAA TAC GAC TCA CTA TAG GG
Class: BAC ends.
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/organism="Triticum aestivum"
                 Email: rwing@genome.arizona.edu
PCR PRimers
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/clone="G118124L19"
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/cultivar="recital"
                                                                                                                                                                                         Location/Qualifiers
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Best Local Similarity 90.0
Matches 18; Conservative
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Length Indels GSS 15-OCT-2002

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Query Match
Best Local Similarity
Matches 18; Conserv
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JOURNAL
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KEYWORDS
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                                                                                                                                              ORIGIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CX682423
ydf10h05.y1 Sea urchin EST Lib1 Strongylocentrotus purpuratus cDNA clone ydf10h05 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 (bases 1 to 673)

Coffman, J. A., Robertson, A.J., Clifton, S., Pape, D., Hillier, L.,

Martin, J., Wylie, T., Dante, M., Meyer, R., Theising, B., Bowers, Y.,

Gibbons, M., Ronko, I., Tsagareishvili, R., Ritter, E., Kennedy, S. and
Wilson, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: est@watson.wustl.edu
DNA sequencing by: Washington University Genome Sequencing Center
Seq primer: -28RPpOT.
                                                                                                                                                                                                                                                                                                                                                                                       /sex="Female"
/cell type="Brain"
/clone_lib="CHONI-210 Segment 2"
/note="Vector: pTARBAC1.3; Site 1: MboI; Site 2: MboI;
CHORI-230 Rat (BN/SBNH8d/MCW) BAC library produced by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Strongylocentrotus purpuratus
Strongylocentrotus perinodermata; Bleutherozoa; Echinozoa;
Echinoidea; Buechinoidea; Echinoidea; Echinoidea;
Strongylocentrotidae; Strongylocentrotus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (2004)
Contact: Dr. James A. Coffman
Contact: Dr. James A. Coffman
WashU Sea urchin EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 666;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               84.0%; Score 16.8; DB 9; Length 6 ilarity 90.0%; Pred. No. 3e+03; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Strongylocentrotus purpuratus"
/mol_type="mRNA"
/db_xref="taxon:7668"
                                    MD 20850, USA
                                                                                                                                                                                                                                                                                             /organism="Rattus norvegicus"
/mol_type="genomic DNA"
/strain="BN/SsNHsd/MCW"
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville,
Tel: 301 838 0208
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                        db_xref="taxon:10116"
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Strongylocentrotus purpuratus
                                                                                                                                                                                                                                                                                                                                                                      /clone="CH230-403G9"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 AAGGAAACACGGACACCCAA 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pieter de Jong"
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Best Local Similarity
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AUTHORS
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/done lib="CSEQENN2"
//done lib="CSEQENN2"
//done lib="CSEQENN2"
//done lib="CSEQENN2"
//done lib="CSEQENN2"
//done lib="CSEQENUATION of library was constructed from site 2. Not1; This normalized library was constructed from l million independent clones. CDNA synthesis was initiated using an oligo(dT) primer, using methylated C in the first strand strand synthesis reaction. Following this first strand reaction, double-stranded cDNA was blunted, ligated to NotI adapters, digested with EcoRI compatible sites of a cloned into the NotI and EcoRI compatible sites of a clustom modified MCS of the pBluescript (KS+) vector. The library was normalized in 2 rounds using conditions adapted from Soares et al., PNAS (1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6 (1996): 791, except that a significantly longer reannealing hybridization was used."
/lab_host="DHIOB"

/clone lib="Sea urchin EST Libl"

/clone lib="Sea urchin EST Libl"

/note="Wector: pCMVSport6.1 (Invitrogen); Site 1: Not1;

Site_2: Smal; Arrayed normalized library of full-length

Site_2: Shal; Arrayed normalized library of full-length

Site_2: Shal; Arrayed plastula stage transcriptome of the sea

urchin Strongylocentrotus purpuratus, cloned into the

vector pCMVSport6.1 (Invitrogen)"
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Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E., Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J. A. Comprehensive Collection of Chicken cDNAs
Curr. Biol. 12 (22), 1965-1969 (2002)
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603471630F1 CSEQRBN22 Gallus gallus cDNA clone ChEST34817 5', mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryoča; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
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                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Department of Biomolecular Sciences
University of Manchester Institute of Science and Technology
                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                             ch 84.0%; Score 16.8; DB 8; Length 673; 1 Similarity 90.0%; Pred. No. 3e+03; 18; Conservative 0; Mismatches 2; Indels
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/mol_type="mRNA"
/strain="Layer and broiler"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PO Box 88, Manchester, M60 1QD, UK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tel: 01612008930
Fax: 01612360409
Email: Simon.Hubbard@umist.ac.uk.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'sex="Male and female"
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/clone="ChEST34817"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
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/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          239 AAGGAAACCCAGACACCCAA 258
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Gallus gallus
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Hattori, M., Toyoda, A., Noguchi, H., Kojima, T. and Sakaki, Y.

Hattori, M., Toyoda, A., Noguchi, H., Kojima, T. and Sakaki, Y.

Direct Submission

L. Direct Submission

L. Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical

and Chemical Research (RIKEN), Genomic Sciences Center (GSC);

1-7-22 Suehiro-chou, Tsurumi-ku, Vokohama, Kanagawa, 230-0045, Japan

(E-mail: hattori@gsc.riken.jp, URL: http://hgp.gsc.riken.go.jp/,

Tel:81-45-503-9111, Fax:81-45-503-9170)

Clones are derived from the mouse BAC library MSMg01. For BAC

library availability, please contect Kuniya Abe (abe@rtc.riken.jp).

Tsukuba Institute (F Physical and Chemical Research (RIKEN) 3-1-1

Koyadai, Tsukuba, 305-0074 Japan

phone: 81-298-36-9189, fax: 81-298-36-9199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AG514370 709 bp DNA linear GSS 22-DEC-2004 Mus musculus molossinus DNA, clone:MSMg01-419D11.T7, genomic survey
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                                                                   Abe,K., Noguchi,H., Tagawa,K., Yuzuriha,M., Toyoda,A., Kojima,T., Ezwa,K., Saitou,N., Hattori,M., Sakaki,Y., Moriwaki,K. and Shiroishi,T. Contribution of Asian mouse subspecies Mus musculus molossinus to genomic constitution of strain C57BL/6J, as defined by BAC-end sequence-SNP analysis Genome Res. 14 (12), 2439-2447 (2004)
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Mus musculus molossinus
Musaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Buarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Abe, K., Noguchi, H., Tagawa, K., Yuzuriha, M., Toyoda, A., Kojima, T., Ezawa, K., Saitou, N., Hattori, M., Sakaki, Y., Moriwaki, K. and Shiroishi, T.
Mammalia; Butheria; Buarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /tissue type="mixture of kidney and spleen"
/clone_lib="MSMg01 Mouse Male BAC Library"
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Pred. No. 3e+03;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /mol_type="genomic DNA"
/sub_species="molossinus"
/db_xref="taxon:57486"
/clone="WSMg01-094110.TJ"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        e-mail: abe@rtc.riken.jp
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: EcoRI
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LIBRARY
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R.Site 1
R.Site 2
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SOURCE
ORGANISM
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JOURNAL
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AUTHORS
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Mus musculus molossinus DNA, clone:MSMg01-094110.TJ, genomic survey
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Brassica oleracea
Extaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

1 (bases 1 to 683)
Ayele,M., Haas,B.J., Kumar,N., Wu,H., Xiao,Y., Van Aken,S., Witterback,T.R., Wortman,J.R., Witte,O.R., and Town,C.D.
Whole genome shotgun sequencing of Brassica oleracea and its application to gene discovery and annotation in Arabidopsis Genome Res. 15 (4), 487-495 (2005)
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Mus musculus molossinus
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
                                                                                               Gaps
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/note="Vector: pHoSl; Site_1: BstXI; 2-3 kb sheared
genomic DNA inserted into pHOSl using BstXI linkers"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
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                                            84.0%; Score 16.8; DB 5; Length 678; 90.0%; Pred. No. 3e+03; ive 0; Mismatches 2; Indels (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: cdtown@tigr.org
DNA is from a doubled haploid provided by Tom Osborn.
Seg primer: TF
Class: sheared ends.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Brassica oleracea"
/mol type="genomic DNA"
/strain="TO1000DH3"
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/clone="BOMQH50"
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BZ510687.1 GI:27035294
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Contact: Chris Town
                                                                                             Conservative
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Fax: 301-838-0208
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.

E 1 (bases 1 to 729)
S NIH-MGC http://mgc.nci.nih.gov/.
I Unpublished (1999)
Contect: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Chung-Der Hsiao, Ming-Yi Chou and Pung-Pung
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               07057597 729 bp mRNA linear EST 11-AUG-2005
AGENCOURT_55704374 NIH_ZGC_21 Danio rerio cDNA clone IMAGE:7919645
Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the mouse BAC library MSMg01. For BAC library availability, please contact Kuniya Abe (abe@rtc.riken.jp). Tsukuba Institude, Bio Resource Center.
The Institute of Physical and Chemical Research (RIKEN) 3-1-1 Koyadai, Tsukuba, 305-0074 Japan
Phone: 81-298-36-9189, fax: 81-298-36-9199
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CDNA Library Preparation: Dr. Yutaka Suzuki
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
Cloud through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov.
Plate: LLAM16325 row: g column: 03
High quality sequence stort: 24
High quality sequence stort: 287.
Localion/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 715;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /tissue_type="mixture of kidney and spleen"
/clone_lib="MSMg01 Mouse Male BAC Library"
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90.0%; Pred. No. 3e+03;
iive 0; Mismatches 2;
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/sub_species="molossinus"
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/clone="MSMg01-324C12.T7"
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/db_xref="taxon:7955"
                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
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: EcoRI
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Best Local Similarity 90.09
Matches 18; Conservative
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                                                                                                              Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa, 230-0045, Japan (E-mail:hattoriogsc.riken.jp, URL:http://hgp.gsc.riken.go.jp/, 7el:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the mouse BAC library MSWg01. For BAC library availability, please contact (Kuniya Abe (abe@rtc.riken.jp). Tsukuba Institude, Bio Resource Center, The Institute of Physical and Chemical Research (RIKEN) 3-1-1 Koyadai, Tsukuba, 305-0074 Japan Phone: 81-298-36-9189, fax: 81-298-36-9199
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Direct Submission
Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical and Chemical Research (RIERN), Genomic Sciences Center (GSC);
1-7-22 Suehiro-chou,Tsurumi-ku, Yokohama, Kanagawa, 230-0045, Japan (R-mail:hattori@gsc.riken.jp, URL:http://hgp.gsc.riken.go.jp/,
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genomic constitution of strain C57BL/6J, as defined by BAC-end
sequence-SNP analysis
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Mammalia; Butheria; Buarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
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Ezawa,K., Saitou,N., Hattori,M., Sakaki,Y., Moriwaki,K. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                             2 (bases 1 to 709)
Hattori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakaki,Y.
Direct Submission
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84.0%; Score 16.8; DB 10; Length 709;
Best Local Similarity 90.0%; Pred. No. 3e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0
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/clone_lib="MSMg01 Mouse Male BAC Library"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Mus musculus molossinus"
/mol_type="genomic DNA"
/sub_species="molossinus"
  Jenome Res. 14 (12), 2439-2447 (2004)
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/clone="MSMg01-419D11.T7"
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                                                                                                                                               ORIGIN
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                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Rukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Rampodinae; Ranogus; Xenogus.
I (bases 1 to 735)
I (bases 2 to 736)
I (bases 3 to 736)
I (bases 4 to 736)
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/lab_host="DH10B TonA"
/clone lib="NIGHD XGC FaB"
/note="Organ: fat_body; Vector: pExpress-1; Site_1: EcoRV;
Site_2: Not1; CDNA was primed using oligo-dT primer:
5'-pGACTAGTTCTAGATCGCGAGCGCGCCC(T) 25-3' and cloned into
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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AGENCOURT_55719638 NICHD_XGC_FaB Xenopus laevis cDNA clone
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84.0%; Score 16.8; DB 8; Length 729;
Best Local Similarity 90.0%; Pred. No. 3e+03;
Matches 18; Conservative 0; Mismatches 2; Indels
'tissue_type="40 pooled samples"
'lab_host="DH10B TonA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Xenopus laevis (African clawed frog)
Xenopus laevis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IMAGE:8072872 5', mRNA sequence.
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/db_xref="taxon:8355"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DT060396.1 GI:72359645
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KEYWORDS
SOURCE
ORGANISM
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TITLE
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COMMENT
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the EcoRV/NotI sites of pExpress-1. Size-selection 1.2kb resulted in an average insert size of 1.8kb. This is a primary library (normalized library is NICHO XGC FabN) and was constructed by Express Genomics (Frederick, MD). Note: this is a (http://xgc.nci.nih.gov/) Xenopus Gene Collection library."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AG429016 737 bp DNA linear GSS 21-DEC-2004
Mus musculus molossinus DNA, clone:MSMg01-303G16.T7, genomic survey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Abe,K., Noguchi,H., Tagawa,K., Yuzuriha,M., Toyoda,A., Kojima,T., Ezawa,K., Saitou,N., Hattori,M., Sakaki,Y., Moriwaki,K. and Shiroishi,T.
Contribution of Asian mouse subspecies Mus musculus molossinus to genomic constitution of strain C57BL/6J, as defined by BAC-end sequence-SNP analysis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Buarchontoglires, Glires, Rodentia,
Sciurognathi, Muridae, Murinae, Mus.
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                                                                                                                                                                                                                                                                                                                                                                                  Length 735;
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/clone lib="MSMg01 Mouse Male BAC Library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus molossinus (Japanese wild mouse)
Mus musculus molossinus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        phone: 81-298-36-9189, fax: 81-298-36-9199
e-mail: abe@rtc.riken.jp
                                                                                                                                                                                                                                                                                                                                                                                  Score 16.8; DB 8;
Pred. No. 3e+03;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Genome Res. 14 (12), 2439-2447 (2004)
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/sub_species="molossinus"
/db_xref="taxon:57486"
/clone="WaNg01-303G16.T7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       159 AAGGAAACACGCACAGCCAA 140
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: EcoRI
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90.0%;
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Best Local Similarity 90.03
Matches 18; Conservative
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R.Site 1
R.Site 2
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DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS

RESULT 73

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Hominidae, Homo.

1 (bases 1 to 756)
Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T.,
Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone lib="RPCI-11 Human Male BAC Library"
/note="Vector: pBACe3.6; Site 1: EcoRI; Site 2: EcoRI;
Male blood DNA was isolated from one randomly chosen donor and partially diseased with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBACe3.6 vector at EcoRI sites"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EST 11-AUG-2005
                                                                                                                                                                                                                                                                                                                                                                        Contact: Mahairas GG, Wallace JC, Hood L.
High Throughput Sequencing Center
High Throughput Sequencing Center
Montershity of Wanhington.

401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Emai: (206) 616-3887
Email: jwallace@u.washington.edu
Clones are derived from the human BAC library RPCI-11. For BAC
Library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu. Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm)
or from Resear h Genetics (info@resgen.com). BAC end Web Server:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
Xenopodinae, Xenopus, Xenopus.

    (bases 1 to 763)

                                                                                      Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                 Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome
Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 763 bp mRNA linear BST 11-7
AGENCOURT 55787745 NICHD_XGC_PABN Xenopus laevis cDNA clone
DT060112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone="Plate=1084 Col=20 Row=K"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA"
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Plate: 1084 row: K column: 20
Seg primer: SP6
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/db_xref="taxon:9606
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Location/Qualifiers
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Best Local Similarity 90.0
Matches 18; Conservative
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estihopterygii, Neopterygii, Teleostei, Buteleostei, Neoteleostei,
Acanthomorpha, Acanthopterygii, Percomorpha, Tetraodontiformes;
Tetradontoidea, Tetraodontidae, Terraodon.
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                                                                                                                                                                                                                              Tetracdon nigroviridis full-length cDNA.
CR693646.2 G1:56286064
HTC; cDNA; full-length; full-length cDNA; Tetracdon nigroviridis
Tetracdon nigroviridis
Bukaryota: were
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                                    Gaps
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                                 Indels
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     Pred. No. 3e+03;
0; Mismatches
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/db_xref="taxon:99883"
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Matches 18; Conservative (
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/clone="InAGE:686561"
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/clone lib="WHH BMAP F10"
/note="Organ: Brain; Vector: pYX-Asc; Site_1: ECOR I;
Site 2: Not 1; The library was constructed according
Sonatido, Lennon and Soares, Genome Research, 6:791-8066,
1996. Denatured RNA was size fractionated on a 1% agarose
gel.First strand cDNA synthesis was primed with oligo-dr
primer containing a Not I site. Double strand cDNA was
size selected according to mRNA size fraction, ligated
with EcoR I adaptor, digested with NotI and then cloned
directionally into pYX-Asc vector. The library tag
sequence located between the Not I site and the polyA tail
is CAGCCACCAC. This library was created for the University
lows Brain Anatomy Project (BMAP): 'Gene Discovery in the
Developing Mouse Nervous System', supported by National
Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,
program coordinator."
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AGENCOURT 55788803 NICHD XGC FabN Xenopus laevis cDNA clone IMAGE:8075729 3', mRNA sequence.
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Contact: Daniela S. Gerhard, Ph.D.
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg: 31 Rml0A07 Betheada, MD 20892
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Tom Sargent
CDNA Library Preparation: Express Genomics
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM1358 row: j column: 15
High quality sequence stop: 671.
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Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus; Xenopus.
1 (bases 1 to 794)
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National Institutes of Health, Mammalian Gene Collection (MGC)
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/mol_type="mRNA"
/db_xref="taxon:8355"
/clone="IMAGE:8075729"
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                                                                                             /strain="C57BL/6"
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Email: cgapbs-r@mail.nih.gov

Email: cgapbs-r@mail.nih.gov

Thisue Procurement: Dr. Jim Lin, University of Iowa

CDNA Library preparation: Dr. M. Bento Soares, University of Iowa

CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

CDNA Expression: MGC clone distribution: MGC clone distribution information can be

found through the I.M.AG.B. Consortium/LINL at:

http://image.llnl.gov
Office of Cancer Genomics

National Cancer Institute / NIH

Bldg. 31 Rm10AO7 Bethesda, MD 20892

Email: cgapbe-remail.nih.gov

Tissue Procurement: Tom Sargent
cDNA Library Preparation: Express Genomics

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LIML)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

http://image.lln.gov

Plate: LiAM17356 row: i column: 21

High quality sequence start: 52

High quality sequence stop: 656.
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1 (bases 1 to 780)

NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'organism="Xenopus laevis"
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Best Local Similarity 90.0
Matches 18; Conservative
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RESULT 76 CB247499/c DEFINITION

ORIGIN

SOURCE ORGANISM

KEYWORDS

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ACCESSION

AUTHORS TITLE JOURNAL COMMENT

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FEATURES

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       1 (bases 1 to 822)
Mandall, T., Dwyer, R.A., Huitema, E., Beyer, K., Cvitanich, C.,
Relkar, H., Dwyer, R.A., Gates, K., Roberte, S., Yatzkan, E., Gaffney, T.,
Law, M., Testa, A., Torto-Alalibo, A., Zhang, M., Zheng, L., Mueller, E.,
Law, M., Testa, A., Birch, P.R.J., Gisi, U., Govers, F., Gow, N.A.,
Mauch, F., van West, P., Waugh, M.E., Yu, J., Boller, T., Kamoun, S.,
Lam, S.T. and Judeleon, H.S.
                                                                                                                                                                                                                                                                                                                                                                                                                    EST 25-JAN-2005
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone lib="mycelium, subtracted infection mimic"
/note="Vector: pSPORT1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Phytophthora infestans (potato late blight agent)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Phytophthora infestans"
|mol_type="mRNA"
|strain="88069"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Webber Hall, Riverside, CA 92521, USA
Tel: 909 787 4199
Fax: 909 787 4294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: howard.judelson@ucr.edu
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Judelson HS
Department of Plant Pathology
University of California
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KEYWORDS
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57 Acceaaagaccacaccaa 38

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/done lib="Hordeum vulgare seedling root EST library HVCDNA0007 (Etiolated and unstressed)"
//done lib="Hordeum vulgare seedling root EST library HVCDNA0007 (Etiolated and unstressed)"
//note="Weetor: lambdaZAP; Site 1: Ecomi, Site 2: Xho1;
Seeds were surface sterilized then germinated under axenic conditions in the dark at room temperature on filter paper with water, nystatin and cefotaxime in covered crystallization dishes: Five-day old seedling roots were then harvested, total RNA was prepared, poly(A) RNA was purified, one primary unamplified cDNA library was made, and imilion pfu were in vivo excised to give pBluescript SK(-) CDNA phagemids. These steps were performed in the TJ Close laboratory at the University of California, Riverside (Choi, Close, Fenton). Phagemids were plated and picked at the Clemson University Genomics Institute (CUGI) (Begum, Palmer, Frisch, Akkins and Wing). Plasmid DNA preparations, DNA sequencing and sequence analysis were performed at CUGI (Wing, Yu, Frisch, Henry, Simmons, Oates, Rambo, Main). The sequence has been trimmed to remove vector sequence and contains a minimum of 100 bases
BF254545
HVSMET60004F07f Hordeum vulgare seedling root EST library HVCDNA0007
(ELiolated and unstressed) Hordeum vulgare subsp. vulgare cDNA
clone HVSMEf0004F07f, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Bukaryota; Viridiplantae; Streptophyta; Enbryophyta; Tracheophyta; Bermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticeae; Hordeum.

1 (bases I to 829)

1 (bases I to 829)

1 (bases T.J., Kleinhofs, A., Wise, R., Begum, D., Frisch, D., Yu, Y., Henry, D., Palmer, M., Rambo, T., Simmons, J., Choi, D.W., Fenton, R.D., Oates, R. and Main, D.

Development of a genetically and physically anchored EST resource for barley genomics: Morex unstressed seedling root cDNA library Unpublished (2001)
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this clone see http://www.genome.clemson.edu/orders Also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                of phred value 20 or above. For more details on library
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                On Nov 16, 2000 this sequence version replaced gi:11183650.
Contact: Wing RA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              see Close TJ, Wing R, Kleinhofs A, Wise R (2001)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'organism="Hordeum vulgare subsp. vulgare"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100 Jordan Hall, Člemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /sub_species="vulgare"
/db_xref="taxon:112509"
/clone="HVSMEf0004F07f"
/tissue_type="Geedling root"
/lab_hosf="TJC121"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Clemson University Genomics Institute
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High quality sequence stop: 659.
Location/Qualifiers
                                                                                                                                                                                                                                                                              Hordeum vulgare subsp. vulgare
Hordeum vulgare subsp. vulgare
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/cultivar="Morex"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: rwing@clemson.edu
                                                                                                                                                                                               BF254545.2 GI:13117195
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CZ511376.1 GI:63235674
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                                                    Hominidae; Homo.
1 (bases 1 to 899)
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// "Mol type="make" |
/ "Mol type="make" |
/ "Mol type="make" |
/ "Ab xref="taxon.835s" |
/ "Cone = "IMAGE:6956191" |
/ "Ab host="DH10B (phage-resistant)" |
/ "Cohe = lin="NICHD XGC Brail |
/ "Cohe = lin="NICHD XGC Brail |
/ "Anote="Organ: Parain; Vector: pCWV-SPORT6; Site 1: NotI;
Site 2: Sall; Cloned unidirectionally. Primer: Oligo dT. |
Average insert size 1.5 kb. Constructed by Life
Technologies. Note: This is a Xenopus Gene Collection (XGC) library."
                                                                                                                                                         CU303542

AGENCOURT 14236123 NICHD XGC Brn1 Xenopus laevis cDNA clone IMAGE:6956191 5', mRNA sequence.
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899 bp mRNA linear EST 15-JUL-2002
AGENCOURT 8062638 NIH_MGC_102 Homo sapiens cDNA clone IMAGE:6211356
EQ674913
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.llhl.gov
Plate: LLAM14582 row: o column: 06
High quality sequence start: 38
Gaps
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Indels
 2,
                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (1999)
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm.0AO7 Bethesda, MD 20892
Email: cgapbs-r@mail.nih.gov
Tissue Procurement:
                                                                                                                                                                                                                                                                                Xenopus laevis (African clawed frog)
Xenopus laevis
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'organism="Xenopus laevis"
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                                                            1 AAGGAAACACGGACACCCAA 20
                                     1 AAGGAAACACGGACACCCAA 20
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EST.
Homo Bapiens (human)
                                                                                                                                                                                                                                             CD303542.1 GI:31083408
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JOURNAL
COMMENT
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KEYWORDS
SOURCE
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                                                                                     In the American Lucach, Mammalian Gene Collection (MGC)

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: ATCC

CONA Library Preparation: Rubin Laboratory

CDNA Library Parayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLCM2373 row: 1 column: 13

High quality sequence stop: 644.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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GMW2-49L8a.gl GMW2 Glycine max genomic, genomic survey sequence.
CZ511376
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Nunberg,A., Bedell,J.A., Citek,R.W., Robbins,D., McMenamy,J.,
Peterson,S., Jones,J., Fries,J., Budiman,M.A., Nguyen,H.,
Clifton,S.W. and Stacey,G.
BAC end sequences from Glycine max Williams 82 cultivar genome Unpublished (2005)
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Washington University School of Medicine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Richard K Wilson
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Homo sapiens
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Best Local Simi
Matches 18;
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AUTHORS
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JOURNAL
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KEYWORDS
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       TITLE
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                                                                                                                                                                                                                                                                                                       CZ517024 916 bp DNA linear GSS 11-MAY-2005
GMW2-49L8a.g2 GMW2 Glycine max genomic, genomic survey sequence.
CZ517024
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus; Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nunberg, A., Bedell, J.A., Citek, R.W., Robbins, D., McMenamy, J., Peterson, S., Jones, J., Fries, J., Budiman, M.A., Nguyen, H., Clifton, S.W. and Stacey, G.
BAC end sequences from Glycine max Williams 82 cultivar genome Unpublished (2005)
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918 bp mRNA linear EST 04.
AGENCOURT_10304322 NICHD_XGC_OO1 Xenopus laevis cDNA clone
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larity 90.0%; Pred. No. 3.1e+03;
Conservative 0; Mismatches 2;
                                                                                                                        84.0%; Score 16.8; DB 10; 90.0%; Pred. No. 3.1e+03; ive 0; Mismatches 2;
/organism="Glycine max"
/mol_type="genomic DNA"
/db_xref="taxon:3847"
/clone lib="GMW2"
/note="Glycine max BAC library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genome Sequencing Center
Washington University School of Medicine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: submissions@watson.wustl.edu
Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       organism="Glycine max"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /mol_type="genomic DNA/db_xref="taxon:3847"
/clone_lib="GMW2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
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                                                                                                                                                                                                                 Contact: Richard K Wilson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 AAGGAAACACGGACACCCAA 20
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                                                                                                                                                                                                                                                                                                                                                                                                   Glycine max (soybean)
Glycine max
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                                                                                                                                                          Conservative
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Best Local Similarity
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Matches 18; Conserv
                                                                                                                                                          18;
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CZ517024/c
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KEYWORDS
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Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Martha Rebbert, Steven L. Klein, Ph.D.
Tissue Procurement: Martha Rebbert, Steven L. Klein, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LIML)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LiNL at:
http://image.llnl.gov.
Plate: LiANAlizes row: a column: 24
High quality sequence start: 19
High quality sequence stor: 732.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /tissue_type="oocytes"
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/lab host="DH10B (phage-resistant)"
/lofne lib="NICHD XGC_OOI"
/note="Vector: pCMV-SPORT6; Site_1: Not1; Site_2: Sal1;
/note="Vector: pCMV-SPORT6; Site_1: Not1; Site_2: Sal1;
Cloned unidirectionally. Primer: Oligo dT. Average insert
size 2.2 kb. Constructed by Life Technologies."
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CDNA Library Preparation: CLONTECH Laboratories, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution and Consortium/LLNL at: image.llnl.gov Plate: LLCM849 row: f column: 12
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1 (bases 1 to 919)

NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /tissue_type="carcinoma, cell line"
/lab_host="DH10B (T1 phage-resistant)".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Xenopus laevis"
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
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/clone="IMAGE:5084447"
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Location/Qualifiers
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                               Tumor Gene Index
Unpublished (1997)
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BU915367
AGENCOURT 10493183 NICHD XGC OO1 Xenopus laevis cDNA clone IMAGE:6642041 5', mRNA sequence.
                                                        BE881640 935 bp mRNA linear EST 20-OCT-2000 601490060F1 NIH_MGC_69 Homo sapiens CDNA clone IMAGE:3892287 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /mol_tope="manna"
/db xref="taxon:9606"
/db xref="taxon:9606"
/db xref="taxon:9606"
/done="manna"
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/clone lib="NHH MGC 69"
/note="Organ: lung' Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: Sal1; Cloned unidirectionally. PrimeT: Oligo dT.
Average insert size 1:1 kb. Library constructed by Life
                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP/Gazdar
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://inage.llnl.gov
Plate: LLAM9678 row: h column: 16
High quality sequence stop: 679.
                                                                                                                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae, Homo.

1 (bases 1 to 935)

11 (bases 1 to 935)

Nath-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Xenopodinae; Xenopus; Xenopus; Xenopus; I (bases 1 to 950)
NGI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
NATional Cancer Institute, Cancer Genome Anatomy Project (CGAP), Thuor Gene Index
Unpublished (1997)
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Martha Rebbert, Steven L. Klein, Ph.D.
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90.0%; Pred. No. 3.1e+03;
cive 0; Mismatches 2;
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/organism="Homo sapiens"
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BU915367.1 GI:24097281
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Homo sapiens
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Best Local Similarity 90.0
Matches 18; Conservative
                                                                                                     mRNA sequence.
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BE881640/c
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BU915367/c
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                                                                                                                                3' adaptor sequence: 5'-CHCGGCCATTATGGCC-3' and 5'-ATTCTAGAGGCGCGAGGCGCGAGGGGTT-6' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.55 kb (range 0.9-4.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA)."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CC694001 930 bp DNA linear GSS 19-JUN-2003 OGVAR91TV ZM_0.7_1.5_KB Zea mays genomic clone ZMMBMa0491014,
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/clone_lib="NIH MGC_53"
/note="Organ: bladder; Vector: pDNR-LIB (Clontech);
site_l: Sfil (ggocgcteggct); Site_2: Sfil
(ggccattatggcc); Double-stranded cDNA was prepared from cell line RNA. 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGGCCATTATGGCC-3' and
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1 (Dases 1 to 930)
Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T., Whitelaw, C.A., Flager, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T., Citek, R.W., Numberg, A., Robbins, D. and Lakey, N.
Consortium for Maize Genomics
Other GSSs: OGTAR91TH
Contact: Cathy Whitelaw
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/note="Vector: pBCSK-; Site_1: HincII; 0.7-1.5 kb
methylation filtered genomic DNA library"
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                                                                                                                                                                                                                                                                                                                                                                Length 919;
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Tel: 301-838-5843
Fax: 301-838-0208
                                                                                                                                                                                                                                                                                                                                                                                                                    2; Indels
                                                                                                                                                                                                                                                                                                                                                                   84.0%; Score 16.8; DB 2; 90.0%; Pred. No. 3.1e+03; iive 0; Mismatches 2;
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/mol_type="genomic DNA"
/strain="B73"
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/clone="ZMMBMa0491014"
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Class: methylation filtered.
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CC694001.1 GI:32098777
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Best Local Similarity 90.0'
Matches 18; Conservative
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Query Match
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BG335613
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                                                                                                                                                                                                                                             /clone="IMAGE:6642041"
/tissue_type="oocytes"
/lab host="NH10B (phage-resistant)"
/clone_lin="WICHD XGC_OO1"
/note="Vector: pCW-SPORT6; Site_1: Not1; Site_2: Sal1;
Cloned unidirectionally. Primer: Oligo dT. Average insert
size_2.2 kb. Constructed by Life Technologies."
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/db xref="taxon:8355"
/clone="lanAGE:637855"
/tissue type="cocytes"
/lab_host="DH10B (phage-resistant)"
/clone lib="NICHD XGC OOl"
/note="Vector: pGW-SPORT6; Site_1: Not!; Site_2: Sall;
/note="Vector: pGW-SPORT6; Site_1: Not!; Site_2: Sall;
/cloned unidirectionally. Primer: Oligo dT. Average insert
size 2.2 kb. Constructed by Life Technologies."
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Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Martha Rebbert, Steven L. Klein, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: NCI-CGAP clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM14215 row: o column: 07
High quality sequence stop: 597.
Location/Qualifiers
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1 (bases 1 to 953)
NCT-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                                                                                                                                                                                                                                                                                                                                                                                       Length 950;
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Pred. No. 3.1e+03;
); Mismatches 2; Indels
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Xenopus laevis
                                                                                                                                                                                         /organism="Xenopus laevis"
/mol_type="mRNA"
/db_xref="taxon:8355"
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90.0%;
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Best Local Similarity 90.0
Marches 18; Conservative
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Unpublished (1997)
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602073196F1 NCI_CGAP_Li9.Mus musculus cDNA clone IMAGE:4210415 5', mENA sequence.
BP532081.1 GI:11619547
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/note="Organ: placenta; Vector: pOTB7; Site_1: Xho1;
Site_2: EcoR1; cDNA made by oligo-dT priming.
Directionally cloned into EcoR1/Xho1 sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp into Horary constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.B. Consortium/LLNL at:
http://mage.llnl.gov.
Plate: LLCM1221 row: a column: 09
High quality sequence stop: 373.
Location/Qualifiers
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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Mammalia; Eutheria; Buarchontoglires; Primates; Catarrhini;
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Length 953;
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Tissue Procurement: ATCC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.B. Consortium (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4541840"
/tissue_type="cioriocarcinoma"
/lab_host="DH10B (phage-resistant)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     84.0%; Score 16.8; DB 2;
90.0%; Pred. No. 3.1e+03;
tive 0; Mismatches 2;
Score 16.8; DB 5;
Pred. No. 3.1e+03;
); Mismatches 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Robert Strausberg, Ph.D.
                                                                                                                                                     900 AAGGAAACACGAAAACCCAA 919
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                                             ;
0
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                                                                                                                                                                                                                                                                                                                                                                                     BG335613.1 GI:13142051
                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hominidae, Homo.
1 (bases 1 to 959)
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Gaps

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us-10-829-474-2.rst

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| 1. 1071 |
| / organism="Homo sapiens" |
| / organism="Homo sapiens" |
| / mol_type="mRNM" |
| / db xref="taxon:9606" |
| / clone="IMAGE:4183723" |
| / tissue_type="glioblastoma with BGFR amplification" |
| / clone lib="NCI_CGAP_Brn64" |
| / clone lib="NCI_CGAP_Brn64" |
| / clone="Organ: brain; Vector: pCWV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT. Saverage insert size 1.57 kb. Constructed by Life |
| Technologies. Note: this is a NCI_CGAP Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BF337949 1071 bp mRNA linear EST 22-NOV-2000 c20353776F1 NCI_CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4183723
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hominidae; Homo.

I (bases 1 to 1071)

Is NIH-MGC http://mgc.nci.nih.gov/.

In Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: capabbe.remail.nih.gov.

Tissue Procurement: David N. Louis, M.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.B. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.B. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLAM9500 row: g column: 20

High quality sequence start: 4

High quality sequence stort: 4

High quality sequence stort: 4
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Euarchontoglires, Primates, Catarrhini,
                /organism="Xenopus tropicalis"
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/clone="ISB1-55G5"
/clone="ISB1-55G5"
/note="Vector: pBeloBAC11; ISB-1 Xenopus tropicalis BAC
Library Segment 1"
                                                                                                                                                                                                                                                                    Length 1032;
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84.0%; Score 16.8; DB 2; Length 1071;
Best Local Similarity 90.0%; Pred. No. 3.1e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0
                                                                                                                                                                                                                                                                                                                      Indels
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ilarity 90.0%; Pred. No. 3.1e+03;
Conservative 0; Mismatches 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5', mRNA sequence.
BF337949
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Best Local Similarity
Matches 18; Conserv
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                                                                                                                                                                                                                                                         Context: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey B. Green, M.D.
Tissue Procurement: Jeffrey B. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC Clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM9977 row: o column: 24
High quality sequence stop: 595.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Xenopus tropicalis (western clawed frog)

Xenopus tropicalis

Xenopus tropicalis

Xenopus tropicalis

Ambibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;

Xenopodinae; Xenopus; Silurana.

1 (bases 1 to 1032)

Kremitzki,C., Carter,J., McPherson,J., Warren,W., Graves,T.,

Mardis,E. and Wilson,R.

A physical map of the xenopus tropicalis genome

Unpublished (2003)
                                                                          Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Buarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone="IMAGE:4210415"
/lab_host="DH10B (T1 phage-resistant)"
/clone lib="NCI CGAP Li9"
/note="Organ: liver; Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: Sall; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.9 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
                                                                                                                                                              1 (bases 1 to 1031)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Washington University School of Medicine
Email: submissions@waten.wustl.edu
Emsert Length: 75000 Std Error: 0.00
Seq primer: Sp6 ATTTAGGTGACACTATAG
Class: BAC ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Mus musculus"
/mol_type="mRNA"
/strain="FVB/N"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        High quality sequence start: 5
High quality sequence stop: 756.
Location/Qualifiers
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                           Mus musculus (house mouse)
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CL111503.1 GI:40605138
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Best Local Similarity 90.0°
Matches 18; Conservative
                                                                                                                                                                                                                                        Unpublished (1999)
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                                                       Mus musculus
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Matches 18; Conserv
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                      GSS 31-DEC-2003
                                                                                                                                                    Xenopus tropicalis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Xenopodinae; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus; Silurana.
I (bases 1 to 1097)
Kremitzki, C., Carter, J., McPherson, J., Warren, W., Graves, T.,
A physical map of the xenopus tropicalis genome
Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianidae; Gallus.

1 (bases 1 to 1123)
Kremitzki, C., Higginbotham, J., Wylie, K., Carter, J., McPherson, J., Warren, W., Graves, T., Mardis, E. and Wilson, R.

Gallus gallus BAC End Reads
Unpublished (2003)
Contact: Richard K. Wilson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /cell_line="Stock 248 F7A2, inbred N7"
/clone_lib="CH216"
/note="Vector: pTARBAC2.1; CHORI-216 Xenopus tropicalis
BAC library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                    CL049473 linear GSS CH216-69P17 Sp6.1 CH216 Kenopus tropicalis genomic clone CH216-69P17, genomic survey sequence.
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                                                                                                                                                                                                                                                                                                                                                                           Washington University School of Medicine
                                                                                                                                      Xenopus tropicalis (western clawed frog)
                                                                                                                                                                                                                                                                                                                                                                                           Email: submissions@watson.wustl.edu
Insert Length: 175000 Std Error: 0.00
Seq primer: Sp6 ATTTAGGTGACACTATAG
Class: BAC ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Xenopus tropicalis"
/mol_type="genomic DNA"
/strain="Nigerian frog"
/db_xref="taxon:8364"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           High quality sequence start: 223
High quality sequence stop: 392.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 114 AAGCAAACACGGACAACCAA 133
                                                                                                                                                                                                                                                                                                                                     Contact: Richard K Wilson
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Gallus gallus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 90.0
Matches 18; Conservative
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SOURCE
ORGANISM
                                      DEFINITION
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JOURNAL
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AUTHORS
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CL049473
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                                                                                                                                                                                                                                                    /cell_line="UCD001, inbred 256"
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/note="Vector: pTARBAC2.1; Site_l: EcoRI; Site_2: EcoRI;
CH261 Female Chicken library - For library and clone
ordering information: http://www.chori.org/bacpag"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Spencer, D. H., Raymond, C. K., Smith, E. E., Sims, E. E., Hastings, M., Burns, J.L., Kanl, R. and Olsen, M. V.
Whole-Genome-Sequence variation among multiple isolates of Psedomonas aeruginosa library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.
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/clone="msh2 5104"
/clone_lib="msh"
/note="Environmental isolate. Whole genomic shotgun
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                                                                                                                                                                                                                                                                                                                                                                                                                        Length 1123;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                   Score 16.8; DB 9;
Pred. No. 3.1e+03;
0; Mismatches 2;
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Box 352145, Seattle, WA 98105-2145, USA
Tel: 2062216954
Fax: 2066857244
                                                                                                                                       /mol_type="genomic_DNA"
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                                                                                                                    organism="Gallus gallus"
Class: BAC ends
High quality sequence start: 91
High quality sequence stop: 469.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: craymond@u.washington.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  organism="Pseudomonas"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           J. Bacteriol. (2002) In press
Contact: Chris K. Raymond
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     genomic survey sequence.
BZ576789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BZ576789.1 GI:27211850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 AAGGAAACACGGACACCCAA
                                                                                                                                                                                                                                   /sex="female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pseudomonas aeruginosa
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90.0%;
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Best Local Similarity 90.03
Matches 18; Conservative
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RESULT 97 CNSOG3AI/c LOCUS

DEFINITION ACCESSION

SOURCE ORGANISM

REFERENCE

VERSION KEYWORDS

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Mauceli, E., Bouneau, L., Fischer, C., Ozouf-Costaz, C., Bernot, A.,
Nicaud, S., Jaffe, D., Fisher, S., Lutfalla, G., Dossat, C.,
Segurens, B., Dassilva, C., Salanoubat, M., Levy, M., Boudet, N.,
Castellano, S., Anthouard, V., Jubin, C., Castelli, V., Katinka, M.,
Vacherie, B., Biemont, C., Skalli, Z., Cattolico, L., Poulain, J., De
Berardinis, V., Cruaud, C., Duprat, S., Brottier, P., Couranceau, J.P.,
Gouzy, J., Parra, G., Lardier, G., Chapple, C., McKernan, K.J.,
McBwan, P., Bosak, S., Kellis, M., Volff, J.N., Guigo, R., Zody, M.C.,
Mesirov, J., Lindblad-Toh, K., Birren, B., Nusbaum, C., Kan, D.,
Robinson-Rechavi, M., Laudet, V., Schachter, V., Quigo, R., San, D.,
Saurin, W., Scarpelli, C., Wincker, P., Lander, E.S., Weissenbach, J.
Garnes d. Collius, H.
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Mauceli,E., Bouneau,L., Fischer,C., Ozouf-Costaz,C., Bernot,A.,
Nicaud,S., Jaffe,D., Fisher,S., Lutfalla,G., Dossat,C.,
Squrens,B., Dasilva,C., Salanoubat,M., Levy,M., Boudet,N.,
Castellano,S., Anthouard,V., Jubin,C., Castelli,V., Katinka,M.,
Vacherie,B., Biemont,C., Skalli,Z., Cattolico,L., Poulain,J., De
Berardinis,V., Craud,C., Duprat,S., Brottier,P., Coutanceau,J.P.,
Gouzy,J., Parra,G., Lardier,G., Chapple,C., McKernan,K.J.,
McEwan,P., Bosak,S., Kellis,M., Volff,J.N., Guigo,R., Zody,M.C.,
Mesirov,J., Lindblad-Toh,K., Birren,B., Nusbaum,C., Kahn,D.,
Robinson-Rechavi,M., Laudet,V., Schachter,V., Quetier,F.,
Saurin,W., Scarpelli,C., Wincker,P., Lander,E.S., Weissenbach,J.
and Roest Crollius,H.
Genome duplication in the teleost fish Tetraodon nigroviridis
reveals the early vertebrate proto-karyotype
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Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetradontoidea; Tetraodontidae; Tetraodon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
Submitted (25-NOV-2004) Genoscope - Centre National de Sequencage
La rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
(B-mail : seqrefégenoscope.cns.fr - Web : www.genoscope.cns.fr)
On Dec 3, 2004 this sequence version replaced gi:51169026.
The sequences are based on single pass reads.
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HTC; CDNA; full-length; full-length cDNA; Tetraodon nigroviridis.
Tetraodon nigroviridis
Tetraodon nigroviridis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           reveals the early vertebrate proto-karyotype Nature 431 (7011), 946-957 (2004)
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/db_xref="taxon:99883"
/tisque_type="Muscle"
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CR647318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           http://www.genoscope.cns.fr/tetraodon.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        More information available at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1158 AAGGAAACACGCAAACCCAA 1139
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Best Local Similarity 90.09
Matches 18; Conservative
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CNS0EYFW/c
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                                          AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Jaillon, O., Aury, J.M., Brunet, F., Petit, J.L., Stange-Thomann, N., Mauceli, E., Bouneau, L., Fischer, C., Ozouf-Costaz, C., Bernot, A., Nicaud, S., Juffe, D., Fisher, S., Lutfalla, G., Dosaét, C., Segurens, B., Dasilva, C., Salanoubat, M., Levy, M., Boudet, N., Vacherie, B., Biemont, C., Skalli, Z., Cattolico, L., Poulain, J., De Berardinis, V., Cruaud, C., Skalli, Z., Cattolico, L., Poulain, J., De Berardinis, V., Cruaud, C., Chapple, C., McKernan, K.J., McEwan, P., Bosak, S., Kellis, M., Volff, J.N., Guigo, R., Zody, M.C., Mesirov, J., Lindblad-Toh, K., Birren, B., Nusbaum, C., Kahn, D., Robinson-Rechavi, M., Laudet, V., Schachter, V., Quetier, F., Saurin, W., Scarpelli, C., Wincker, P., Lander, E.S., Weissenbach, J. and E. S., Weissenbach, J. Lander, M., Lander, W., Schachter, V., Cause, J., Lander, J., Lander, E.S., Weissenbach, J. Lander, L., Lander,
                                                                                                                                                                  HTC 05-JUL-2005
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HTC; CDNA; full-length CDNA; Tetraodon nigroviridis.
Tetraodon nigroviridis
Tetraodon nigroviridis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopeerygii; Teleostei; Buteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetradontoidea; Tetraodontidae; Tetraodon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; settinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei; Acanthomerpha; Acanthopterygii; Percomorpha; Tetraodontiformes; Tetradontoidea; Tetraodontidae; Tetraodon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (24-NOV-2004) Genoscope - Centre National de Sequencage : 2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE (Email: seqref@genoscope.cns.fr. Web : www.genoscope.cns.fr) On Dec 3, 2004 this sequence version replaced gi:51198195. The sequences are based on single pass reads.
                                                                                                                                                                                                                                                                                 CR700286.2 GI:56289005
HTC; cDNA; full-length; full-length cDNA; Tetraodon nigroviridis
Tetraodon nigroviridis
Tetraodon nigroviridis
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                                                                                                                                                                      linear
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0; Mismatches 2
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CR672581
                                                                                                                                                                  CNSOG3AI 1338 bp mRNA Tetraodon nigroviridis full-length cDNA.
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Direct Submission
Submitted (24.NOV-2004) Genoscope - Centre National de Sequencage submitted (24.NOV-2004) Genoscope - Centre National de Sequencage : 2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE (8-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr) On Dec 3, 2004 this sequence version replaced gi:51143763.

The sequences are based on single pass reads.

More information available at http://www.genoscope.cns.fr/tetraodon.

Location/Qualifiers
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84.0%; Score 16.8; DB 4; Length 1541;
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GenCore version 5 Copyright (c) 1993 - 2006 B OM nucleic - nucleic search, using sw model Run on: March 9, 2006, 00:09:45; Sea	Title: US-10-829-474-4  Perfect score: 25 Sequence: 1 tccgctgcagagttgcccgttacga 25 Scoring table: IDENTITY_NUC Gapop 10.0, Gapext 1.0 Searched: 5883141 seqs, 28421725653 residues Total number of hits satisfying chosen parameters: Minimum DB seq length: 0 Maximum DB seq length: 2000000000	Post-processing: Minimum Match 1008 Listing first 500 summaries Listing first 500 summaries GenEmbl:* 1: qb ba:* 2: qb_in:* 3: qb_on:* 4: gb_on:* 5: qb_on:* 6: qb_pat:* 7: qb_ph:* 8: qb_pr:* 10: qb_pr:* 11: qb_pr:* 12: qb_pr:* 13: qb_pr:* 13: qb_pr:* 14: qb_pr:*	Pred. No. is the number of results predictions of greater than or equal to the score and is derived by analysis of the total and is derived by analysis of the total of the total of the score match Length DB ID  25 100.0 73 13 AY18933 25 100.0 109 13 EXUSSER 25 100.0 109 13 EXUSSER 25 100.0 109 13 EXUSSER 25 100.0 109 13 EYUSSER 25 100.0 115 13 AY189159 25 100.0 116 13 AY189161 25 100.0 116 13 AY189161 25 100.0 116 13 AY189161 25 100.0 116 13 AY189163 25 100.0 116 13 AY189163 25 100.0 116 13 AY189163 25 100.0 116 13 AY189164 25 100.0 116 13 AY189165 25 100.0 116 13 AY189165 25 100.0 116 13 AY189166

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Enterovirus sp.

Enterovirus sp.

Viruses; ssRNA positive-strand viruses, no DNA stage;

Picornaviridae; Enterovirus.

1 (bases 1 to 100)

Muir, P., Nicholson, F., Spencer, G.T., Ajetunmobi, J.F., Starkey, W.G., Khan, M., Archard, L.C., Cairns, N.J., Anderson, V.E.R., Leigh, P.N., Broward, R.S. and Banatvala, J.B.

Enterovirus infection of the central nervous system of humans: lack J. Gen. Virol. 77 (Pt 7), 1469-1476 (1996)
 Khan,M., Archard,L.C., Cairns,N.J., Anderson,V.E.R., Leigh,P.N., Howard,R.S. and Banatvala,J.E.
Enterovirus infection of the central nervous system of humans: lack of association with chronic neurological disease
J. Gen. Virol. 77 (Pt 7), 1469-1476 (1996)
                                                                                                                                                 Direct Submission
Submitted (22-APR-1996) Peter Muir, Virology, UMDS, Lambeth Palace
Road, London SE1 7EH, UK
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/organism="Enterovirus sp/mol_type="genomic RNA"
/db_xref="texon:47681"
/note="from patient B6"
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/db_xref="taxon:47681"
/note="from patient A23"
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/organism="Enterovirus
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                                                                                                         2 (bases 1 to 83)
Muir, P.
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Best Local Similarity 100.0
Matches 25; Conservative
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Human enterovirus 71 isolate NSW/167/97 5' untranslated region,
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Picornaviridae; Enterovirus.
1 (bases 1 to 83)
Muir,P., Nicholson,F., Spencer,G.T., Ajetunmobi,J.F., Starkey,W.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 (bases 1 to 73)
Craig, M.E., Howard, N.J., Silink, M. and Rawlinson, W.D.
Direct Submission
Submitted (03-DEC-2002) Virology Division, University of New South Wales, Prince of Wales Hospital, High Street, Randwick, NSW 2031, Australia
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Picornaviridae; Enterovirus.
I (bases 1 to 73)
Craig, M.E., Howard, N.J., Silink, M. and Rawlinson, W.D.
Reduced Frequency of HLA DRB1*03-DQB1*02 in Children with Type 1
Diabetes Associated with Enterovirus RNA
J. Infect. Dis. 187 (10), 1562-1570 (2003)
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                                                                                                                                                                 Score 25; DB 13; Length 73; Pred. No. 0.32;
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Enterovirus sp. 5' NTR sequence from patient B6.
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// Organism="Human enterovirus 71"
//mol type="genomic RNA"
//isolate="NSW/167/97"
               1. .73
/organism="Human enterovirus B"
/mol type="genomic RNA"
/isolate="NSW/51/97"
/db xref="taxon:138949"
<1. .>73
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tive 0; Mismatch
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Human enterovirus 71
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VRL 23-MAY-1996

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VRL 29-MAY-2005

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                    0; Mismatches
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Best Local Similarity 100.0%; Pred. No. 0
Matches 25; Conservative 0; Mismatche
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Bankowski, M.J.
Best Local Similarity 100.0
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E7U00872/c
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AY189929/c
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                                                                                                                                                                                                             phenotypes
Umpulished (2005)
2 (bases 1 to 109)
Gharbi,J., Elhiar,R., Ben M'Hadheb,M., Jaidane,H., Bouslama,L.,
N'Saibia,S. and Aouni,M.
Direct Submission
Direct Submission
Submitted (06-MAY-2005) Virology, Faculty of Pharmacy & Higher
Institute of Biorechnology, Avicenne Street, Monastir 5000, Tunisia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (17-AUG-1993) Bankowski M. J., Diagnostic Services, Inc., Clinical Virology & Molecular Medicine, 340 Goodlette Road South, Naples, FL 33940, USA
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                                                Human echovirus 11

Human echovirus 11

Yuruses; saRNA positive-strand viruses, no DNA stage;

Picornaviridae; Enterovirus.

1 (bases 1 to 109)

Gharbi,J., Elhiar,R., Ben M'Hadheb,M., Jaidane,H., Bouslama,L.,
N'Saibia,S. and Aouni,M.

N'Saibia,S. and Aouni,M.

Noclectide sequences of the IRES domains IV and V of natural isolates ECHO virus type 11 with different replicative capacities
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human enterovirus 71

Picornaviridae; Enterovirus.

1 (bases 1 to 109)

Zheng, Z.M., He, P.J., Caueffield, D., Neumann, M., Specter, S.,

Baker, C.C. and Bankcwskt, M.J.

Enterovirus 71 isolated from China is serologically similar to the prototype E71 BrCr strain but differs in the 5'-noncoding region 30, Med. Virol. 47 (2), 161-167 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="domain V of IRES (internal ribosome entry site)"
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/organism="Human enterovirus 71"
/mol_type="unassigned DNA"
/strain="prototype BrCr"
/db_xref="taxon:39054"
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                                                                                                                                                                                                                                                                                                                                                                                              'organism="Human echovirus 11"
                                                                                                                                                                                                                                                                                                                                                                                                                             /mol_type="genomic RNA"
/strain="Gregory prototype"
/db_xref="taxon:12078"
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DQ029093
DQ029093.1 GI:66473301
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Bankowski, M.J.
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Best Local Similarity
Matches 25; Conserva
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SOURCE
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E7U00871/c
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ACCESSION
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                                   KEYWORDS
SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                             Human enterovirus 71
Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
1 (bases 1 to 109)
Zheng, Z.M., He, P.J., Caueffield, D., Neumann, M., Specter, S.,
Baker, C.C. and Bankowski, M.J.
Barterovirus 71 isolated from China is serologically similar to the prototype E71 BrCs strain but differs in the 5'-noncoding region J. Med. Virol. 47 (2), 161-167 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
Submitted (17-ANG-1993) Bankowski M.J., Diagnostic Services, Inc.,
Clinical Virology & Molecular Medicine, 340 Goodlette Road South,
Naples, FL 33940, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human enterovirus B
Human enterovirus B
Human enterovirus B
Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
1 (bases 1 to 112)
Craig, M.E., Howard, N.J., Silink, M. and Rawlinson, W.D.
Craig, M.E., Howard, N.J., Silink, M. and Rawlinson, W.D.
Diabetes Associated with Enterovirus RNA
J. Infect. Dis. 187 (10), 1562-1570 (2003)
Gaps
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Indele
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Enterovirus E71 H 5' untranslated region.
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/strain="E 71 H"
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Gaps

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VRL 08-MAY-2003

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Gaps

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VRL 08-MAY-2003

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Craig, M.B., Howard, N.J., Silink, M. and Rawlinson, W.D.
Craig, M.B., Howard, N.J., Silink, M. and Rawlinson, W.D.
Direct Submission
Submitted (29-NOV-2002) Virology Division, South Eastern Area
Laboratory Services, University of New South Wales/Prince of Wales
Hospital, High Street, Randwick, NSW 2031, Australia
Location/Qualifiers
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Craig, M.E., Howard, N.J., Silink, M. and Rawlinson, W.D.
Direct Submission
Submitted (29-NOV-2002) Virology Division, South Eastern Area
Laboratory Services, University of New South Wales/Prince of Wales
Hospital, High Street, Randwick, NSW 2031, Australia
Location/Qualifiers
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Human enterovirus B
Viruses; sBRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
1 (bases 1 to 116)
Craig, M.E., Howard, N.J., Sllink, M. and Rawlinson, W.D.
Reduced Frequency of HLA DRB1*03-DQB1*02 in Children with Type 1
Diabetes Associated with Enterovirus RNA
0. Infect. Dis. 187 (10), 1562-1570 (2003)
 Reduced Frequency of HLA DRB1*03-DQB1*02 in Children with Type Diabetes Associated with Enterovirus RNA J. Infect. Dis. 187 (10), 1562-1570 (2003)
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Human enterovirus B isolate NSW/07/97 5' UTR, partial sequence.
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Human enterovirus B isolate NSW/02/97 5' UTR, partial sequence
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                                                                                                                                                                                                                                 /organism="Human enterovirus
                                                                                                                                                                                                                                             /mol type="genomic RNA"
/isolate="NSW/01/97"
/db_xref="taxon:138949"
<1._.>116
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/isolate="NSW/02/97"
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<1._.>116
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Matches 25; Conserv
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12721936
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AY189160/c
LOCUS
DEFINITION
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LOCUS
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VERSION
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TITLE
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AUTHORS
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JOURNAL
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SOURCE
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Direct Submission
Submitted (29-NOV-2002) Virology Division, South Eastern Area
Laboratory Services, University of New South Wales/Prince of Wales
Hospital, High Street, Randwick, NSW 2031, Australia
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human enterovirus B
Human enterovirus B
Viruses; saRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
I (bases 1 to 115)
Craig, M.E., Howard, N.J., Silink, M. and Rawlinson, W.D.
Reduced Prequency of HLA DRB1*03-DQB1*02 in Children with Type 1
Diabetes Associated with Enterovirus RNA
J. Infect. Dis. 187 (10), 1562-1570 (2003)
                                                                                                                                                                                                                                                                                                                                                                                                             Human enterovirus B isolate NSW/100/98 5' UTR, partial sequence.
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AV189158.1 GI:28274181
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Human enterovirus B
Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridas Enterovirus.
1 (bases 1 to 116)
Craig, M.E., Howard, N.J., Silink, M. and Rawlinson, W.D.
                                                                                                                                                                                        13; Length 112;
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                                   1. .112
/organism="Human enterovirus B"
/mol_type="genomic RNA"
/isoTate="NSW/47/97"
/db_xref="taxon:138949"
<1. .>112
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                                                                                                                                                                                          DB
                                                                                                                                                                                    Query Match
100.0%; Score 25; DB
Best Local Similarity 100.0%; Pred. No. 0.3
Matches 25; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /mol_type="genomic RNA"
/isolate="NSW/100/98"
/db_xref="taxon:138949"
<1._.>115
                                                                                                                                                                                                                                                                                    74 TCCGCTGCAGAGTTGCCCGTTACGA 50
                                                                                                                                                                                                                                                              1 TCCGCTGCAGAGTTGCCCGTTACGA 25
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Australia
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ORIGIN
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AY189179/c
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AY189158/c
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Submitted (29-NOV-2002) Virology Division, South Eastern Area
Laboratory Services, University of New South Wales/Prince of Wales
Hospital, High Street, Randwick, NSW 2031, Australia
Location/Qualifiers
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                               Human enterovirus B
Human enterovirus B
Viruses; ssRNA positive-strand viruses, no DNA stage;
Viruses; ssRNA positive-strand viruses, no DNA stage;
1 (bases I Howard, N.J., Silink, M. and Rawlinson, W.D.
Craig, M.B., Howard, N.J., Silink, M. and Rawlinson, W.D.
Reduced Prequency of HLA DRB1*03-DQB1*02 in Children with Type 1
Joinbetes Associated with Enterovirus RNA
J. Infect. Dis. 187 (10), 1562-1570 (2003)
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Picornaviridae; Enterovirus.
1 (bases 1 to 116)
Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
Diabetes Frequency of HLA DRB1*03-DQB1*02 in Children with Type 1
Diabetes Associated with Enterovirus RNA
J. Infect. Dis. 187 (10), 1562-1570 (2003)
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Human enterovirus 71 isolate NSW/08/97 5' UTR, partial sequence.
AY189161
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 13; Length 116;
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Craig, M.E., Howard, N.J., Silink, M. and Rawlinson, W.D.
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/mol_type="genomic RNA"
/isolate="NSW/08/97"
/db_xref="taxon:39054"
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                                                                                                                                                                                                                                                                                                                                                                /mol_type="genomic RNA"
/isolate="NSW/07/97"
/db_xref="taxon:138949"
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AY189160.1 GI:28274383
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Human enterovirus 71
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Craig, M.E., Howard, N.J., Silink, M. and Rawlinson, W.D.
Direct Submission
Submitted (29-NOV-2002) Virology Division, South Eastern Area
Laboratory Services, University of New South Wales/Prince of Wales
Hospital, High Street, Randwick, NSW 2031, Australia
Location/Qualifiers
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Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
Reduced Frequency of HLA DRB1*03-DQB1*02 in Children with Type 1
Diabetes Associated with Enterovirus RNA
J. Infect. Dis. 187 (10), 1562-1570 (2003)
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Picornaviridae; Enterovirus.

( bases 1 to 116)
Craig, M.E., Howard, N.J., Silink, M. and Rawlinson, W.D.
Reduced Frequency of HIA DRBH*03-DQBH*02 in Children with Type 1
Diabetes Associated with Enterovirus RNA
J. Infect. Dis. 187 (10), 1552-1570 (2003)
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Human enterovirus B isolate NSW/14/97 5' UTR, partial sequence.
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Craig, M.E., Howard, N.J., Silink, M. and Rawlinson, W.D.
Direct Submission
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Picornaviridae; Enterovirus.
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/isolate="NSW/14/97"
/db xref="taxon:138949"
74 TCCGCTGCAGAGTTGCCCGTTACGA 50
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Human enterovirus B
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Matches 25; Conservative
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Craig, M. B., Howard, N. J., Silink, M. and Rawlinson, W. D.
Direct Submission
Submitted (29-NOV-2002) Virology Division, South Bastern Area
Laboratory Services, University of New South Wales/Prince of Wales
Hospital, High Street, Randwick, NSW 2031, Australia
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1 (base 1 to 116)
Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
Reduced Frequency of HLA DRB1*03-DQB1*02 in Children with Type 1 blabetes Associated with Enterovirus RNA
J. Infect. Dis. 187 (10), 1562-1570 (2003)
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Picornaviridae; Enterovirus.
I (bases 1 to 116)
Craig, M.E., Howard, N.J., Silink, M. and Rawlinson, W.D.
Reduced Frequency of HLA DRB1*03-DQB1*02 in Children with Type 1
Diabetes Associated with Enterovirus RNA
J. Infect. Dis. 187 (10), 1562-1570 (2003)
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Human enterovirus B isolate NSW/17/97 5' UTR, partial sequence.
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/organism="Human enterovirus B"
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                                                                                     Query Match 100.0%; Score 25; DE Best Local Similarity 100.0%; Pred. No. 0.3 Matches 25; Conservative 0; Mismatches
/mol_type="genomic RNA"
/isolate="NSW/16/97"
/db_xref="taxon:138949"
<1...>116
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/isolate="NSW/17/97"
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Human enterovirus B
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Best Local Similarity 100.
Matches 25; Conservative
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AX189167 116 bp RNA linear VRL 08-MAY-2003
Human enterovirus B isolate NSW/25/97 5' UTR, partial sequence.
AX189167
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2 (bases 1 to 116)
Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
Direct Submission
Submitted (29-NOV-2002) Virology Division, South Eastern Area
Laboratory Services, University of New South Wales/Prince of Wales
Hospital, High Street, Randwick, NSW 2031, Australia
Location/Qualifiers
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Picornaviridae; Enterovirus.
1 (bases 1 to 116)
Craig, M.E., Howard, N.J., Silink, M. and Rawlinson, W.D.
Reduced Frequency of Hith DRB1*03-DOB1*02 in Children with Type
Diabetes Associated with Enterovirus RNA
J. Infect. Dis. 187 (10), 1562-1570 (2003)
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Human enterovirus B isolate NSW/45/97 5' UTR, partial sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 (bases 1 to 116)
Craig, M.E., Howard, N.J., Silink, M. and Rawlinson, W.D.
Direct Submission
                                                                                                                                                                             1. .116
/organism="Human enterovirus NSW/23/97"
/mol_type="genomic RNA"
/isolate="NSW/23/97"
/db_xref="taxon:220228"
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/mol type="genomic RNA"
/isolate="NSW/25/97"
/db_xref="taxon:138949"
<11. ->116
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VRL 08-MAY-2003
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Craig, M.E., Howard, N.J., Silink, M. and Rawlinson, W.D.
Direct Submission
Submitted (29-N0V-2002) Virology Division, South Eastern Area
Laboratory Services, University of New South Wales/Prince of Wales
Hospital, High Street, Randwick, NSW 2031, Australia
Location/Qualifiers
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Direct Submission
Submitted (29-NOV-2002) Virology Division, South Bastern Area
Laboratory Services, University of New South Wales/Prince of Wales
Hospital, High Street, Randwick, NSW 2031, Australia
Location/Qualifiers
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Craig, M.E., Howard, N.J., Silink, M. and Rawlinson, W.D.
Diabetes Associated with Enterovirus RNA
J. Infect. Dis. 187 (10), 1562-1570 (2003)
                                                                                                                                                   Human enterovirus B
Human enterovirus B
Yūruses; saRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.

1 (bases 1 to 116)
Craig,M.E., Howard,N.J., Sllink,M. and Rawlinson,W.D.
Reduced Frequency of HLA DRB1*03-DQB1*02 in Children with Type 1
Diabetes Associated with Enterovirus RNA
J. Infect. Dis. 187 (10), 1562-1570 (2003)
                                           AY189171 116 bp RNA linear VRL 08-MAY-.
Human enterovirus B isolate NSW/60/97 5' UTR, partial sequence.
AY189171
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Human enterovirus B isolate NSW/73/97 5' UTR, partial sequence.
AY189173.1 GI:28274396
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Human enterovirus B
Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
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ilarity 100.0%; Pred. No. 0.32;
Conservative 0; Mismatches 0;
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/mol_type="genomic RNA"
/isolate="NSW/73/97"
/db_xref="taxon:138949"
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/mol_type="genomic RNA"
/isolate="NSW/60/97"
/db_xref="taxon:138949"
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            Viruees; BSRNA positive-strand viruses, no DNA stage;
Viruees; BSRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.

E 1 (bases 1 to 116)

Craig, M.E., Howard, N.J., Silink, M. and Rawlinson, W.D.
Reduced Frequency of HLA DRB1*03-DQB1*02 in Children with Type 1
Diabetes Associated with Enterovirus RNA
L J. Infect. Dis. 187 (10), 1562-1570 (2003)
D 12721936
E 2 (bases 1 to 116)
Craig, M.E., Howard, N.J., Silink, M. and Rawlinson, W.D.
Direct Submission
L Submitted (29-NOV-2002) Virology Division, South Eastern Area
Laboratory Services, University of New South Wales/Prince of Wales
Hospital, High Street, Randwick, NSW 2031, Australia
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Craig, M.E., Howard, N.J., Silink, M. and Rawlinson, W.D.
Direct Submission
Submitsed (29-NOV-2002) Virology Division, South Eastern Area
Laboratory Services, University of New South Wales/Prince of Wales
Hospital, High Street, Randwick, NSW 2031, Australia
Location/Qualifiers
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Picornaviridae; Enterovirus.

1 (Dases 1 to 116)
Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
Reduced Frequency of HLA DRB1*03-DDB1*02 in Children with Type 1
Diabetes Associated with Enterovirus RNA
J. Infect. Dis. 187 (10), 1562-1570 (2003)
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Human enterovirus B isolate NSW/48/97 5' UTR, partial sequence.
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/organism="Human enterovirus B"
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Pred. No.
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/isolate="NSW/45/97"
/db_xref="taxon:138949"
<1._.>116
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/isolate="NSW/48/97"
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Best Local Similarity 100.
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VRL 08-MAY-2003
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Direct Submission
Direct (29-NOV-2002) Virology Division, South Eastern Area
Laboratory Services, University of New South Wales/Prince of Wales
Hospital, High Street, Randwick, NSW 2031, Australia
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Viruses, SRRNA positive-strand viruses, no DNA stage,
Picornaviridae, Enterovirus.

1 (bases 1 to 116)
1 carigy,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
Reduced Frequency of HLA DREL*03-DOB1*02 in Children with Type 1
Diabetes Associated with Enterovirus RNA
J. Infect. Dis. 187 (10), 1562-1570 (2003)
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Human enterovirus B isolate NSW/111/98 5' UTR, partial sequence.
                                                                                                                                                                                                                                                                                                                                                                      AX189176 116 bp RNA linear VRL 08-MAY.
Human enterovirus B isolate NSW/83/97 5' UTR, partial sequence.
AY189176
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                                                                                                                                                                                  Length 116;
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Piocornavizidae; Enterovirus.
1 (bases 1 to 116)
Craig, M.E., Howard, N.J., Silink, M. and Rawlinson, W.D.
High Street, Randwick, NSW 2031, Australia
Location/Qualifiers
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100.0%; Pred. No. 0.32;
ive 0; Mismatches 0;
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/mol_type="genomic RNA"
/isolate="NSW/83/97"
/db_xref="taxon:138949"
                                                     /organism="Human enterovirus
                                                                      /mol_type="genomic_RNA"
/isolate="NSW/82/97"
                                                                                                    /db_xref="taxon:138949"
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Human enterovirus B
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Best Local Similarity 100.
Matches 25, Conservative
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Submitted (19-NOV-2002) Virology Division, South Eastern Area Laboratory Services, University of New South Wales/Prince of Wales
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (29-NOV-2002) Virology Division, South Eastern Area Laboratory Services, University of New South Wales/Prince of Wales Hospital, High Street, Randwick, NSW 2031, Australia Location/Qualifiers
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Picornaviridae; Enterovirus.

1 (bases 1 to 116)

Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
Reduced Frequency of HLA DRB1*03-DOB1*02 in Children with Type 1
Diabetes Associated with Enterovirus RNA
J. Infect. Dis. 187 (10), 1562-1570 (2003)
                                                                                                                                                                                                                                                                                                                                                                                               Craig, M.E., Howard, N.J., Silink, M. and Rawlinson, W.D. Reduced Prequency of HLA DRB1*03-DQB1*02 in Children with Type Diabetes Associated with Enterovirus RNA J. Infect. Dis. 187 (10), 1562-1570 (2003)
                                                                                                                                                                                                                                 5' UTR, partial sequence.
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Human enterovirus B isolate NSW/82/97 5' UTR, partial sequence.
AY189175
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Picornavizidae; Enterovirus.
1 (bases 1 to 116)
Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
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                 Length 116;
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             Score 25; DB 13;
Pred. No. 0.32;
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Human enterovirus B isolate NSW/76/97
                                                 0; Mismatches
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/isolate="NSW/76/97"
/db_xref="taxon:138949"
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             Query Match
Best Local Similarity 100.0%;
Matches 25; Conservative 0
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Human enterovirus B
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Human enterovirus B
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AY189174/c
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VRL 08-MAY-2003
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Craig, M.B., Howard, N.J., Silink, M. and Rawlinson, W.D.
Direct Submission
Submitted (29-NOV-2002) Virology Division, South Eastern Area
Laboratory Services, University of New South Wales/Prince of Wales
Hospital, High Street, Randwick, NSW 2031, Australia
Location/Qualifiers
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Submitted (29-NOV-2002) Virology Division, South Eastern Area
Laboratory Services, University of New South Wales/Prince of Wales
Hospital, High Street, Randwick, NSW 2031, Australia
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Picornaviridae; Enterovirus.
1 (bases 1 to 116)
Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
Diabetes Associated with Enterovirus RNA
J. Infect. Dis. 187 (10), 1562-1570 (2003)
                                                                                                                      Picornaviridae, Enterovirus.

L (Dases 1 to 116)

Craig, M.E., Howard, N.J., Silink, M. and Rawlinson, W.D.

Reduced Frequency of HLA DRB1*03-DQB1*02 in Children with Type 1
Diabetes Associated with Enterovirus RNA
J. Infect. Dis. 187 (10), 1562-1570 (2003)
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Human enterovirus B isolate NSW/147/98 5' UTR, partial sequence.
AY189186
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                                                                                                     Viruses; ssRNA positive-strand viruses, no DNA stage;
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100.0%; Score 25; DB 13;
Best Local Similarity 100.0%; Pred. No. 0.32;
Matches 25; Conservative 0; Mismatches 0;
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/mol_type="genomic RNA"
/isolate="NSW/143/98"
/db_xref="taxon:138949"
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100.0%; Score 25; DB
Best Local Similarity 100.0%; Pred. No. 0.3
Matches 25; Conservative 0; Mismatches
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/isolate="NSW/147/98"
/db_xref="taxon:138949"
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    AY189184.1 GI:28274407
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Human enterovirus B
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Human enterovirus B isolate NSW/143/98 5' UTR, partial sequence.
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                                                                            Craig, M.E., Howard, N.J., Silink, M. and Rawlinson, W.D.
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Location/Qualifiers
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Human enterovirus B
Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
1 (bases 1 to 116)
Craig, M.E., Howard, N.J., Silink, M. and Rawlinson, W.D.
Diabetes Associated with Enterovirus RNA
J. Infect. Dis. 187 (10), 1562-1570 (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AY189183 116 bp RNA linear VRL 08-MAY-2
Human enterovirus B isolate NSW/141/98 5' UTR, partial sequence.
AY189183
Reduced Frequency of HLA DRB1*03-DQB1*02 in Children with Type
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100.0%; Pred. No. 0.32;
tive 0; Mismatches 0; Indels
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    Diabetes Associated with Enterovirus RNA
J. Infect. Dis. 187 (10), 1562-1570 (2003)
12721936
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/ organism="Human enterovirus B'/mol type="genomic RNA"
/isolate="NSW/111/98"
/ db_tef="taxon:138949"
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100.0%; Pred. No. 0.32;
:ive 0; Mismatches
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/isolate="NSW/141/98"
/db_xref="taxon:138949"
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Best Local Similarity 100.
Matches 25; Conservative
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les 25; Conserv
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AY189183/c
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ORGANISM
                                                                                                   AUTHORS
TITLE
JOURNAL
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VERSION
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Gaps ; 0

KEYWORDS SOURCE ORGANISM

AUTHORS TITLE

REFERENCE

JOURNAL PUBMED REFERENCE AUTHORS

TITLE JOURNAL

PEATURES

RESULT 30 AY189187/c

ò 셤 DEFINITION

ACCESSION VERSION

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AY189192 116 bp RNA linear VRL 08-MAY-2003
Human entercovirus 71 isolate NSW/157/98 5' UTR, partial sequence.
AY189192 GI:28274415
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Craig, M.E., Howard, N.J., Silink, M. and Rawlinson, W.D.
Reduced Frequency of HLA DRB1*03-DQB1*02 in Children with Type 1
Diabetes Associated with Enterrovirus RNA
J. Infect. Dis. 187 (10), 1562-1570 (2003)
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Human enterovirus 71
Human enterovirus 71
Viruses, no DNA stage;
Viruses, saRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
1 (bases 1 to 116)
Craig, M.E., Howard, N.J., Silink, M. and Rawlinson, W.D.
Craig, M.E., Howard, N.J., Silink, M. and Rawlinson, W.D.
Saduced Frequency of HLA DRB1*03-DQB1*02 in Children with Type.
Diabetes Associated with Enterovirus RNA
J. Infect. Dis. 187 (10), 1562-1570 (2003)
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                                                                                                                                             Length 116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
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Craig, M.E., Howard, N.J., Silink, M. and Rawlinson, W.D.
Direct Submission
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100.0%; Pred. No. 0.32;
ive 0; Mismatches 0;
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  /isolate="NSW/156/98"
/db_xref="taxon:39054"
/note="Human enterovirus 71"
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/mol type="genomic RNA"
/isolate="NSW/157/98"
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Conservative 0
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Human enterovirus 71
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Best Local Similarity
Matches 25; Conserv
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ORIGIN
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AY189191.1 GI:28274414
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Direct Submission
Submitted (29-NOV-2002) Virology Division, South Eastern Area
Laboratory Services, University of New South Wales/Prince of Wales
Hospital, High Street, Randwick, NSW 2031, Australia
Location/Qualifiers
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Edduced Frequency of HLA DRB1*03-DQB1*02 in Children with Type 1
Diabetes Associated with Enterovirus RNA
J. Infect. Dis. 187 (10), 1562-1570 (2003)
                                                                                                                                             AXIB9187 116 bp RNA linear VRL 08-MAY-2
Human enterovirus B isolate NSW/149/98 5' UTR, partial sequence.
AY189187
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Human enterovirus 71

Human enterovirus 71

Viruses; ssRNA positive-strand viruses, no DNA stage;

Picornaviridae; Enterovirus.

1 (bases 1 to 116)

Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.

Reduced Frequency of HLA DRB1*03-DQB1*02 in Children with Type Diabeters Associated with Enterovirus RNA

J. Infect. Dis. 187 (10), 1562-1570 (2003)
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Submitted (29-NOV-2002) Virology Division, South Eastern Area Laboratory Services, University of New South Wales/Prince of Whospital, High Street, Randwick, NSW 2031, Australia Location/Qualifiers
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Viruses; BSRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
I bases I to 116
Craig, M.E., Howard, N.J., Silink, M. and Rawlinson, W.D.
Reduced Frequency of HLA DRB1*03-DQB1*02 in Children w
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/isolate="NSW/149/98"
/db_xref="taxon:138949"
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                          74 TCCGCTGCAGAGTTGCCCGTTACGA 50
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TCCGCTGCAGAGTTGCCCGTTACGA
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Best Local Similarity 100.0
Matches 25; Conservative
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5'UTR ORIGIN

KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS

TITLE

JOURNAL PUBMED

RESULT 31 AY189191/c

Š 셤 DEFINITION ACCESSION VERSION

LOCUS

source

PEATURES

REFERENCE AUTHORS TITLE JOURNAL

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Gaps

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08-MAY-2003 sequence.

5'UTR ORIGIN

Matches

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source

FEATURES

REFERENCE AUTHORS

JOURNAL

PUBMED

RESULT 34 AY189196/c LOCUS

DEFINITION ACCESSION VERSION KEYWORDS ORGANISM

SOURCE

REFERENCE AUTHORS TITLE

TITLE JOURNAL

FEATURES

AUTHORS

JOURNAL PUBMED REFERENCE

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VRL 08-MAY-2003
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Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
Direct Submission
Direct Submission
Laboratory Services, University of New South Wales/Prince of Wales
Hospital, High Street, Randwick, NSW 2031, Australia
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                           Laboratory Services, University of New South Wales/Prince of Wales Hospital, High Street, Randwick, NSW 2031, Australia Location/Qualifiers
                               Human enterovirus 71

Human enterovirus 71

Viruses; ssRNA positive-strand viruses, no DNA stage;

Viruses; ssRNA positive-strand viruses, no DNA stage;

1 (bases 1 to 116)

Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.

Reduced Frequency of HLA DRB1*03-DQB1*02 in Children with Type 1

Diabetes Associated with Enterovirus RNA
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Craig, M.B., Howard, N.J., Silink, M. and Rawlinson, W.D.
Reduced Frequency of HLA DRB1*03-DQB1*02 in Children with Type 1
Diabetes Associated with Enterovirus RNA
J. Infect. Dis. 187 (10), 1562-1570 (2003)
                                                                                                                                                                                                                                                                              Craig, M.E., Howard, N.J., Silink, M. and Rawlinson, W.D. Direct Submission Submitted (29-NOV-2002) Virology Division, South Eastern Area
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Human enterovirus 71 isolate NSW/182/98 5' UTR, partial
AY189199
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Human enterovirus 71
Viruses; sekovirus 71
Picornaviridae; Enterovirus.
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/noTe="Human enterovirus 71"
<1. .>116
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/note="Human enterovirus 71"
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/isolate="NSW/182/98"
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/isolate="NSW/180/98"
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AY189198.1 GI:28274421
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Matches 25; Conservative
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Human enterovirus 71 isolate NSW/169/98 5' UTR, partial sequence.
AX189196
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Human enterovirus 71 isolate NSW/180/98 5' UTR, partial sequence.
AY189198
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                  2 (bases 1 to 116)
Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
Direct Submission
Submitted (29-NOV-2002) Virology Division, South Eastern Area
Laboratory Services, University of New South Wales/Prince of Wales
Hospital, High Street, Randwick, NSW 2031, Australia
Location/Qualifiers
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Craig, M.E., Howard, N.J., Silink, M. and Rawlinson, W.D.
Direct Submission
Submitted (29-NOV2002) Virology Division, South Eastern Area
Laboratory Services, University of New South Wales/Prince of Wales
Hospital, High Street, Randwick, NSW 2031, Australia
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Viruses, SERNA positive-strand viruses, no DNA stage,
Picornaviridae, Enterovirus.

( Chaig, M.E., Howard, N.J., Silink, M. and Rawlinson, W.D.
Reduced Frequency of HLA DRB1*03-DCB1*02 in Children with Type 1
Diabetes Associated with Enterovirus RNA
J. Infect. Dis. 187 (10), 1562-1570 (2003)
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                                                                                                                                                                                                                 /mol type="genomic RNA"
/isolate="NSW/166/98"
/db_xref="taxon:39054"
/note="Human enterovirus 71"
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'isolate="NSW/169/98"
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Human enterovirus 71
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hes 25; Conserv
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AY189198/c

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DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM

AUTHORS

REFERENCE

TITLE JOURNAL

PEATURES

PUBMED AUTHORS REFERENCE

JOURNAL

RESULT 37 AY189201/c

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Craig, M.E., Howard, N.J., Silink, M. and Rawlinson, W.D.
Craig, M.E., Howard, N.J., Silink, M. and Rawlinson, W.D.
Direct Submissaton
Submitted (29-NOV-2002) Virology Division, South Eastern Area
Laboratory Services, University of New South Wales/Prince of Wales
Hospital, High Street, Randwick, NSW 2031, Australia
Location/Qualifiers
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Human enterovirus B
Viruses; asRNA positive-strand viruses, no DNA stage;
Viruses; asRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.

(Casig, M.E., Howard, N.J., Silink, M. and Rawlinson, W.D.
Reduced Frequency of HLA DRB1*03-DQB1*02 in Children with Type 1
Diabetes Associated with Enterovirus RNA
J. Infect. Dis. 187 (10), 1562-1570 (2003)
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Human enterovirus B
Viruses; seRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
1 (bases 1 to 116)
Craig, M.E., Howard, N.J., Silink, M. and Rawlinson, W.D.
Reduced Frequency of HLA DRB1*03-DQB1*02 in Children with Type 1
Diabetes Associated with Enterovirus RNA
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Human enterovirus B isolate NSW/338/99 5' UTR, partial sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                            linear VRL 08-MAY-2
5' UTR, partial sequence.
                                                                                                                                                                             Length 116;
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organism="Human enterovirus 71"
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/organism="Human enterovirus B"
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                                                                                     71"
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                                                              /db xref="taxon:39054"
/note="Human enterovirus
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/isolate="NSW/208/99"
/db_xref="taxon:138949"
<1. .>116
                    /mol_type="genomic RNA"
/isolate="NSW/196/99"
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AY189215.1 GI:28274438
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Best Local Similarity
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AY189215/c
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Human enterovirus 71 isolate NSW/194/99 5' UTR, partial sequence.
AY189201
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Human enterovirus 71 isolate NSW/196/99 5' UTR, partial sequence.
AY189202
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Direct Submission
Submitted (29-NOV-2002) Virology Division, South Eastern Area
Laboratory Services, University of New South Wales/Prince of Wales
Hospital, High Street, Randwick, NSW 2031, Australia
Location/Qualifiers
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Picornaviridae; Enterovirus.

Craig, M.E., Howard, N.J., Silink, M. and Rawlinson, W.D.
Reduced Frequency of HLA DRB1*03-DQB1*02 in Children with Type 1
Diabetes Associated with Enterovirus RNA
J. Infect. Dis. 187 (10), 1562-1570 (2003)
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Picornaviridae, Enterovirus.

1 (bases 1 to 116)

Craig, M.E., Howard, N.J., Silink, M. and Rawlinson, W.D.
Reduced Frequency of HLA DRBS*03-DQBI*02 in Children with Type 1
Diabetes Associated with Enterovirus RNA
J. Infect. Dis. 187 (10), 1562-1570 (2003)
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Pred. No. 0.32;
; Mismatches 0; Indels
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/mol type="genomic RNA"
/isoTate="NSW/194/99"
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100.0%; Pred. No. v.
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/note="Human enterovirus 71"
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                1 TCCGCTGCAGAGTTGCCCGTTACGA 25
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Human enterovirus 71
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Best Local Similarity 100.00
-hos 25; Conservative
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DEFINITION ACCESSION VERSION KEYWORDS

RESULT 38 AY189202/c

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SOURCE ORGANISM

REPERENCE AUTHORS

TITLE

JOURNAL

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PEATURES

TITLE JOURNAL REFERENCE AUTHORS

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VRL 08-MAY-2003
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Craig, M. E., Howard, N.J., Silink, M. and Rawlinson, W.D.
Direct Submission
Submitted (19-NOV-2002) Virology Division, South Eastern Area
Laboratory Services, University of New South Wales/Prince of Wales
Hospital, High Street, Randwick, NSW 2031, Australia
Location/Qualifiers
                                                                                                                                  Human enterovirus B
Human enterovirus B
Viruses; saRNA positive-strand viruses, no DNA stage;
Viruses; saRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.

(Craig, M. E., Howard, N. J., Sllink, M. and Rawlinson, W. D.
Reduced Frequency of HLA DRB1*03-DQB1*02 in Children with Type 1
Diabetes Associated with Enterovirus RNA
J. Infect. Dis. 187 (10), 1562-1570 (2003)
                        AY189205
Human enterovirus B isolate NSW/204/99 5' UTR, partial sequence.
AY189205
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Viruses: ssRNA positive-strand viruses, no DNA stage;
Viruses: strand positive-strand viruses, no DNA stage;
Viruses: Loston therovirus.

I (bases 1 to 154)
Singh,S., Chow,V.T.K., Phoon,M.C., Chan,K.P. and Poh,C.L.
Direct Detection of Enterovirus 71 (EVT) in Clinical Specimens from a Hand, Foot, and Mouth Disease Outbreak in Singapore by Reverse Transcription-PCR with Universal Enterovirus and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (18-000-2000) Microbiology, National University of Singapore, 5 Science Drive 2, Singapore 117597, Singapore 3 (Dases 1 to 154)
Singapore, 5 Chow, V.T.K. and Poh, C.L.
Bingapore, 5 Science Drive 2, Singapore 117597, Singapore Singapore, 5 Science Drive 2, Singapore 117597, Singapore 5 Sequence update by submitter of Singapore 2, Singapore 3, 2001 this sequence version replaced gi:12667228.

Location/Qualifiers
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AP314005
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J. Clin. Microbiol. 40 (8), 2823-2827 (2002)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Human enterovirus B"
/mol_type="genomic RNA"
/isolate="NSW/204/99"
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Singh,S., Chow,V.T.K. and Poh,C.L.
Direct Submission
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Pujimoto, T., Munemura, T. and Chikahira, M.

Direct Submission

Submitted (30-31Ns-2004) Tsuguto Fujimoto, Hyogo Prefectural

Institute of Public Health and Environmental Sciences, Infectious

Disease Research Division; 2-1-29, Arata-Cho, Hyogo-Ku, Kobe, Hyogo
652-0032, Japan (E-mail:Tsuguto_Fujimoto@pref.hyogo.jp,

URL:http://www.lphes.pref.hyogo.jp/, Tel:81-78-511-6640(ex.236),

Fax:81-78-531-7080)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   117 bp RNA linear VRL 02-JUL-2004
Human enterovirus 71 genomic RNA, 5' UTR, partial sequence,
1801ate: 2279/EV71/Hyogo/2003.
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                            Craig, M.E., Howard, N.J., Silink, M. and Rawlinson, W.D.
Craig, M.E., Howard, N.J., Silink, M. and Rawlinson, W.D.
Direct Submission
Submitted (29-NOV-2002) Virology Division, South Eastern Area
Laboratory Services, University of New South Wales/Prince of Wales
Hospital, High Street, Randwick, NSW 2031, Australia
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fujimoto, T., Yoshida, S., Munemura, T., Yoshida, H., Chikahira, M. and
                                                                                                                                                                                                                                                                                                                                                                                Gaps
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Unpublished
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Human enterovirus 71
Human enterovirus 71
Viruses; seRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
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J. Infect. Dis. 187 (10), 1562-1570 (2003)
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/mol_type="genomic RNA"
/isolate="NSW/338/99"
/db_xref="taxon:138949"
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/isolate="2279/EV71/Hyogo/2003"
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Pred. No. 0.32;
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Pred. No.
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/db_xref="taxon:39054"
/country="Japan:Hyogo"
<1. .>117
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Best Local Similarity 100.
Matches 25; Conservative
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Best Local
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myocardium tissue of subject
            Unpublished
2 (bases 1 to 162)
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/db_xref="taxon:12072"
/country="USA"
                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                    Lednicky, J.A. and Ohr, J.S.
Lednicky, J.A. and Ohr, J.S.
Direct Submission Submission Submitted (14-MAY-2004) Pathology, Loyola University Medical
Center, 2160 South, First Avenue, Maywood, IL 60153, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lednicky, J.A. and Ohr, J.S.
5' untranslated region (5' UTR) of Human coxsakievirus B in
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                                                                                                          DB 13; Length 154;
                                                                                                                                                                                                                                                                                                                                                     Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
1 (bases 1 to 162)
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Human coxeackievirus B3
Viruses; seRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
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Human coxsackievirus B3 isolate subject 9 5' UTR.
AY626236
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Human coxsackievirus B3 isolate subject 6 5' UTR.
AY626235
           organism="Enterovirus 5656/SIN/002209"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'organism="Human coxsackievirus B3"
mol type="genomic RNA"
isolate="subject 6"
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                                                                                                       Score 25; DB 13
Pred. No. 0.32;
                                                                                         100.0%; Sco.
100.0%; Pred. No. v..
... 0; Mismatches
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Coxsackievirus B in myocardium tissue
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                   /mol_type="mRNA"
/strain="5656/SIN/002209"
/db_xref="taxon:150720"
<1._.>154
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Pred. No.
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Conservative 0;
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Human coxsackievirus B3
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                                                                                                       Query Match
Best Local Similarity 100.
Matches 25; Conservative
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Best Local Similarity
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                                                     5'UTR
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ORGANISM
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AY626235/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Manzara, S., Muscillo, M., La Rosa, G., Marianelli, C., Cattani, P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Molecular identification and typing of enteroviruses isolated from
                                                                                                                                                                          /mol type="genomic RNA"
/isolate="gubject 9"
/isolation_source="myocardium tissue from patient that died of myocarditis"
/db_xref="taxon:12072"
/country="USA"
/note="Enterovirus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (08-MAY-2001) Muscillo M., Environmental Hygiene,
Istituto Superiore di Sanita', Viale Regina Elena 299, Rome, RM
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/db xref="taxon:39054"
/lab_host="vero cell cultures"
/note="throat swab from child with aseptic meningitis, identified by immunofluorescence assay"
<1. .>172
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Lednicky, J.A. and Ohr, J.S.
Direct Submission
Submitted (14-MAY-2004) Pathology, Loyola University Medical
Center, 2160 South First Avenue, Maywood, IL 60153, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HEN312088 172 bp RNA linear VR
Human enterovirus 71 partial 5'UTR, strain /di/Roma98.
AJ312088
                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 25; DB 13; Length 162; 100.0%; Pred. No. 0.32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human enterovirus 71
Human enterovirus 71
Viruses; sesta positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
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J. Clin. Microbiol. 40 (12), 4554-4560 (2002)

    162
/organism="Human coxsackievirus B3"

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100.0%; Score 25; DB 13;
Best Local Similarity 100.0%; Pred. No. 0.32;
Matches 25; Conservative 0; Mismatches 0;
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/strain="/di/Roma98"
/isolate="IT98-5114"
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                                                                                                        Location/Qualifiers
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Conservative
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Best Local Similarity
Matches 25; Conserv
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Best Local Similarity
Matches 25; Conserv
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AF521447/c
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                                                                                 ESP295207 177 bp RNA linear VRL 15-MAY-2001
Echovirus sp. genomic RNA for partial 5'UTR, isolate ATCC VR-322.
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Human echovirus 30

Viruses; saRNA postive-strand viruses, no DNA stage;

Viruses; saRNA postive-strand viruses, no DNA stage;

1 (bases 1 to 185)

Thoelen,I., Lemey,P., Van Der Donck,I., Beuselinck,K.,

Mindberg,A.M. and Van Ranst,M.

Molecular typing and epidemiology of enteroviruses identified from an outbreak of aseptic meningitis in Belgium during the summer of
                                                                                                                                                                                                                                                   Muscillo,M., La Rosa,G., Marianelli,C., Capobianchi,M.R.,
Zaniratti,S., Cattani,P., Manzara,S., Fadda,G., Comparcola,D. and
                                                                                                                                                                                                                                                                                                     A phylogenetic analysis of the two echovirus 30 isolated in Rome (Italy) in 1997 from an outbreak of aseptic meningitis associated with swimming pools
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /isolate="ATCC VR-122"
/db_xref="taxon:145390"
/note="isolated from fecal specimen of 10-year-old boy virth symptoms of headache, stiff neck, fever"
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                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (03-NOV-2000) Muscillo M., Environmental Hygiene,
Istituto Superiore di Sanita', Viale Regina Elena 299, Rome,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AF521433 11near VRL 17-J
Human echovirus 30 isolate BE00-14 5' UTR, partial sequence.
AF521433
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Lindberg,M.A. and Van Ranst,M.
Direct Submission
                                                                                                                                                                                      Echovirus sp.
Viruses; ssRNA positive-strand viruses, no DNA stage;
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2767006
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100.0%; Pred. No. 0.3
:ive 0; Mismatches
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/organism="Echovirus sp.
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/strain="Bastianni"
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                                                                                                                                                                                                                       Picornaviridae, Enterovirus.
 90 TCCGCTGCAGAGTTGCCCGTTACGA
                                                                                                                                  AJ295207.1 GI:14140008
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2 (bases 1 to 177)
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Best Local Similarity 100.
Matches 25; Conservative
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                                                                                                                                                                   Echovirus sp.
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ORIGIN
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VERSION
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REFERENCE
AUTHORS
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AUTHORS
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PUBMED
                                                RESULT 47
ESP295207
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KEYWORDS
SOURCE
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Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological Virology, Department of Microbiology and Immunology, Rega Institute for Medical Research, University of Leuven, Minderbroedersstraat 10, Leuven BE-3000, Belgium Location/Qualifiers
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Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological
Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiology
Vicology, Department of Microbiology and Immunology, Rega Institute
for Medical Research, University of Leuven, Minderbroedersstraat
10, Leuven BB-3000, Belgium
Location/Qualifiers
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Human echovirus 30

Viruses; saRNA positive-strand viruses, no DNA stage;

Viruses; saRNA positive-strand viruses, no DNA stage;

Dicornaviridae; Enterovirus.

1 (bases 1 to 185)

Thoelen,I., Lemey,P., Van Der Donck,I., Beuselinck,K.,

Lindberg,A.M. and Van Ranst,M.

Molecular typing and epidemiology of enteroviruses identified from an outbreak of aseptic meningitis in Belgium during the summer of
                                                                                                                                                                                                                                                                                /isolation_source="patient 14 - zipcode Belgium 9310"
/db_xref="taxon:41846"
<1._.>185
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/db_xref="taxon:41846"
<1._.>185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    185 bp RNA linear VRL 17-AP51436 TO GI:31790778
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Thoelen, I., Lemey, P., van der Donck, I., Beuselinck, K., Lindberg, M.A. and Van Ranst, M.
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                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 25; DB 13; Length 185; 100.0%; Pred. No. 0.32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                      1. .185
/organism="Human echovirus 30"
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/isolate="BE00-2"
                                                                                                                                                                                                                               /mol_type="genomic RNA"
/isolate="BE00-14"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 TCCGCTGCAGAGTTGCCCGTTACGA 25
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(bases 1 to 185)
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Best Local Similarity 100.0
Matches 25, Conservative
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Human echovirus 30
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Matches 25; Conserva
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KEYWORDS
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Thochen, I., Lemey, P., van der Donck, I., Beuselinck, K.,
Lindberg, M.A. and Van Ranst, M.
Lindberg, M.A. and Van Ranst, M.
Submission

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Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological
Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological
Virology, Department of Microbiology and Immunology, Rega Institute
for Medical Research, University of Leuven, Minderbroedersstraat
10, Leuven BE-3000, Belgium
Location/Qualifiers
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                                                                                                                          Human echovirus 30
Human echovirus 30
Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
1 (bases 1 to 185)
Thoelen, I., Lemey, P., Van Der Donck, I., Beuselinck, K.,
Lindberga, A.M. and Van Ranst, M.
Molecular typing and epidemiology of enteroviruses identified from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VRL 17-JUN-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /mol.type="genomic RNA"
/isolate="BE00-30"
/isolation.source="patient 30 - zipcode Belgium 9310"
/db_xref="taxon:41846"
<1...>185
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     AF521447
Human echovirus 30 isolate BE00-30 5' UTR, partial sequence
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Lindberg,M.A. and Van Ranst,M.
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Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
1 (bases 1 to 185)
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Pred. No. 0.32;
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100.0%; Pred. No. v.
0; Mismatches
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  185 bp
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                                                                         AF521447.1 GI:31790789
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AF521449.1 GI:31790791
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Best Local Similarity
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Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological Virology, Department of Microbiology and Immunology, Rega Institute for Medical Research, University of Leuven, Minderbroedersstraat 10, Leuven BE-3000, Belgium Location/Qualifiers
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Human echovirus 30 isolate BE00-34 5' UTR, partial sequence.
AF521451
AF521451.1 GI:31790793
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Viruses; ssRNA positive-strand viruses, no DNA stage;
prograviridae; Enterovirus.
1 (bases 1 to 185)
Thoelen,I., Lemey,P., Van Der Donck,I., Beuselinck,K.,
Indoberg,A.M. and Van Ranst,M.
Molecular typing and epidemiology of enteroviruses identified from
                                                                                              /isolation_source="patient 32 - zipcode Belgium 1703"
/db_xref="taxon:41846"
<1._.>185
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/db xref="taxon:41846"
<1. .>185
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AF521450
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; Pred. No. 0.32;
0; Mismatches

    .185
    organism="Human echovirus 30"

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1. .185
/organism="Human echovirus
/virion
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                                                                  /mol_type="genomic_RNA"
/isolate="BE00-32"
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/isolate="BE00-33"
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Thoelen, I., Lemey, P., van der Donck, I., Beuselinck, K., Lindberg, M.A. and Van Ranst, M. Diract Submission

Diract Submission

Submitted (12-37N-2002) Laboratory of Clinical & Epidemiological Virology, Department of Microbiology and Immunology, Rega Institute for Medical Research, University of Leuven, Minderbroedersstraat 10, Leuven BE-3000, Belgium

Location/Qualifiers
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Human echovirus 30 isolate BE00-16 5' UTR, partial sequence.
AF521474
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.

1 (bases 1 to 185)
Thoelen, I., Lemey, P., Van Der Donck, I., Beuselinck, K.,
Lindberg, A.M. and Van Ranst, M.
Molecular typing and epidemiology of enteroviruses identified from an outbreak of aseptic meningitis in Belgium during the summer of
/isolation_source="patient 43 - zipcode Belgium 9402"
/db_xref="taxon:41846"
<1._.>185
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/db_xref="taxon:41846"
<1. .>185
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Human echovirus 30 isolate BE00-48 5' UTR, partial sequence.
AF521461
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                                                                                                                  Score 25; DB 13; Length 185;
Pred. No. 0.32;
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larity 100.0%; Pred. No. 0.32;
Conservative 0; Mismatches 0; Indels C
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Picornaviridae; Enterovirus.
1 (bases 1 to 185)
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                                                                                                                                                           0; Mismatches
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/isolate="BE00-48"
                                                                                                                                                                                                    1 TCCGCTGCAGAGTTGCCCGTTACGA 25
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ilarity 100.0%;
Conservative 0
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Best Local Similarity
Matches 25; Conserv
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AF521461/c
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                                                                                                                                                                                                                                                                            Thoelen, I., Lewey, P., van der Donck, I., Beuselinck, K., Lindberg, M. A. and Van Ranst, M. Direct Submission

Direct Submission
Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological Virology, Department of Microbiology and Immunology, Rega Institute for Medical Research, University of Leuven, Minderbroedersstraat 10, Leuven BB-3000, Belgium
Location/Qualifiers
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Lindberg, M.A. and Van Ranst, M.
Lindberg, M.A. and Van Ranst, M.
Direct Submission
Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological
Virology, Department of Microbiology and Immunology, Rega Institute
for Medical Research, University of Leuven, Minderbroedersstraat
10, Leuven BE-3000, Belgium
Location/Qualifiers
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                                                                                                                                                           Molecular typing and epidemiology of enteroviruses identified from an outbreak of aseptic meningitis in Belgium during the summer of
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Lindberg, A.M. and Van Ranst, M.
Molecular typing and epidemiology of enteroviruses identified from
an outbreak of aseptic meningitis in Belgium during the summer of
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/db_xref="taxon:41846"
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Human echovirus 30 isolate BE00-43 5' UTR, partial sequence.
AF521458
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            Human echovirus 30
Human echovirus 30
Human echovirus 30
Voiruses; SBRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
1 (Dases 1 to 185)
1 (Dases 1 to 185)
1 Thoelen, I., Lemey, P., Van Der Donck, I., Beuselinck, K., Lindberg, A.M. and Van Ranst, M.
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Human echovirus 30
Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
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    /organism="Human echovirus 30"

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12767006
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/isolate="BE00-34"
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/isolate="BE00-43"
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2 (bases 1 to 185)
Thoelen,I., Lemey,P., van der Donck,I., Beuselinck,K.,
Lindberg,M.A. and Van Ranst,M.
Direct Submission
Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological
Virology, Department of Microbiology and Immunology, Rega Institute
for Medical Research, University of Leuven, Minderbroedersstraat
10, Leuven BE-3000, Belgium
Location/Qualifiers
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Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological Virology, Department of Microbiology and Immunology, Rega Institute for Medical Research, University of Leuven, Minderbroedersstraat 10, Leuven BB-3000, Belgium
Location/Qualifiers
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Human echovirus 30

Yuruses; saRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.

1 (bases 1 to 185)

Thoelen, I., Lemey, P., Van Der Donck, I., Beuselinck, K.,
Lindberg, A.M. and Van Ranst, M.
Molecular typing and epidemiology of enteroviruses identified from
Thoelen, I., Lemey, P., Van Der Donck, I., Beuselinck, K.,
Lindberg, A.M. and Van Ranst, M.
Molecular typing and epidemiology of enteroviruses identified from
an outbreak of aseptic meningitis in Belgium during the summer of
                                                                                                                                                                                                                                                                                                                                                              /isolation_source="patient 16 - zipcode Belgium 3294"
/db_xref="taxon:41846"
<1. .>185
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/virion
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                                                                                       J. Med. Virol. 70 (3), 420-429 (2003)
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/isolate="BE00-16"
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/isolate="BE00-17"
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AF521475/c
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Thoelen! I. Lemey, P., van der Donck, I., Beuselinck, K., Lindberg, M.A. and Van Ranst, M. Dindberg, M.A. and Van Ranst, M. Direct Submitseion
Direct Submitted (12-70N-2002) Laboratory of Clinical & Epidemiological Submitted (12-70N-2002) Laboratory of Clinical & Epidemiological Virology, Department of Microbiology and Immunology, Rega Institute for Medical Research, University of Leuven, Minderbroedersstraat 10, Leuven BE-3000, Belgium
Location/Qualifiers
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Picornaviridae; Enterovirus.
1 (bases I to 185)
Thoelen,I., Lemey,P., Van Der Donck,I., Beuselinck,K.,
Lindberg,A.M. and Van Ranst,M.
Molecular typing and epidemiology of enteroviruses identified from an outbreak of aseptic meningitis in Belgium during the summer of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Thoelen, I., Lemey, P., Van Der Donck, I., Beuselinck, K., indoerg, A.M. and Van Ranst, M. Molecular typing and epidemiology of enteroviruses identified from an outbreak of aseptic meningitis in Belgium during the summer of
                                                      Gaps
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Picornaviridae, Enterovirus.
1 (bases 1 to 185)
       Length 185;
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100.0%; Score 25; DB 13;
llarity 100.0%; Pred. No. 0.32;
Conservative 0; Mismatches 0;
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/db_xref="taxon:41846"
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/isolate="BE00-18"
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VRL 17-JUN-2003

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Thoelen, I., Lemey, P., van der Donck, I., Beuselinck, K.,
Lindberg, M.A. and Van Ranst, M.
Lindberg, M.A. and Van Ranst, M.
Direct Submission
Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological
Virology, Department of Microbiology and Immunology, Rega Institute
for Medical Research, University of Leuven, Minderbroedersstraat
10, Leuven BE-3000, Belgium
Location/Qualifiers
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Piconnaviridae; Enterovirus.

1 (bases 1 to 185)
Thoelen,I., Lemey,P., Van Der Donck,I., Beuselinck,K.,
Lindberg,A.m. and Van Ranst,M.
Molecular typing and epidemiology of enteroviruses identified from an outbreak of aseptic meningitis in Belgium during the summer of
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/db_xref="taxon:41846"
<1._.>185
                                                                                                                              AF521483 linear VRL 17-J
Human echovirus 30 isolate BE00-74 5' UTR, partial sequence.
                                                                                                                                                                                                                                                                           Viruses, SERNA positive-strand viruses, no DNA stage, Picornaviridae, Enterovirus.

1 (bases 1 to 185)

Thoslen, I., Lemey, P., Van Der Donck, I., Beuselinck, K., Lindberg, A.M. and Van Ranst, M.
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Lindberg,M.A. and Van Ranst,M.
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Human echovirus 30 isolate BE00-76 5' UTR,
AP521485
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/organism="Human echovirus 30"
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12767006
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/isolate="BE00-74"
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1 TCCGCTGCAGAGTTGCCCGTTACGA 25
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Human echovirus 30
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Human echovirus 30
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AF521483/c
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                                                           Thoelen, I., Lemey, P., van der Donck, I., Beuselinck, K., Lindborg, M.A. and Van Ranst, M. Direct Submission
Direct Submission
Submitted (12-7UN-2002) Laboratory of Clinical & Epidemiological Virology, Department of Microbiology and Immunology, Rega Institute for Medical Research, University of Leuven, Minderbroedersstraat 10, Leuven BE-3000, Belgium
Location/Qualifiers
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Direct Submission
Submitted (12-7UN-2002) Laboratory of Clinical & Epidemiological Virology, Department of Microbiology and Immunology, Rega Institute for Medical Research, University of Leuven, Minderbroedersstraat 10, Leuven BE-3000, Belgium
Location/Qualifiers
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/db_xref="taxon:41846"
<1._.>185
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/db_xref="taxon:41846"
<1. _.>185
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Human echovirus 30 isolate BE00-20 5′ UTR, partial sequence.
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Human echovirus 30
Viruses; sBRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
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    Virol. 70 (3), 420-429 (2003)
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                                                                                                                                                                                                                                                                                                /mol type="genomic RNA"
/isolate="BE00-19"
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/isolate="BE00-20"
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AF521478.1 GI:31790820
                                             (bases 1 to 185)
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Direct Submission
Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological
Virology, Department of Microbiology and Immunology, Rega Institute
for Medical Research, University of Leuven, Minderbroedersstraat
10, Leuven BE-3000, Belgium
Location/Qualifiers
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Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological
Virology, Department of Microbiology and Immunology, Rega Institute
for Medical Research, University of Leuven, Minderbroedersstraat
10, Leuven BE-3000, Belgium
Location/Qualifiers
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                                                                                                                                                                                 - zipcode Belgium 8930"
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/db_xref="taxon:41846"
<1._.>185
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Human echovirus 30 isolate BE00-77 5' UTR, partial sequence.
AF521486
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indberg,M.A. and Van Ranst,M.
                                                                                                                                                                                                                                                          Score 25; DB 13; Length 185; Pred. No. 0.32;
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Picornaviridae; Enterovirus.
1 (bases 1 to 185)
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ilarity 100.0%; Pred. No. 0.3
Conservative 0; Mismatches
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                                                                                                                                                /mol_type="genomic RNA"
/isolate="BE00-76"
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/isolate="BE00-77"
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Human echovirus 30
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Best Local Similarity
Matches 25; Conserv
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Matches 25; Conserv
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AF521486/c
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RESULT

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AF521492 17-JUN-2003
Human echovirus 30 isolate BE00-83 5' UTR, partial sequence.
AF521492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological Virology, Department of Microbiology and Immunology, Rega Institute for Medical Research, University of Leuven, Minderbroedersstraat 10, Leuven BE-3000, Belgium
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Lindberg, M.A. and Van Ranst, M.
Direct Submission
Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological
Virology, Department of Microbiology and Immunology, Rega Institute
for Medical Research, University of Leuven, Minderbroedersstraat
10, Leuven BB-3000, Belgium
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Picornaviridae; Enterovirus.
1 (bases 1 to 185)
Thoelen, I., Lemey, P., Van Der Donck, I., Beuselinck, K.,
Lindberg, A.M. and Van Ranst, M.
Molecular typing and epidemiology of enteroviruses identified from an outbreak of aseptic meningitis in Belgium during the summer of
                                                                                                                                                                                                                                                                                                             Thoelen,I., Lemey,P., Van Der Donck,I., Beuselinck,K.,
Lindberg,A.M. and Van Ranst,M.
Molecular typing and epidemiology of enteroviruses identified from
an outbreak of aseptic meningitis in Belgium during the summer of
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/db_rref="taxon:41846"
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Human echovirus 30 isolate BE00-58 5' UTR, partial sequence.
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Thoelen,I., Lemey,P., van der Donck,I., Beuselinck,K.,
Lindberg,M.A. and Van Ranst,M.
Direct Submission
                                                                                                                                                                                                                          Viruses, BBRNA positive-strand viruses, no DNA stage,
Picornaviridae, Enterovirus.
1 (bases 1 to 185)
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/isolate="BE00-83"
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Human echovirus 30
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AUTHORS
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PUBMED
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                                                                                                                                                                                                                   AUTHORS
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Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological
Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological
Virology, Department of Microbiology and Immunology, Rega Institute
for Medical Research, University of Leuven, Minderbroedersstraat
10, Leuven BB-3000, Belgium
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /isolation_source="patient 59 - zipcode Belgium 2300"
/db_xref="taxon:41846"
<1. .>185
                                                                                           58 - zipcode Belgium 2340"
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Human echovirus 30 isolate BE00-64 5' UTR, partial sequence.
AF521501.1 GI:31790843
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Human echovirus 30 isolate BE00-59 5' UTR, partial sequence
AF521496
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Lindberg, M.A. and Van Ranst, M.
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Human echovirus 30
Viruses; seRNA positive-strand viruses, no DNA stage;
Picornavirides Enterovirus.
1 (bases 1 to 185)
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1 Similarity 100.0%; Pred. No. 0.32;
25; Conservative 0; Mismatches 0; Indels ()
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                              organism="Human echovirus 30"
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ilarity 100.0%; Pred. No. 0.32;
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12767006
                                                                                        /isolation_source="patient/db_xref="taxon:41846"
<1._.>185
                                                        /mol_type="genomic_RNA"
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/isolate="BE00-59"
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Lindberg, M.A. and Van Ranst, M.
Dindberg, M.A. and Van Ranst, M.
Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological
Virology, Department of Microbiology and Immunology, Rega Institute
for Medical Research, University of Leuven, Minderbroedersstraat
10, Leuven BE-3000, Belgium
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1 (bases 1 to 185)
Thoelen,I., Lemey,P., Van Der Donck,I., Beuselinck,K.,
Indoberg,A.M. and Van Ranst,M.
Molecular typing and epidemiology of enteroviruses identified from an outbreak of aseptic meningitis in Belgium during the summer of
Viruses; BSRNA positive-strand viruses, no DNA stage;
1 (bases 1 to 185)
Thoelen,I., Lemey,P., Van Der Donck,I., Beuselinck,K.,
IndhergyA.M. and Van Ranst,M.
Molecular typing and epidemiology of enteroviruses identified from an outbreak of aseptic meningitis in Belgium during the summer of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /isolation_source="patient_64 - zipcode_Belgium_2400"
/db_xref="taxon:41846"
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/isolate="BE00-64"
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The Chaese 1 to 185)
Thoelen, I., Lemey, P., van der Donck, I., Beuselinck, K.,
Lindberg, M.A. and Van Ranst, M.
Direct Submission
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Virology, Department of Microbiology and Immunology, Rega Institute
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Submitted (12-JUM-2002) Laboratory of Clinical & Epidemiological
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10, Leuven BE-3000, Belgium
Location/Qualifiers
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Human echovirus 30

Viruses; saRNA positive-strand viruses, no DNA stage;

Viruses; saRNA positive-strand viruses, no DNA stage;

Dicornaviridae; Enterovirus.

1 (bases 1 to 185)

Thoelen,I., Lemey,P., Van Der Donck,I., Beuselinck,K.,
Lindberg,A.M. and Van Ranst,M.

Molecular typing and epidemiology of enteroviruses identified from an outbreak of aseptic meningitis in Belgium during the summer of
       1 (bases 1 to 185)
Thoelen, I., Lemey, P., Van Der Donck, I., Beuselinck, K.,
Lindberg, A.M. and Van Ranst, M.
Molecular typing and epidemiology of enteroviruses identified from
an outbreak of aseptic meningitis in Belgium during the summer of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /isolation_source="patient_90 - zipcode_Belgium_8560"
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/db_xref="taxon:41846"
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Thoelen,I., Lemey,P., van der Donck,I., Beuselinck,K.,
Lindberg,M.A. and Van Ranst,M.
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/organism="Human echovirus 30"
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                                                                                                                                               J. Med. Virol. 70 (3), 420-429 (2003)
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Human echovirus 30 isolate BE00-92
AF521517
AF521517.1 GI:31790859
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /mol_type="genomic RNA"
/isolate="BE00-90"
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/isolate="BE00-92"
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Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological
Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological
Virology, Department of Microbiology and Immunology, Rega Institute
for Medical Research, University of Leuven, Minderbroedersstraat
10, Leuven BE-3000, Begjuum
Location/Qualifiers
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Picornaviridae, Enterovirus.

1 (bases 1 to 185)
Thoelen, I., Lemey, P., Van Der Donck, I., Beuselinck, K.,
Lindberg, A. M. and Van Ranst, M.
Molecular typing and epidemiology of enteroviruses identified from an outbreak of aseptic meningitis in Belgium during the summer of
                               - zipcode Belgium 2340"
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Human echovirus 30 isolate BE00-68 5' UTR, partial sequence.
AF521505
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Human echovirus 30 isolate BE00-90 5' UTR, partial sequence.
AFS21515
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Lindberg, M.A. and Van Ranst, M.
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Human echovirus 30
Viruses; seRMA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
                                                                                                                                               DB 13; Length 185;
                                                                                                                                                                                          0; Indels
/isolate="BE00-67"
/isolation_source="patient_67"
/db_xref="taxon:41846"
<1. .185
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12767006
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100.0%; Pred. No. 0.3
tive 0; Mismatches
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/isolate="BE00-68"
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Human echovirus 30
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FEATURES

SOURCE ACCESSION VERSION KEYWORDS

REFERENCE AUTHORS

TITLE

JOURNAL PUBMED REFERENCE AUTHORS TITLE

DEFINITION ACCESSION VERSION

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RESULT 70

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KEYWORDS SOURCE ORGANISM

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VRL 17-JUN-2003

partial sequence.

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Thoelen, I., Lemey, P., van der Donck, I., Beuselinck, K.,
Lindberg, M.A. and Van Ranst, M.
Lindberg, M.A. and Van Ranst, M.
Direct Submission
Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological
Virology, Department of Microbiology and Immunology, Rega Institute
for Medical Research, University of Leuven, Minderbroedersstraat
10, Leuven BB-3000, Belgium
Location/Qualifiers
                                        Thoelen, I., Lemey, P., van der Donck, I., Beuselinck, K.,
Lindberg, M.A. and Van Ranst, M.
Lindberg, M.A. and Van Ranst, M.
Direct Submission
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for Medical Research, University of Leuven, Minderbroedersstraat
10, Leuven BE-3000, Belgium
Location/Qualifiers
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Human echovirus 30

Viruses; ssRNA positive-strand viruses, no DNA stage;

Viruses; ssRNA positive-strand viruses, no DNA stage;

1 (bases 1 to 185)

Thoelen,I., Lemey,P., Van Der Donck,I., Beuselinck,K.,

Lindberg,A.M. and Nanst,M.

Molecular typing and epidemiology of enteroviruses identified from an outbreak of aseptic meningitis in Belgium during the summer of
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/db_xref="taxon:41846"
<1._.>185
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AF521538.1 GI:31790880
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100.0%; Score 25; DB 13; Length 185;
Best Local Similarity 100.0%; Pred. No. 0.32;
Matches 25; Conservative 0; Mismatches 0; Indels 0
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/db_xref="taxon:41846"
<1._.>185
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J. Med. Virol. 70 (3), 420-429 (2003)
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/isolate="BE00-111"
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/isolate="BE00-54"
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Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological
Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological
Virology, Department of Microbiology and Immunology, Rega Institute
for Medical Research, University of Leuven, Minderbroedersstraat
10, Leuven BE-3000, Belgium
Location/Qualifiers
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Human echovirus 30
Viruses; sBRNA positive-strand viruses, no DNA stage;
Viruses; sBRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
1 (bases 1 to 185)
Thoelen, I., Lemey, P., Van Der Donck, I., Beuselinck, K.,
Lindberg, A.M. and Van Ranst, M.
Molecular typing and epidemiology of enteroviruses identified from an outbreak of aseptic meningitis in Belgium during the summer of
                                                                                                                                                                                                                                                                                                                                                              Human echovirus 30
Human echovirus 30
Yuruses; asRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
1 (bases 1 to 185)
Thoelen, I., Lemey, P., Van Der Donck, I., Beuselinck, K.,
Lindberg, A.M. and Van Ranst, M.
Molecular typing and epidemiology of enteroviruses identified from
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Human echovirus 30 isolate BE00-54 5' UTR, partial sequence.
AF521525
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Human echovirus 30 isolate BE00-95 5' UTR, partial sequence.
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Lindberg, M.A. and Van Ranst, M.
100.0%; Score 25; DB 13; Length 185; 100.0%; Pred. No. 0.32;
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                                               0; Mismatches
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/isolate="BE00-95"
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AF521519.1 GI:31790861
                       Best Local Similarity 100.
Matches 25; Conservative
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Best Local &
    Query Match
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AF521525/c
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AF521519/c
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KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS

TITLE

JOURNAL PUBMED REFERENCE · AUTHORS

TITLE JOURNAL

RESULT 75 AF521539/c

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LOCUS

ACCESSION VERSION

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Lindberg, M.A. and Van Ranst, M.

Direct Submission

Submitted (12-UTN-2002) Laboratory of Clinical & Epidemiological
Submitted (12-UTN-2002) Laboratory of Clinical & Epidemiological
Virology, Department of Microbiology and Immunology, Rega Institute
for Medical Research, University of Leuven, Minderbroedersstraat
10, Leuven BR-3000, Belgium
Location/Qualifiers
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Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological
Virology, Department of Microbiology and Immunology, Rega Institute
for Medical Research, University of Leuven, Minderbroedersstraat
10, Leuven BE-3000, Belgium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human coxeackievirus B4
Human coxeackievirus B4
Viruses; seRNA positive-strand viruses, no DNA stage;
Viruses; seRNA positive-strand viruses, no DNA stage;
Vicornaviridae; Enterovirus.

(bases 1 to 185)
Thochen, I., Lemey, P., Van Der Donck, I., Beuselinck, K.,
Thochen, J., Amey Van Anst, M.
Molecular typing and epidemiology of enteroviruses identified from an outbreak of aseptic meningitis in Belgium during the summer of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AF521543 17-JUN-200
Human coxsackievirus B4 isolate BE00-117 5' UTR, partial sequence.
AF521543
                                                                                                                                                                                                                                                                                /isolation_source="patient 116 - zipcode Belgium 3000"
/db_xref="taxon:41846"
<1._.>185
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                                                                                                                                                                                                                                                                                                                                                                                                   Length 185;
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Pred. No. 0.32;
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/db_xref="taxon:12073"
                                                                                                                                                                                        /organism="Human echovirus 30"
/virion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             J. Med. Virol. 70 (3), 420-429 (2003)
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                                                                                                                                                                                                                                        /mol_type="genomic RNA"
/isolate="BE00-116"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /mol_type="genomic RNA"
/isolate="BE00-117"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 TCGCTGCAGAGTTGCCCGTTACGA 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                74
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological Virology, Department of Microbiology and Immunology, Rega Institute for Medical Research, University of Leuven, Minderbroedersstraat 10, Leuven BE-3000, Belgium
Location/Qualifiers
                                                                                                                                                                VRL 17-JUN-2003
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Human echovirus 30 isolate BE00-116 5' UTR, partial sequence.
AF521542
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /isolation_source="patient 113 - zipcode Belgium 2570"
/db_xref="taxon:46018"
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                                                                                                                                                           AF521539 1865 bp RNA linear VRL 17-.
Human echovirus 7 isolate BE00-113 5' UTR, partial sequence
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Thoelen,I., Lemey,P., van der Donck,I., Beuselinck,K.,
Lindberg,M.A. and Van Ranst,M.
Direct Submission
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Thoelen,I., Lemey,P., van der Donck,I., Beuselinck,K.,
                                                                                                                                                                                                                                                                                                 Human echovirus 7
Viruses; seRNA positive-strand viruses, no DNA stage;
Picornaviriade; Enterovirus.
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Picornaviridae; Enterovirus.
1 (bases 1 to 185)
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isolate="BE00-113"
  25
                       98 TCCGCTGCAGAGTTGCCCGTTACGA 74
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TCCGCTGCAGAGTTGCCCGTTACGA
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Human echovirus 30
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Best Local Similarity
Matches 25; Conserv
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PEATURES

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AF521542/c LOCUS DEFINITION ACCESSION VERSION

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ORGANISM

KEYWORDS

REFERENCE AUTHORS

TITLE

PUBMED REFERENCE AUTHORS

JOURNAL

Gaps

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VRL 17-JUN-2003
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Human echovirus 30 patient BE00-CC2313 5' UTR, partial sequence.
AY342855
                                                                                                                   /isolation_source="patient 121 - zipcode Belgium 3060"
/db_xref="taxon:41846"
<1. .>185
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5' UTR, partial sequence.
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<1. .>185
                                  1. .185
/organism="Human echovirus 30"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /mol_type="genomic_RNA"
/isolate="patient_BE00-CC2313"
/db_xref="taxon:41846"
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Human echovirus 30 isolate BE00-37
AF521454
AF521454.1 GI:31790796
                                                                                    /mol_type="genomic RNA"
/isolate="BE00-121"
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10, Leuven BE-3000, Belgium
Location/Qualifiers
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Conservative (
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Human echovirus 30
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Best Local Similarity
Matches 25; Conserv
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Best Local Similarity
Matches 25; Conserv
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ACCESSION
VERSION
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AY342855/c
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ORGANISM
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Direct Submission
Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological Virology, Department of Microbiology and Immunology, Rega Institute for Medical Research, University of Leuven, Minderbroedersstraat
                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological Virology, Department of Microbiology and Immunology, Rega Institute for Medical Research, University of Leuven, Minderbroedersstraat 10, Leuven BE-3000, Belgium Location/Qualifiers
                                      VRL 17-JUN-2003
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locoraviridae; Enterovirus.
1 (bases 1 to 185)
Thoelen,I., Lemey,P., Van Der Donck,I., Beuselinck,K.,
Lindberg,A.M. and Van Ranst,M.
Molecular typing and epidemiology of enteroviruses identified from an outbreak of aseptic meningitis in Belgium during the summer of
                                                                                                                                                                                                                                       Molecular typing and epidemiology of enteroviruses identified from an outbreak of aseptic meningitis in Belgium during the summer of 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /mol_type="genomic RNA"
/isolate="BE00-120"
/isolation_source="patient 120 - zipcode Belgium 9890"
/db_xref="Taxon:41846"
-1. ->185
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Human echovirus 30 isolate BE00-121 5' UTR, partial sequence.
AF521547
                       אראביניבלאל 19-5 pp. RNA linear VRL 17-UI
Human echovirus 30 isolate BE00-120 5' UTR, partial sequence.
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Lindberg, M.A. and Van Ranst, M.
Direct Submission
                                                                                                                       Human echovirus 30
Human echovirus 30
Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
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Human echovirus 5
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AY343038/c
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Lindberg, M.A. and Van Ranst, M.
Lindberg, M.A. and Van Ranst, M.
Direct Submission
Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological
Virology, Department of Microbiology and Immunology, Rega Institute
for Medical Research, University of Leuven, Minderbroedersstraat
10, Leuven BE-3000, Belgium
Location/Qualifiers
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Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological
Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological
Virology, Department of Microbiology and Immunology, Rega Institute
for Medical Research, University of Leuven, Minderbroedersstraat
10, Leuven BE-3000, Belgium
Location/Qualifiers
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                                                                                 Thoelen,I., Lemey,P., Van Der Donck,I., Beuselinck,K.,
Lindberg,A.M. and Van Ranst,M.
Molecular typing and epidemiology of enteroviruses identified from
an outbreak of aseptic meningitis in Belgium during the summer of
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Lindberg,A.M. and Van Ranst,M.
Molecular typing and epidemiology of enteroviruses identified from
an outbreak of aseptic meningitis in Belgium during the summer of
                                                                                                                                                                                                                                                                                                                                                                                                                /isolation_source="patient 37 - zipcode Belgium 2110"
/db_xref="taxon:41846"
<1._.>186
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Thoelen, I., Lemey, P., van der Donck, I., Beuselinck, K.,
Lindberg, M.A. and Van Ranst, M.
                                 Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
1 (bases 1 to 186)
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AF521479
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100.0%; Pred. No. v.--.
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/isolate="BE00-23"
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1 (bases 1 to 186)
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Human echovirus 30
Human echovirus 30
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Human echovirus 30
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Picornaviridae; Enterovirus.
1 (bases 1 to 180,
Thoelen, I., Moes, E., Lemey, P., Mostmans, S., Wollants, E.,
Lindberg, A.M., Vandamme, A.-M. and Van Ranst, M.
Analysis of the serotype and genotype correlation of VP1 and the S'
moncoding region in an epidemiological survey of the human enterovirus B species
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (16-JUL-2003) Department of Microbiology and Immunology, Laboratory of Clinical and Epidemiological Virology, Rega Institute for Medical Research, Minderbroedersstraat 10, Leuven 3000, Belgium Location/Qualifiers
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Human echovirus 30 patient BE02-7181 5' UTR, partial sequence.
AY343032
  - zipcode Belgium 9472'
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Human echovirus 5 patient BE02-3792 5' UTR, partial sequence.
AY343038
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Human echovirus 30

Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.

1 (bases 1 to 187)

Thoelen,I., Moes,E., Lemey,P., Mostmans,S., Wollants,E.,
Lindberg,A.M., Vandamme,A.-M. and Van Ranst,M.
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                                                                                                                                                                                  Indels
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2 (bases I to 186)
Thoelen, I., Moes, E., Lemey, P., Mostmans, S., Wo Lindberg, A.M., Vandamme, A.-M. and Van Ranst, M. Direct Submission
                                                                                                                            100.0%; Score 25; DB 13;
ilarity 100.0%; Pred. No. 0.32;
Conservative 0; Mismatches 0;
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/isolation_source="patient_23"/db_xref="taxon:41846"
<1._.>186
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/note="isolated in July 2002"
<1. .>186
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/isolate="patient BE02-3792"
/db_xref="taxon:40280"
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VRL 04-MAR-2004

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Viruses; SERNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.

1 (Dases I to 188)
Thoelen,I., Mose,E., Lemey,P., Mostmans,S., Wollants,E.,
Lindberg,A.M., Vandamme,A.-M. and Van Ranst,M.
Analysis of the serotype and genotype correlation of VP1 and the snoncoding region in an epidemiological survey of the human enterovirus B species
J. Clin. Microbiol. 42 (3), 963-971 (2004)
E. 2 (Dases I to 188)
Thoelen,I., Mose,E., Lemey,P., Mostmans,S., Wollants,E.,
Lindberg,A.M., Vandamme,A.-M. and Van Ranst,M.
Direct Submission
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2 (bases 1 to 188)
Thoelen, I., Moes, E., Lemey, P., Mostmans, S., Wollants, E.,
Lindberg, A.M., Vandamme, A.-M. and Van Ranst, M.
Direct Submitssion
Submitted (16-JUL-2003) Department of Microbiology and Immunology,
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Human echovirus 11 patient BE99-1509 5' UTR, partial sequence.
AY342838
                                                                                                                                            AL342837
Human echovirus 11 patient BE99-135 5' UTR, partial sequence.
AY342837
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Human echovirus 11

Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.

1 (bases 1 to 188)

Thoelen, I., Moes, E., Lemey, P., Mostmans, S., Wollants, E., Lindberg, A.M., Vandamme, A.M. and Van Ranst, M.
Analysis of the serotype and genotype correlation of VP1 an enterovirus B species
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100.0%; Score 25; DB 13; Length 188;
Best Local Similarity 100.0%; Pred. No. 0.32;
Matches 25; Conservative 0; Mismatches 0; Indels C
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/note="isolated in January 1999"
<1. .>188
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/mol_type="genomic RNA"
/isolate="patient BE99-135"
/db_xref="taxon:12078"
         TCCGCTGCAGAGTTGCCCGTTACGA 25
                               101 TCCGCTGCAGAGTTGCCCGTTACGA 77
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Human echovirus 11
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AY342838/c
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Analysis of the serotype and genotype correlation of VP1 and the 5' noncoding region in an epidemiological survey of the human enterovirus B species

1. Clin. Microbiol. 42 (3), 963-971 (2004)

2. (bases 1 to 187)

Thoselar,I., Moes, B., Lemey,P., Mostmans,S., Wollants,B.,
Lindberg,A.M., Vandamme,A.-M. and Van Ranst,M.

Direct Submission
Submitted (16-JUL-2003) Department of Microbiology and Immunology,
Laboratory of Clinical and Epidemiological Virology, Rega Institute
for Medical Research, Minderbroedersstraat 10, Leuven 3000, Belgium
Location/Qualifiers
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1 (bases 1 to 188)
Thoelen,I., Lemey,P., Van Der Donck,I., Beuselinck,K.,
Indbergy,A.M. and Van Ranst,M.
Molecular typing and epidemiology of enteroviruses identified from an outbreak of aseptic meningitis in Belgium during the summer of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /isolation source="patient 26 - zipcode Belgium 1770"
/db_xref="Taxon:41846"
<1...>188
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Thoelen, I., Lemey, P., van der Donck, I., Beuselinck, K.,
Lindberg, M.A. and Van Ranst, M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 13; Length 187;
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Human echovirus 30 isolate BE00-26 5' UTR,
AF521468
                                                                                                                                                                                                                                                                                                                                                                      /country="Belgium"
/note="isolated in December 2002"
<1. .>187
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                                                                                                                                                                                                                                                                                                                /mol_type="genomic RNA"
/isolate="patient BE02-7181"
/db_xref="taxon:41846"
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/isolate="BE00-26"
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Laboratory of Clinical and Epidemiological Virology, Rega Institute for Medical Research, Minderbroedersstraat 10, Leuven 3000, Belgium Location/Qualifiers
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Human coxsackievirus B4 patient BE99-3672 5' UTR, partial sequence.
AY342840
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Picornaviridae; Enterovirus.
I (bases 1 to 188)
Thoelen, I., Moes, E., Lemey, P., Mostmans, S., Wollants, E.,
Lindberg, A.M., Vandamme, A.-M. and Van Ranst, M.
Analysis of the serotype and genotype correlation of VP1 and the 5'
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                                                                                                                                                                                                                                         0; Indels
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J. Clin. Microbiol. 42 (3), 963-971 (2004)
2 (bases 1 to 188)
Thoelen, I., Moes, E., Lemey, P., Mostmans, S., Wol
Lindberg, A.M., Vandamme, A.-M. and Van Ranst, M.
Direct Submission
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                                                                             /mol_type="genomic RNA"
/isolate="patient BE99-1509"
/b_xref="taxon:12078"
/country="Belgium"
/note="isolated in February 1999"
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                                                              organism="Human echovirus 11"
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Pred. No. 0.32;
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/isolate="patient BE99-3672"
/db_xref="taxon:12073"
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Human coxsackievirus B4
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                                                                                                                                                                                                                                       Conservative
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Submitted (16-JUL-2003) Department of Microbiology and Immunology, Laboratory of Clinical and Epidemiological Virology, Rega Institute for Medical Research, Minderbroedersstraat 10, Leuven 3000, Belgium Location/Qualifiers
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Human coxsackievirus A9
Human coxsackievirus A9
Human coxsackievirus A9
Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
1 (bases 1 to 188)
1 (bases 1 to 188)
1 Lindberg, A.M., Vandamme, A.-M. and Van Ranst, M.
Analysis of the serotype and genotype correlation of VP1 and the 5'
noncoding region in an epidemiological survey of the human
enterovirus B species
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Human coxsackievirus A9 patient BE99-5750 5' UTR, partial sequence.
Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
1 (bases 1 to 188)
Thoelen! L., Moes.E., Lemey, P., Mostmans, S., Wollants, E.,
Lindberg, A.M., Vandamme, A.-M. and Van Ranst, M.
Analysis of the serotype and genotype correlation of VPI and the noncoding region in an epidemiological survey of the human
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2 (bases 1 to 188)
2 Thoden, I., Mose, E., Lemey, P., Mostmans, S., Wollants, E.,
Lindberg, A.M., Vandamme, A.-M. and Van Ranst, M.
Direct Submission
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J. Clin. Microbiol. 42 (3), 963-971 (2004)
2 (bases 1 to 188)
Inhoelen, I., Moes, E., Lemey, P., Mostmans, S., Wo
Dirdberg, M., Vandamme, A.-M. and Van Ranst, M.
Direct Submission
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Best Local Similarity 100.0%; Pred. No. 0.32;
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/note="isolated in April 1999"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /mol_type="genomic RNA"
/isolate="patient BE99-4376"
/db_xref="taxon:12078"
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/isolate="patient BB99-5750"
/db_xref="taxon:12067"
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/note="isolated in May 1999"
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Query Match
Best Local Similarity
Matches 25; Conserv
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Best Local Similarity
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2 (bases 1 to 188)
Thoselen, I., Moss, E., Lemey, P., Mostmans, S., Wollants, E.,
Lindberg, A.M., Vandamme, A.-M. and Van Ranst, M.
Direct Submission
Submitted (16-JUL-2003) Department of Microbiology and Immunology,
Laboratory of Clinical and Epidemiological Virology, Rega Institute
for Medical Research, Minderbroedersstraat 10, Leuven 3000, Belgium
Location/Qualifiers
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Viruses; SRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
1 (Dases 1 to 188)
Thoelen,I., Moes,E., Lemey,P., Mostmans,S., Wollants,E.,
Lindberg,A.M., Vandamme,A.-M. and Van Ranst,M.
Analysis of the serotype and genotype correlation of VP1 and the 5'
enterovirus B species
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Human coxeackievirus B4 patient BE99-6504 5' UTR, partial sequence.
AY342844
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Human coxsackievirus B4

Viruses, ssRNA positive-strand viruses, no DNA stage;

Viruses, ssRNA positive-strand viruses, no DNA stage;

Dicornaviridae; Enterovirus.

I (bases 1 to 188)

Thoelen, I., Moes, B., Lemey, P., Mostmans, S., Wollants, E.,

Lindberg, A.M., Vandamme, A.-M. and Van Ranst, M.

Analysis of the serotype and genotype correlation of VP1 and the S'

Analysis of the serotype and genotype correlation of VP1 and the S'

enterovirus B species
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Human echovirus 11 patient BE99-7222 5′ UTR, partial sequence
AY342846
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/note="isolated in June 1999"
<1. .>188
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/isolate="patient BE99-6504"
/db_xref="taxon:12073"
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Best Local Similarity 100.
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J. Clin. Microbiol. 42 (3), 963-971 (2004)

2 (bases 1 to 188)

Thoelen, I., Moes, E., Lemey, P., Mostmans, S., Wollants, E.,
Lindberg, A.M., Vandamme, A.-M. and Van Ranst, M.

Direct Submission
Submitted (16-JUL-2003) Department of Microbiology and Immunology,
Laboratory of Clinical and Epidemiological Virology, Rega Institute
for Medical Research, Minderbroedersstraat 10, Leuven 3000, Belgium
Location/Qualifiers
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Viruses; SSRNA positive-strand viruses, no DNA stage;
1 (bases 1 to 188)
Thochen, I., Moes, E., Lemey, P., Mostmans, S., Wollants, E.,
Lindberg, A.M., Vandamme, A.-M. and Van Ranst, M.
Analysis of the serotype and genotype correlation of VP1 and the 5'
noncoding region in an epidemiological survey of the human entervirus E species
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2 (bases I too 188)
Thoelen, I., Moes, E., Lemey, P., Mostmans, S., Wollants, E.,
Lindberg, A.M., Vandamme, A.-M. and Van Ranst, M.
Direct Submission
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                                                                                                                                                                                                                                                                               1. .188
/organism="Human echovirus 11"
/mol type="genomic RNA"
/isolate="patient BE99-7222"
/db_xref="taxon:12078"
/country="Belgium"
/note="isolated in June 1999"
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/mol_type="genomic RNA"
/isolate="patient BE00-518"
/db_xref="taxon:41846"
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Human echovirus 30
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AY342859/c
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Viruses; SeRNA positive-strand viruses, no DNA stage;
Picornavitidae; Enterovirus.

E 1 (bases 1 to 188)
S Thoelen, I., Moss, E., Lemey, P., Mostmans, S., Wollants, E.,
Lindberg, A.M., Vandamme, A.-M. and Van Ranst, M.
Analysis of the serotype and genotype correlation of VP1 and the S'
noncoding region in an epidemiological survey of the human
enterovirus B species
J. Clin. Microbiol. 42 (3), 963-971 (2004)
E 2 (bases 1 to 188)
S Thoelen, I., Moss, E., Lemey, P., Mostmans, S., Wollants, E.,
Lindberg, A.M., Vandamme, A.-M. and Van Ranst, M.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (16-JUL-2003) Department of Microbiology and Immunology, Laboratory of Clinical and Epidemiological Virology, Rega Institute for Medical Research, Minderbroedersstraat 10, Leuven 3000, Belgium Location/Qualifiers
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                                                                                                                                                                      Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
1 (bases 1 to 188)
Thoelen,I. Moes,E., Lemey,P., Mostmans,S., Wollants,E.,
Lindberg,A.M., Vandamme,A.-M. and Van Ranst,M.
Analysis of the serotype and genotype correlation of VP1 and the 5'
noncoding region in an epidemiological survey of the human
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                                            VRL 04-MAR-2004
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Human echovirus 30 patient BE00-CC3574 5' UTR, partial sequence.
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J. Clin. Microbiol. 42 (3), 963-971 (2004)
2 (bases 1 to 188)
Thoelen,I., Moes,E., Lemey,P., Mostmans,S., Wollants,E., Lindberg,A.M., Vandamme,A.-M. and Van Ranst,M.
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/isolate="patient BE00-CC3574"
/db_xref="taxon:41846"
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/note="isolated in April 2000"
<1. .>188
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100.0%; Pred. No.
:ive 0; Mismatch
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Matches 25; Conservative
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AY342856/c
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Viruses; SaRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
1 (bases 1 to 188)
Thoelen, I., Mose, E., Lemey, P., Mostmans, S., Wollants, E.,
Lindberg, A.M., Vandamme, A.-M. and Van Ranst, M.
Analysis of the serotype and genotype correlation of VP1 and the S.
noncoding region in an epidemiological survey of the human enterovirus B species
I. Clin. Microbiol. 42 (3), 963-971 (2004)
E. Classes 1 to 188)
Thoelen, I., Mose, E., Lemey, P., Mostmans, S., Wollants, E.,
Lindberg, A.M., Vandamme, A.-M. and Van Ranst, M.
Direct Submission
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AY342858
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Human echovirus 30 patient BE00-CC4049 5' UTR, partial sequence.
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Human echovirus 30
Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
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Pred. No. 0.32;
/mol_type="genomic RNA"
/isolate="patient BE00-CC2641"
/db xref="taxon:41846"
/country="Belgium"
/note="isolated in March 2000"
<1. .>188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Human echovirus 30"
/mol type="genomic RNA"
/isolate="patient BE00-CC3916"
/db xref="taxon:41846"
/country="Belgium"
/note="isolated in April 2000"
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25; Conservative 0
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Matches 25; Conserv
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AY342864.1 GI:37623517
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Thoelen, I., Moes E., Lemey, P., Mostmans, S., Wollants, E.,
Lindberg, A.M., Vandamme, A.-M. and Van Ranst, M.
Lindberg, A.M., Vandamme, A.-M. and Genotype correlation of VP1 and the S'
nalysis of the serotype and genotype correlation of VP1 and the S'
noncoding region in an epidemiological survey of the human
enterovirus B species
L. J. Clin. Microbiol. 42 (3), 963-971 (2004)
E. S. (bases 1 to 188)
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Indberg, A.M., Vandamme, A.-M. and Van Ranst, M.
Direct Submission
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Picornaviridae; Enterovirus.

E 1 (Dasses 1 to 188)
S Thoelen, I., Moss, E., Lemey, P., Mostmans, S., Wollants, E.,
Lindberg, A.M., Vandamme, A.-M. and Van Ranst, M.
Analysis of the serotype and genotype correlation of VP1 and the serotype and genotype correlation of the human noncoding region in an epidemiological survey of the human enterovirus B species
U. Clin. Microbiol. 42 (3), 963-971 (2004)
E 2 (Dasses 1 to 188)
S Thoelen, I., Mostmans, S., Wollants, E.,
Lindberg, A.M., Vandamme, A.-M. and Van Ranst, M.
Direct, Submission
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Human echovirus 30 patient BE00-CC3821 5' UTR, partial sequence.
AY342860
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/isolate="patient BE00-CC4049"
/db xref="taxon:41846"
/country="Belgium"
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isolate="patient BE00-CC3821"
db_xref="taxon:41846"
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/note="isolated in April 2000"
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Viruses; seRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.

El (bases 1 to 188)

Thoelen, I., Mosey, E., Mostmans, S., Wollants, E.,
Lindberg, A.M., Vandamme, A.-M. and Van Ranst, M.
Analysis of the serotype and genotype correlation of VP1 and the snoncoding region in an epidemiological survey of the human enterovirus B species
J. Clin. Microbiol. 42 (3), 963-971 (2004)

E. (bases 1 to 188)

Thoelen, I., Mosey, E., Lemey, P., Mostmans, S., Wollants, E.,
Lindberg, A.M., Vandamme, A.-M. and Van Ranst, M.
Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae; Enterovirus.

1 (Dases 1 to 188)
Thoelen,I., Moes,E., Lemey,P., Mostmans,S., Wollants,E., Lindberg,A.M., Vandamme,A.-M. and Van Ranst,M.
Analysis of the serotype and genotype correlation of VP1 and the S' noncoding region in an epidemiological survey of the human
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Human echovirus 30 patient BE00-CC3917 5' UTR, partial sequence.
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J. Clin. Microbiol. 42 (3), 963-971 (2004)
2 (bases 1 to 188)
Thoelen, I. Moes, E., Lemey, P., Mostmans, S., Wollants, E.,
Lindberg, A. M., Vandamme, A.-M. and Van Ranst, M.
Direct Submission
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JOURNAL Submitted (16-JUL-2003) Department of Microbiology and Immunology,
Laboratory of Clinical and Epidemiological Virology, Rega Institute
for Medical Research, Minderbroedersstraat 10, Leuven 3000, Belgium
Location/Qualifiers

1. 188
| Location/Qualifiers | Location/Qualifiers |
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                                                                                                                                                                                   APPLICANT: CHANG, EDWARD L.
APPLICANT: CHANG, EDWARD L.
APPLICANT: CHANG, EDWARD L.
APPLICANT: DEVELOPMENT CENTER FOR BIOTECHNOLOGY
TITLE OF INVENTION: SWINE VESICULAR DISEASE VIRUS AND MUTANT STRAINS AND
TITLE OF INVENTION: PREPARATION PROCESS AND USE THEREOF
FILE REFERENCE: 9751.790501
CURRENT APPLICATION NUMBER: US/09/116,032
CURRENT APPLICATION NUMBER: CHINA 86105814
EARLIER PILING DATE: 1997-05-01
NUMBER OF SEQ ID NOS: 39
SOFTWARE: PATENTIN VEY: 2.0
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APPLICANT: JENG, KING-SONG
APPLICANT: JENG, KING-SONG
APPLICANT: CHANG, EDWARD L.
APPLICANT: CHANG, EDWARD L.
APPLICANT: CHANG, EDWARD L.
APPLICANT: DEVELOPMENT CENTER FOR BIOTECHNOLOGY
TITLE OF INVENTION: SWINE VESICULAR DISEASE VIRUS AND MUTANT STRAINS AND
TITLE OF INVENTION: PREPRAGATION PROCESS AND USE THEREOF
FILE REFERENCE: 9751.79US01
CURRENT APPLICATION NUMBER: US/09/116,032
CURRENT FILING DATE: 1998-07-15
EARLIER PILING DATE: 1998-07-15
EARLIER FILING DATE: 1997-05-01
NUMBER OF SEQ ID NOS: 39
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0; Mismatches 1;
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; ORGANISM: SWINE VESICULAR DISEASE VIRUS
US-09-116-032-2
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ORGANISM: SWINE VESICULAR DISEASE VIRUS
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                    Sequence 2, Application US/09116032
Patent No. 6200576
GENERAL INFORMATION:
APPLICANT: HWONG, CHING LONG
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Patent No. 6200576
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ilarity 96.0%;
Conservative
                                                                                           APPLICANT: HWONG, CHING LONG
APPLICANT: LO, CHENG-KAI
APPLICANT: YANG, YING-CHUAN
APPLICANT: JENG, KING-SONG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: HWONG, CHING LONG APPLICANT: LO, CHENG-KAI
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SEQ ID NO 1
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Best Local Similarity 96.0
Matches 24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 24; Conserva
US-09-116-032-2/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-116-032-1/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 1220
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RESULT 4

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APPLICANT: Lee, Kang-Hung
APPLICANT: Bair, Chi-Horng
APPLICANT: Bair, Chi-Horng
APPLICANT: Bair, Chi-Horng
APPLICANT: Wang, Yih-Weng
APPLICANT: Wang, Xih-Weng
APPLICANT: Wang, Shing-Hwan
TITLE OF INVENTION: Methods for Detecting and differentiating Enteroviruses and the P
TITLE OF INVENTION: and Probes Therefor
FILE REFERENCE: TAI 316
CURRENT APPLICATION NUMBER: US/09/724,678D
CURRENT PILLING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 16
SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RELATING TO KLEBSIELLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: WHITE, Owen R.
APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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APPLICANT: GATY Brecon et. al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATI

TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAFEUTICS

TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAFEUTICS

CURRENT APPLICATION NUMBER: US/09/489,039A

CURRENT FILING DATE: 2000-01-27

PRIOR APPLICATION NUMBER: US 60/117,747

PRIOR FILING DATE: 1999-01-29

NUMBER OF SEQ ID NOS: 14342

SEQ ID NO 680
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: Artificial Sequence is Synthesized
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 23; DB 3
Pred. No. 0.17;
5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 18.8; D
Pred. No. 28;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27 TCCGCYRCRGASTTGCSCGTTACGA 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-489-039A-680/c; Sequence 680, Application US/09489039A; Patent No. 6610836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1112 ccecreceaserescerrae 1091
Application US/09724678D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 CCGCTGCAGAGTTGCCCGTTAC 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2, Application US/09103840A Patent No. 6294328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ); ORGANISM: Klebsiella pneumoniae
US-09-489-039A-680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: FLEISCHMAN, Robert D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 80.0%;
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 90.9%;
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 TCCGCTGCAGAG1
                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Patent No. 6818397
US-09-724-678D-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-103-840A-2
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Gaps

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70.4%; Score 17.6; DB 3; Length 10082; 83.3%; Pred. No. 1.2e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: VANDERBILT UNIVERSITY
305 Kirkland Hall
Nashville, TN 37240
TITLE OF INVENTION: MAMMALIAN GENES INVOLVED IN VIRAL
INPECTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Needle & Rosenberg, P.C.
STREET: 127 Peachtree Street, Suite 1200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Selby, Elizabeth
REGISTRATION NUMBER: 38,298
REFERENCE/DOCKET NUMBER: 22000.0061/P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US97/06067
FILING DATE: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION UNBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-0-03
PRIOR PILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FREESEQ for Windows Version 4.0
SEQ ID NO 15569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/171,209
FILING DATE: 08-Mar-1999
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8354 rccrcrccadadcrcccccrrace 8377
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NOLECULE TYPE: DNA (genomic)

SEQUENCE DESCRIPTION: SEQ ID NO: US-09-171-209-45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 TCCGCTGCAGAGTTGCCCGTTACG 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-171-209-45; Sequence 45, Application US/09171209; Patent No. 6448000; GENERAL INPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 30303-1811
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: 404 688 0770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 404 688 9880 INFORMATION FOR SEQ ID NO: 45:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 83
                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 83.3
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Atlanta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: USA
                                                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                         US-09-949-016-15569
                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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Batent No. 6012319
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TILLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION:
PLITE OF DETECTION AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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                                                                                                                                                                                                                                                              ; OTHER INFORMATION: CDC 1551
; OTHER INFORMATION: "n" bases at various positions throughout the sequence
; OTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Pompejus, Markus
APPLICANT: Froger, Burkhard
APPLICANT: Schroder, Hartwig
APPLICANT: Schroder, Hartwig
APPLICANT: Haberhauer, Gregor
TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING NOVEL
TITLE OF INVENTION: PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 72.8%; Score 18.2; DB 3; Length 4403765; Best Local Similarity 87.0%; Pred. No. 1.1e+02; Matches 20; Conservative 0; Mismatches 3; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/605,703B
CURRENT FILIDEN DATE: 2000-06-27
PRIOR APPLICATION NUMBER: 60/142,764
PRIOR APLICATION NUMBER: 60/142,764
PRIOR FILING DATE: 1999-07-08
PRIOR FILING DATE: 1999-09-03
                       FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
CUNBER OF EQ. ID NOS: 2
SOFTWARE: Patentin Ver: 2.1
SEQ. ID NO 2
LENGTH: 4403765
TYPE: DNA
ORGANISM: Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. 91;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            356580 ccearcccaciriccccarace 356602
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1619, Application US/09605703B Patent No. 6962989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 CCGCTGCAGAGTTGCCCGTTACGA 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 CCGCTGCAGAGTTGCCCGTTACG 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA ORGANISM: Corynebacterium glutamicum
     TUBERCULOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | NAME/KEY: CDS
| LOCATION: (1101)...(1282)
| OTHER INFORMATION: RXA00159
| US-09-605-703B-1619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 83.3
       TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 8
US-09-949-016-15569
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Gaps

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TITLE OF INVENTION: Preparation of heterodimeric PDGF-AB using a TITLE OF INVENTION: Dicistronic vector system in mammalian cells NUMBER OF SEQUENCES: 16 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25 (EPA) CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/387,845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "non-authentic sequence
due to a base pair substitution from C to
at position 610"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "shown are the first
628 nt of the 5' non-translated region of
poliovirus Typ 1 (Mahoney)"
  GENERAL INFORMATION:
APPLICANT: Lefebyre, Daniel D.
APPLICANT: Malboobi, Mohammad A.
TITLE OF INVENTION: PHOSPHATE STARVATION-INDUCIBLE PROTEINS
FILE REFERENCE: PPL96-03
CURRENT APPLICATION NUMBER: US/08/688,988B
CURRENT FILING DATE: 1996-07-31
NUMBER OF SEQ ID NOS: 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 628;
                                                                                                                                                                                                                                                                                                                            Length 319;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear ORIGINAL SOURCE:
ORGANISM: Poliovirus Typ 1 (Mahoney strain)
IMMEDIATE SOURCE:
CLONE: pGEM 3-5'Polio (M) (4708 bp), (Sarnow, 1989)
                                                                                                                                                                                                                                                                                                                          Score 17; DB 3; I
Pred. No. 1.5e+02;
0; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             68.0%; Score 17; DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      162 recectrcacartreccectreaca 186
                                                                                                                                                                                                                                                                                                                                                                                                               25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 5, Application US/08387845
Patent No. 5665567
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                          68.0%;
80.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 435
INFORMATION FOR SEQ ID NO: 5
SEQUENCE CHARACTERISTICS:
LENGTH: 628 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 80.0
Matches 20; Conservative
                                                                                                                                                                                                                                       TYPE: DNA
CORGANISM: Brassica Nigra
US-08-688-988-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PUBLICATION INFORMATION:
AUTHORS: Sarnow, P.
JOURNAL: J. Virol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PEATURE:
NAME/KEY:
LOCATION: 610
OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCATION: 1..628
OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-387-845-5/c
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                                                                                                                                                                                                                       LENGIH: 319
                                                                                                                                                                                               SEQ ID NO 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Rebischung, Corinne
TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPII
TITLE OF INVENTION: AND USES THEREOF
NUMBER OF SEQUENCES: 1152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    68.8%; Score 17.2; DB 3; Length 824;
                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: Research Triangle Park
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: No. 6239264th Carolina
COUNTRY: USA
ZIP: 27709
COMPUTER: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/998,416
FILING DATE: 24-DEC-1997
CLASSIFICATION NUMBER: CH 0016/97
FILING DATE: 31-DEC-1996
ATPONEY/AGENT INPOMMER: CH 0016/97
FILING DATE: 31-DEC-1996
ATPONEY/AGENT INPOMMER: 38,241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PF/5-30306/A/CGC1976
      1.1e+02;
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                          Mismatches
Best Local Similarity 94.7%; Pred. No. Matches 18; Conservative 0; Mismat
                                                                                                                                                                                       US-08-998-416-523/c
; Sequence 523, Application US/08998416
; Patent No. 6239264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 27, Application US/08688988B; Patent No. 6096545
                                                                                                        491 Crecacaciriscorcitae 509
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8689
INFORMATION FOR SEQ ID NO: 523:
SEQUENCE: CHARACTERISTICS:
LENGTH: 824 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                   5 CTGCAGAGTTGCCCGTTAC 23
                                                                                                                                                                                                                                                                          Philippsen, Peter
Pohlmann, Rainer
Steiner, Sabine
                                                                                                                                                                                                                                                                                                                                         Mohr, Christine
Wendland, Jurgen
Knechtle, Philipp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: DNA (genomic) ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    86.48;
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Best Local Similarity 86.4
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 623920
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                                                                                                                                                                                                                                                        GENERAL INFORMATION:
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APPLICANT:
APPLICANT:
APPLICANT:
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                     Gaps
                                                                                                                                                                                                                                                                   TITLE OF INVENTION: Preparation of heterodimeric PDGF-AB using a TITLE OF INVENTION: bicistronic vector system in mammalian cells NUMBER OF SEQUENCES: 16
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "non-authentic sequence
due to a base pair substitution from C to
at position 610"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "shown are the first
628 nt of the 5' non-translated region of
poliovirus Typ 1 (Mahoney)"
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80.0%; Pred. No. 1.6e+02;
iive 0; Mismatches 5; Indels
                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.25 (EPA)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/778,275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Poliovirus Typ 1 (Mahoney strain)
IMMEDIATE SOURCE:
CLONE: pGEM 3-5'Polio (M) (4708 bp), (Sarnow, 1989)
Pred. No. 1.6e+02;
0; Mismatches 5
                                                                                             535 rcceccaceacrirececerracea 511
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                                                       1 TCCGCTGCAGAGTTGCCCGTTACGA 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/387,845
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US-08-867-352-5/c
; Sequence 5, Application US/08867352
; Betent No. 6060273
; GENERAL INFORMATION:
                                                                                                                                                                                     Sequence 5, Application US/08778275
Patent No. 5935819
GENERAL INFORMATION:
APPLICANT:
Best Local Similarity 80.0%;
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
INFORMATION FOR SEQ ID NO: 5
SEQUENCE CHARACTERISTICS:
LENGITH: 628 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION: 610
CTHER INFORMATION: /no
OTHER INFORMATION: due
OTHER INFORMATION: at
PUBLICATION INFORMATION: at
AUTHORS: SATION, P.
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NAME/KEY:
LOCATION:
OTHER INFORMATION:
OTHER INFORMATION:
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DATE: 1989
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                                                                                                                                                     RESULT 13
US-08-778-275-5/c
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NAME/KEY:
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RESULT 15
US-09-221-017B-435/C
; Sequence 435, Application US/09221017B
; Patent No. 6444799
; GENERAL INFORMATION:
; APPLICANT: Ross, Bruce C.
; TITLE OF INVENTION: P. GINGIVALIS NUCLEOTIDES AND USES THEREOF
; NUMBER OF SEQUENCES: 1120
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
; CITY: Palo Alto
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TITLE CART.

THE CART.

THE CART.

NUMBER OF SEQUENCES: 25

COMPOTER READABLE PORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25 (EPA)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/867,352
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due to a base pair substitution from C to
at Location 610"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "shown are the first
628 nt of the 5' non-translated region of
poliovirus Typ 1 (Mahoney)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORIGINAL SOURCE:
ORGANISM: Poliovirus Typ 1 (Mahoney strain)
IMMEDIATE SOURCE:
CLONE: pGEM3-5'Polio (M) (4708 bp), (Sarnow, 1989)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 68.0%; Score 17; DB 3; I Best Local Similarity 80.0%; Pred. No. 1.6e+02; Matches 20; Conservative 0; Mismatches 5:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/387,847
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 628 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM Compatible OPERATING SYSTEM: Windows
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PEATURE:
NAME/KEX:
LOCATION:
COTALION:
OTHER INFORMATION:
OTHER INFORMATION:
AUTHORN INFORMATION:
AUTHORN INFORMATION:
AUTHORNAME:
JOURNAME:
OTHER INFORMATION:
AUTHORNAME:
OTHER INFORMATION:
AUTHORNAME:
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ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: -.628
LOCATION: 1..628
OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
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; DATE: 1989
US-08-867-352-5
                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
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FENCERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;

CURRENT APPLICATION NUMBER: 60/241, 755

PRIOR FILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/231, 768

PRIOR APPLICATION NUMBER: 60/231, 498

PRIOR PILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FastsEQ for Windows Version 4.0

SEQ ID NO SOFTWARE: FastsEQ for Windows Version 4.0
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Patent No. 5587289
GENERAL INFORMATION:
APPLICANT: Lurquin, Christophe; Boon-Falleur, Thierry
ITILE OF INVENTION: Isolated Nucleic Acid Molecules Which Are
TITLE OF INVENTION: Members of The Mage-Xp Family and Uses Thereof
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                                                    Length 1865;
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                                                Score 17; DB 3; Length 186
Pred. No. 1.8e+02;
0; Mismatches 5; Indels
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Pred. No. 1.8e+02;
0; Mismatches 5;
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REFERENCE/DOCKET NUMBER: LUD 5408
                                                                                                                                                                                                                                                                                                         Sequence 5301, Application US/09949016
Patent No. 6812339
                                                                                                                                           1 TCCGCTGCAGAGTTGCCCGTTACGA
                                                  68.0%;
80.0%;
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80.0%;
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STREET: 805 Third Avenue
CITY: New York City
                                                Query Match
Best Local Similarity 80.0°
Matches 20; Conservative
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Best Local Similarity 80.0
Matches 20; Conservative
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & Ly
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                                                                                                                                                                                                                                                                                    US-09-949-016-5301/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: DNA
; ORGANISM: Human
US-09-949-016-5301
       US-09-949-016-5300
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Patent No. 6812339
GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF FILE REPERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/231,768
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR PILING DATE: 2000-10-09
PRIOR PILING DATE: 2000-10-09
PRIOR PILING DATE: 2000-09-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         68.0%; Score 17; DB 3; Length 1823;
80.0%; Pred. No. 1.8e+02;
Live 0; Mismatches 5; Indels
SOPTWARE: FastSEQ for Windows Version 2.0b CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/221,017B FILING DATE: 23-DEC-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27340-20021.00
                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: PP1182
FILING DATE: 31-DEC-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PP1546
FILING DATE: 30-JAN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PP2911
FILING DATE: 09-APR-1998
FILING DATE: 10-DEC-1998
APPLICATION NUMBER: PCT/AU98/01023
FILING DATE: 10-DEC-1998
APPLICATION NUMBER: PCT/AU98/01023
FILING DATE: NAME: MONTON, GLAGAB H
REGISTRATION NUMBER: 32,430
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SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 5300
LENGTH: 1865
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 TCCGCTGCAGAGTTGCCCGTTACGA 25
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REFERENCE/DOCKET NUMBER: 2734C
TELECOMMUNICATION INFORMATION:
TELEPAK: 650-494-0792
TELEX: 706141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: UNKNOWN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 1823 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEX: 706141
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc_feature
LOCATION: 1...1823
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Best Local Similarity 80.03
Matches 20; Conservative
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US-09-949-016-5300/c
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ORGANISM: Human
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US-09-221-017B-435
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APPLICANT: Lurquin, Christophe; Brasseur, Francis;
APPLICANT: Lurquin, Christophe; Brasseur, Francis;
APPLICANT: Lurquin, Christophe; Brasseur, Francis;
APPLICANT: Boon-Falleur, Thierry
TITLE OF INVENTION: Members of The Mage-Xp Family and Uses Thereof
INVERSPONDENCE: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York City
STRTE: New York City
STRTE: New York
INVENTION:
COMPUTER: Librabale FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
                                                                                                                                                                                                                                                                                                  Gaps
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Pred. No. 1.8e+02;
0; Mismatches 5; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
SOCTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/658,578
FILING DATE: 5-MAY-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/403,388
FILING DATE: 14-MARCH-1995
ATTORNEY/ACENT INFORMATION:
NAME: HANSON, NO. 5759783man D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: 30,946
REFERENCE/DOCKET NUMBER: 100 5444
TELEPHON: (212) 688-9200
TELEPAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1866 base pairs
                                                                                                                                                                                                                                                                                                                                                                                       973 rcgereccacacricccrrraaca 949
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TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                 68.0%;
80.0%;
                TELEPHONE: (212) 688-9200
TELEPAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1866 base pairs
                                                                                                                                                                                                                                          Query Match
Best Local Similarity 80.0
Matches 20; Conservative
                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                               ; TOPOLOGY: linear
US-08-403-388-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-658-578-1
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RESULT 20

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                                                                            GENERAL INFORMATION:
APPLICANT: Lurquin, Christophe; Brasseur, Francis;
APPLICANT: Boon-Falleur, Thierry
TITLE OF INVENTION: Isolated Nucleic Acid Molecules Which Are
TITLE OF INVENTION: Members Of The Mage-B Family and Uses Thereof
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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; Betent No. 6287569
; GENERAL INFORMATION:
APPLICANT: KIPES, THOMAS J.
APPLICANT: WI, YUNQI
TITLE OF INVENTION: PROCESSING
TITLE OF INVENTION: PROCESSING
FILE REFERENCE: 233/221
CURRENT FILING DATE: 1998-04-06
BARLIER FILING DATE: 1998-04-10
SARLIER FILING DATE: 1998-04-10
NUMBER OF SEQ ID NOS: 35
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 18-06
SEQ
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STREET: 805 Third Avenue
CITY: New York City
ZTATE: New York
ZIP: 10022-7513
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
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Pred. No. 1.8e+02;
0; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Hanson, No. 6017705man D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5444.1
TELECHONICATION INFORMATION:
TELEPHONE: (212) 689-9200
IELEPHONE: (212) 838-3884
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1866 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: 180
COMPUTER: 180
COPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect For DOS 6.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/846,111D
FILING DATE: 25-APRIL-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/658,578
FILING DATE: 5-MAY-1996
FILING DATE: 14-WARCH-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       973 rcccrcccacacrrccccrrraaca 949
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; Sequence 1, Application US/08846111D
; Patent No. 6017705
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illarity 80.0%;
Conservative
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STRANDEDNESS: single
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US-08-846-111D-1
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Best Local Similarity
Matches 20; Conserv
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TYPE: DNA ORGANISM: Artificial Sequence
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TELEX: 42253 COOP UTELEX: 42253 COOP UTELEX: 5EQUENCE CHARACTERISTICS: LENGTH: 7432 base_pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: DNA (genomic)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         20; Conservative
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CLASSIFICATION: 435
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TYPE: NUCLEIC ACID
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
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STATE: New York
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
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                                                                                                                                                                                                                                                                                                                                                                         US-09-202-904A-10
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US-07-852-260-1/c
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                                                                                                                                                                                                                              SEQ ID NO 10
LENGTH: 2320
                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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                                                                                                                                                                                                                                                                            Sequence 1, Application US/09443077
Sequence 1, Application US/09443077
Patent No. 6392016
GENERAL INFORMATION:
APPLICANT: Lurquin, Christophe; Brasseur, Francis;
Boon-Falleur, Thierry.
TITLE OF INVENTION: Isolated Nucleic Acid Molecules Which Are
Members Of The Mage-B Family and Uses Thereof
                                                                                                         Gaps
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                                                               Score 17; DB 3; Length 1866; Pred. No. 1.8e+02;
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                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE: New York
ZIP: 10022-7513
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 68.0%; Score 17; DB 3; Length 18¢
Best Local Similarity 80.0%; Pred. No. 1.8e+02;
Matches 20; Conservative 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect For DOS 6.0b
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: LUD 5444.1
                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/09/443,077
FILING DATE: 26-Jun-2001
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Hanson, No. 6392016man D. REGISTRATION NUMBER: 30,946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: <Unknown>
APPLICATION WUNBER: 08/403,388
FILING DATE: 14-MARCH-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 08/846,111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-443-077-1
                                                                                                                                                                                  973 rcgcroccacaciriccccrrraaca 949
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                                                                                                                                            1 TCCGCTGCAGAGTTGCCCGTTACGA 25
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; Sequence 10, Application US/09202904A
; Patent No. 6395471
; GENERAL INFORMATION:
; APPLICANT: Kang, Sung Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York City
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (212) 838-3884
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 1866 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
                                                            Query Match 68.0%;
Best Local Similarity 80.0%;
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                              -09-443-077-1/c
                  US-09-056-105-19
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TITLE OF INVENTION: Hepatitis C Surrogate Virus for Testing
TITLE OF INVENTION: the Activity of Hepatitis C Virus Protease, a Recombinant
TITLE OF INVENTION: Gene and a Use Thereof
FILE REFERENCE: A32210-PCT-USA 0.7244.0104
CURRENT APPLICATION NUMBER: US/09/202,904A
CURRENT APPLICATION NUMBER: BCT/KR97/00120
PRIOR PILING DATE: 1997-06-25
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PASESEQ for Windows Version 3.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: Genetically engineered virus derived from OTHER INFORMATION: poliovirus and hepatitis C virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Racaniello, Vincent
APPLICANT: Tatem, Joanne M.
APPLICANT: Weeks-Levy, Carolyn L.
TITLE OF INVENTION: METHODS FOR PRODUCING RNA VIRUSES FROM
TITLE OF INVENTION: CDNA
NUMBER OF SEQUENCES: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 2320;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READBALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/852,260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 17; DB 3; Pred. No. 1.9e+02;
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; Patent No. 5525715
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ADDRESSEE: Cooper & Dunham
STREET: 30 Rockefeller Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 36
TELECOMMUNICATION INFORMATION:
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US-08-465-250-1/c
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                                                                                                                         Query Match 68.0%; Score 17; DB 2; Length 7432; Best Local Similarity 80.0%; Pred. No. 2.1e+02; Matches 20; Conservative 0; Mismatches 5; Indels
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80.0%; Pred. No. 2.1e+02;
iive 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Racaniello, Vincent
APPLICANT: Tatem, Joanne M.
APPLICANT: Weeks-Levy, Carolyn L.
TITLE OF INVENTION: METHODS FOR PRODUCING RNA VIRUSES
TITLE OF INVENTION: FROM CDNA
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:

SOFTWARE PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/461,503
FILING DATE: 5-UN-1995
CLASSIFICATION: 435-1095
ATTONREY AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 36607-D-PCT-US
TELEPHONICATION INFORMATION:
TELEPHONICATION INFORMATION:
TELEPHONICATION INFORMATION:
TELEPHONICATION INFORMATION:
TELEPHONICATION INFORMATION:
TELEPHONICATION INFORMATION:
TELEFEX: 422523 COOP UI
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Cooper & Dunham STREET: 1185 Avenue of the Americas CITY: New York STATE: New York COUNTRY: U.S.A. ZIP: 10112
COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: ISM PC compatible COMPUTER: ISM PC COMPATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                538 rcccccccccccrrcccccrracca 514
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Patent No. 5834302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               : 7432 base pairs
nucleic acid
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Best Local Similarity 80.0
Matches 20; Conservative
                       CDS
743..7361
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; NAME/KEY:
; LOCATION:
US-08-461-503-1
                     NAME/KEY:
LOCATION:
US-07-852-260-1
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FEATURE:
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GENERAL INCREMENTATION:

APPLICANT: RACCARIATION:

APPLICANT: Tatem, Joanne M.

APPLICANT: Weeks-Levy, Carolyn L.

TITLE OF INVENTION: METHODS FOR PRODUCING RNA VIRUSES FROM TITLE OF INVENTION: CONA STREET: 1185 Avenue of the Americas

CITY: New York

STREET: 1185 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: U.S.A.

ZIP: 10036

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: ENP Compastible

COMPUTER: LIB MP Compastible

COMPUTER: OFFICE OFFICE

COMPUTER: CONFORTION: DATACLE

COMPUTER: D
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APPLICANT: Yong Soo, Bae
APPLICANT: Jung, Hye Rhan
TITLE CANT: Jung, Hye Rhan
TITLE OF INVENTION: Replication-Competent Sabin Type 1 Strain
FILE REFERENCE: Docket No. 6696289: 4220-109 US
CURRENT APPLICATION NUMBER: US/09/284,349B
CURRENT FILING DATE: 1999-06-04
PRIOR APPLICATION NUMBER: PCT/KR98/00242
PRIOR FILING DATE: 1998-07-08
PRIOR APPLICATION NUMBER: KR 97/37812
RICH DATE: 1999-07-08
NUMBER OF SEQ ID NOS: 30
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Best Local Similarity 80.0%; Pred. No. 2.1e+02;
Matches 20; Conservative 0; Mismatches 5; Indels
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NAME: White, Obn P.
REGISTRATION NUMBER: 28,678
REPERENCE/DOCKET NUMBER: 36607-E-PCT-US
TELEPHONE: (212) 279-0400
TELEPHONE: (212) 391-0525
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APPLICATION NUMBER: US/08/465,250
FILLING DATE: 6-JUN-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SYSTEM: PC-DOS/MS-DOS
PatentIn Release 1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-284-349B-1/c
; Sequence 1, Application US/09284349B
; Patent No. 6696289
; Sequence 1, Application US/08465250
; Patent No. 6136570
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7432 base pairs
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743..7361
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STRANDEDNESS: sing
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OPERATING SYSTEM:
SOFTWARE: PatentI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
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RESULT 26

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IBM
    US-09-949-016-17043
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US-09-949-016-17043/C
is Sequence 17043, Application US/09949016
is Patent No. 6812339
is GENERAL INFORMATION:
TYTIZE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
ITITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
ITITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
ITITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
ITITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
ITITLE DEATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/231,768
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR PILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FASELSEQ for Windows Version 4.0
SEQ ID NO 17043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REPERENCE: CLOO1307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-10-20

PRIOR PILING DATE: 2000-10-20

PRIOR PILING DATE: 2000-10-20

PRIOR PILING DATE: 2000-10-09

PRIOR PILING DATE: 2000-10-09

PRIOR PILING DATE: 2000-10-09

PRIOR PILING DATE: 2000-09-08
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                                                                                                                                                                  DB 3; Length 7441;
                                                                                                                                                                                                                 5; Indels
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                                                                                                                                                                  Score 17; DB 3; )
Pred. No. 2.1e+02; 0; Mismatches 5
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SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 17042
LENGTH: 12309
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Patent No. 6812339
                                                                                                                                                                Query Match 68.0%;
Best Local Similarity 80.0%;
Matches 20; Conservative
SOFTWARE: PatentIn version 3.1
                                                                     TYPE: DNA
ORGANISM: Human poliovirus 1
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Best Local Similarity 80.0°
Matches 20; Conservative
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; ORGANISM: Human
US-09-949-016-17042
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ORGANISM: Human
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                                              LENGTH: 7441
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                        SEQ ID NO 1
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Patent No. 6017705
GENERAL INFORMATION:
APPLICANT: Lurdun, Christophe; Brasseur, Francis;
APPLICANT: Long Constant Christophe; Brasseur, Francis;
TITLE OF INVENTION: Isolated Nucleic Acid Molecules Which Are
TITLE OF INVENTION: Members Of The Mage-B Family and Uses Thereof
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & Lynch
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    Length 12309;
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           Indels
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Boon-Falleur, Thierry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: New York
ZIP: 10022-7513
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2.6e+02;
  Score 17; DB 3;
Pred. No. 2.3e+02
0; Mismatches
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SOFTWARE: Wordperfect For DOS 6.0b
CURRENT APPLICATION DATA:
APPLICATION NATA:
APPLICATION NATA:
CLASSIPICATION 1435
PILING DATE: 25-APRIL-1997
CLASSIPICATION DATA:
APPLICATION NUMBER: 08/658,578
FILIND DATE: 5-MAY-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/658,388
APPLICATION NUMBER: 08/403,388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             38797 rcgcrcccacacacrcccrrraaca 38773
                                                                                                                                9414 TCGGTGCCAGAGTTGCCCTTTAAGA 9390
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REFERENCE/DOCKET NUMBER: LUD 5444.1
                                                                                     25
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                                                                                     1 TCCGCTGCAGAGTTGCCCGTTACGA
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 15, Application US/09443077; Patent No. 6392016; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION
  68.0%;
80.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (212) 688-9200
TELEPAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York City
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 40352 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
Query Match
Best Local Similarity 80.0
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 68.0
Best Local Similarity 80.0
Matches 20; Conservative
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US-08-846-111D-15
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51764 rcrecrecadadarecererae 51786
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; Sequence 12171, Application US/09949016
; Patent No. 6812339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANIEM: Mycobacterium tuberculosis
OTHER INCRMATION: H37Rv
US-09-103-840A-1
                   1 TCCGCTGCAGAGTTGCCCGTTAC 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 1, Application US/09103840A; Patent No. 6294328; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; LOCATION: (1)...(85369)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-12171
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Best Local Similarity 82.6%;
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Human
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US-09-103-840A-1
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APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Stater, Steven C.
APPLICANT: Misgand, Roger C.
TITLE OF INVENTION: Mycococcus xanthus Genome Sequences and Uses Thereof FILE REFERENCE: 38-10(15849)8
CURRENT FILING DATE: 2001-07-10
CURRENT FILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 16825
SEQ ID NO 11326
LENGTH: 13226
TITLE OF INVENTION: Isolated Nucleic Acid Molecules Which Are
Members Of The Mage-B Family and Uses Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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Pred. No. 3.6e+02;
0; Mismatches 4; Indels 0:
                                           Length 40352;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 17; DB 3; Length 403
Pred. No. 2.6e+02;
0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Hanson, No. 6392016man D. REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5444.1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEPHONE: (212) 688-3884
INFORMATION FOR SEQ ID NO: 15:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           38797 rccereccacacircccrrraaca 38773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear SEQUENCE DESCRIPTION: SEQUENCE DESCRIPTION: SEQ ID NO: 15:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 TCCGCTGCAGAGTTGCCCGTTACGA 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 32
US-09-902-540-1132/c
'S Equence 1132, Application US/09902540
'Patent No. 6833447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 40152 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       68.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 82.6%;
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGANISM: Myxococcus xanthus US-09-902-540-1132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 80.0
Matches 20; Conservative
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FALCHAN TO SELICANT: VENTER, J. Craig et al.

APPLICANT: VENTER, J. Craig et al.

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
TITLE REFERENCE: CLOO1307

CURRENT APPLICATION NUMBER: 06/241,755

PRIOR APPLICATION NUMBER: 66/241,755

PRIOR PELING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOUTHAND SES SEQ ID NOS: 207012

SEQ ID NO 12171

LENGTH: 85369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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APPLICANT: FLEISCHAMN, Robert D.
APPLICANT: FRASER, Claire M.
APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: TUBRECULOSIS
FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO.1
FURNATION NO.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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Pred. No. 4.4e+02;
0; Mismatches 4; Indels 0;
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Sequence 16889, Application US/09949016

Sequence 16889, Application US/09949016

Batent No. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;

FILE REPRENEUE. CLOO1307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

FRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOCTWARE: PEAGESEQ for Windows Version 4.0

SEQ ID NO 16889

LENGTHAL: 17154
                                                                  GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISRASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: 60/241, 755
FRIOR FILING DATE: 2000-10-20
PRIOR PELING DATE: 2000-10-03
PRIOR PELING DATE: 2000-10-03
PRIOR PELING DATE: 2000-09-08
PRIOR PELING DATE: 2000-09-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 16.2; DB 3; Length 17154;
Pred. No. 5.7e+02;
); Mismatches 3; Indels 0:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                64.8%; Score 16.2; DB 3; Length 3378; 85.7%; Pred. No. 4.6e+02; ive 0; Mismatches 3; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FRAESEQ for Windows Version 4.0
SEQ ID NO 5147
LENGTH: 3378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 13873, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14079 CTGCATAGATGCCCGTTACTA 14099
                             Application US/09949016
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2711 CTGCATAGATGCCCGTTACTA 2731
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Best Local Similarity 85.7
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 85.7
Matches 18; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Human
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US-09-949-016-16889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-949-016-5147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 38
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                                                                                                                                                              GENERAL INFORMATION:

APPLICANT: ROSE, Bruce C.

TITLE OF INVENTION:

NUMBER OF SEQUENCES: 1120

CORRESPONDENCE ADDRESS:

ADDRESSEE: MORRISON & FOERSTER

STREET: 755 PAGE MILL ROAD

CITY: Palo Alto

STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: FastSEQ for Windows Version 2.0b CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/221,017B FILING DATE: 23-DEC-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: PP1182
FILING DATE: 31-DEC-1997
FRIOR APPLICATION DATA:
APPLICATION NUMBER: PP1546
FILING DATE: 30-JAN-1998
FILING DATE: 09-APR-1998
FILING DATE: 09-APR-1998
FILING DATE: 10-DEC-1998
ATTORNEY/AGENT INFORMATION:
NAMB: MORICOY, Gladys H
REGISTRATION NUMBER: 32,4330
356524 CCAATGCCGAGTTGCCCGATACG 356546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: PORYPHYROMONAS GINGIVALIS
                                                                                      US-09-221-017B-301/c; Sequence 301, Application US/09221017B; Patent No. 6444799
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      201 GCTGCAGAGTAGCCCATTTCG 181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 27
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-813-5600
TELEFAX: 650-494-0792
                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  : 508 base pairs
nucleic acid
EDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: misc feature LOCATION: 1...508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEX: 706141
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               UNKNOWN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORIGINAL SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; LOCATION:
US-09-221-017B-301
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LENGTH:

RESULT 36

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Gaps

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US-09-252-991A-4736/c

| Sequence 4736, Application US/09252991A |
| Sequence 4736, Application US/09252991A |
| Sequence 4736, Application US/09252991A |
| Patent No. 6551795 |
| GENERAL INPORMATION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS |
| TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS |
| TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS |
| TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS |
| TITLE OF INVENTION NUMBER: US/09/252,991A |
| CURRENT FILING DATE: 1998-02-18 |
| PRIOR PILING DATE: 1998-02-18 |
| PRIOR PILING DATE: 1998-07-27 |
| PRIOR FILING DATE: 1998-07-27 |
| SEQ ID NO 4736 |
| LENGTH: 447 |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 4772. Application US/09252991A

Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: ABRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 10196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
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                                                                                                                                                                                                                                                                                                             Length 50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5; Indels
                                                                                                                                                                                                                                                                                                             Score 16; DB 3; I
Pred. No. 3.5e+02;
0; Mismatches 5;
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Pred. No. 4.4e+02
0; Mismatches
                                         60/296,764
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18 ccecrccaecrirecacerireca 41
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-4772
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA ORGANISM: Pseudomonas aeruginosa
        PRIOR FILING DATE: 2001-10-22
PRIOR APPLICATION NUMBER: US 60/
PRIOR FILING DATE: 2001-06-08
NUMBER OF SEQ ID NOS: 9090
SOFTWARE: Patentin version 3.1
SEQ ID NO 4079
LENGTH: 50
                                                                                                                                                                                                                                                                                                             64.0%;
ilarity 79.2%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 79.2%;
Matches 19; Conservative
                                                                                                                                                                                                   TYPE: DNA; ORGANISM: Homo sapiens
US-10-131-827-4079
                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 19; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-252-991A-4772
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APPLICANT: Wohlgemuth, Jay
APPLICANT: Wohlgemuth, Jay
APPLICANT: Wohlgemuth, Jay
APPLICANT: Woodward, Robert
APPLICANT: Ly, Ngoc
TITLE OF INVENTION: CRRONIC INFLAMMATORY DISEASES
FILE REFERENCE: 506612000120
CURRENT APPLICATION NUMBER: US/10/131,827
CURRENT FILING DATE: 2002-09-06
PRIOR APPLICATION NUMBER: US 10/006,290
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR PAPLICATION NUMBER: 60/241,755
PRIOR PAPLICATION NUMBER: 60/241,756
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR PILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
PRIOR PILING DATE: 2000-09-08
PRIOR PILING DATE: 2000-09-08
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Pred. No. 3.3e+02;
0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              64.8%; Score 16.2; DB 3;
85.7%; Pred. No. 6.9e+02;
iive 0; Mismatches 3;
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APPLICANT: No. 65118370zymes A/S
APPLICANT: TEULEUM: No. 6511837iko
; TITLE OF INVENTION: Lipolytic Enzymes
FILE REPERENCE: 10057.200-US
CURRENT APPLICATION NUMBER: US/09/891,735
CURRENT FILING DATE: 2001-06-06
; NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          64365 rcrecrecadadricerrerr 64345
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Patent No. 6905827
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US-09-891-735-5
; Sequence 5, Application US/09891735
...ant No. 6511837
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 79.2%;
Matches 19; Conservative
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Best Local Similarity 85.7
Matches 18; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-949-016-13873
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US-10-131-827-4079
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LENGTH: 32
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| Sequence 30653, Application US/09949016
| Patent No. 6812339
| GENERAL INFORMATION: Craig et al. | APPLICANT: VENTER, J. Craig et al. | TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED | TITLE OF INVENTION: POLYMORPHISMS IN ENOWN GENES ASSOCIATED | TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF | FILE REFERENCE: CL001307 | CURRENT APPLICATION NUMBER: US/09/949,016
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 16462, Application US/09270767

Patent No. 6703491

GENERAL INFORMATION:

APPLICANT: Homburion:

TITLE OF INVENTION:

FILE REFERENCE: File Reference: 7326-094

CURRENT APPLICANTE: NUMBER: US/09/270,767

CURRENT APPLICANTE: 1999-03-17

NUMBER OF SEQ ID NOS: 62517

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 16462

LENGTH: 465
                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
TITLE OF INVENTION: Nucleic 3326-094
CURRENT APPLICATION NUBER: 13/99/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62217
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1180
LENGTH: 465
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       Length 447;
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Query Match 64.0%; Score 16; DB 3; Length 447
Best Local Similarity 79.2%; Pred. No. 4.5e+02;
Matches 19; Conservative 0; Mismatches 5; Indels
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Pred. No. 4.5e-
0; Mismatches
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Pred. No.
                                                                                                                                             376 recerrecada acrececeda as a
                                                                                                 1 TCCGCTGCAGAGTTGCCCGTTACG 24
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                                                                                                                                                                                                                                                        Sequence 1180, Application US/09270767 Patent No. 6703491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-1180
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US-09-270-767-16462
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ilarity 79.2%;
Conservative
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Best Local Similarity 79.2%;
Matches 19; Conservative
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Matches 19; Conserv
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Sequence 73150

Sequence 73150

Sequence 73150

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;

FILE REPREMENCE: CLOOM, 1307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-03

SPRIOR FILING DATE: 2010-10-03

SPRIOR FILING DATE: 2010-
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Bequence 133356, Application US/09949016
Bequence 133356, Application US/09949016
Bequence 133356, Application US/09949016
Better No. 6812339
GENERAL INFORMATION: Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF FILE REFERENCE: CLO01307
CURRENT APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/241,756
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
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                               PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: PASLESE FOR Windows Version 4.0
SEQ ID NO 30653
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2000-04-14
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Best Local Similarity 79.2%;
Matches 19; Conservative
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; ORGANISM: Human
US-09-949-016-30653
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Length 942;
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Sequence 154, Application US/09640211A
Patent No. 6833446

GENERAL INFORMATION:
APPLICANT: Shenk, Michael A.
APPLICANT: Shenk, Michael A.
APPLICANT: Glenn, Matthew
TITLE OF INVENTION: Compositions and Methods for the
TITLE OF INVENTION: Composition of Gene Transcription
FILE REFERENCE: 11000.1021C1U
CURRENT PAPLICATION NUMBER: US/09/640,211A
CURRENT FILING DATE: 2000-08-16
NUMBER OF SEQ ID NOS: 2368
SEQ ID NO 154
LENGTH: 1144
    Indels
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TITLE OF INVENTION: No. 6783969el Nucleic Acids and
TITLE OP INVENTION: Polypeptides
FILE REFERENCE: 803
CURRENT APPLICATION NUMBER: US/09/799,451
CURRENT FILING DATE: 2001-03-05
NUMBER OF SEQ ID NOS: 948
SEQ TWARE: pt_Ft_genes Version 2.0
LENGTH: 942
      2,
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Pred. No. 4.9e+02;
O; Mismatches 5;
  0; Mismatches
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                                             2 CCGCTGCAGAGTTGCCCGTTACGA 25
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                                                                                    26 ccerrecadacriererarricas 3
                                                                                                                                                                                        Sequence 300, Application US/09799451
Patent No. 6783969
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Ma, Yunqing
Yamazaki, Victoria
Chen, Rui-hong
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79.2%;
                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Tang, Y. Tom
APPLICANT: Zhou, Ping
APPLICANT: Goodrich, Ryle
APPLICANT: Asundi, Vinod
APPLICANT: Ren, Feiyan
                                                                                                                                                                                                                                                                                                                                                                               Xue, Aidong J.
Zhao, Qing A.
Wang, Jian-Rui
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, Yonghong
    19; Conservative
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Ghosh, Reena
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        , NAME/KEY: CDS
, LOCATION: (52)..(807)
US-09-799-451-300
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Best Local Similarity
Matches 19; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wang,
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US-09-799-451-300/c
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APPLICANT:
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APPLICANT: Rebischung, Corinne
TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPII
TITLE OF INVENTION: AND USES THEREOF
NUMBER OF SEQUENCES: 1152
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 6239264artis Corporation
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: No. 6239264th Carolina
COUNTRY: USA
                                                                                                                                                                                                                Length 601;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      64.0%; Score 16; DB 3; Length 718; 79.2%; Pred. No. 4.8e+02;
                                                                                                                                                                                                                                                     5; Indels
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ZIP: 27709

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/998,416
FILING DATE: 24-DEC-1997
FILING DATE: 24-DEC-1997
PRIOR APPLICATION UNDER: CH 0016/97
FILING DATE: 1-DEC-1996
ATPOREX/AGENT INFORMATION:
NAME: Med-198 J. Timochy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: 38,241
REFERENCE/DOCKET NUMBER: 38,241
REFERENCE/DOCKET NUMBER: 38,241
REFERENCE/DOCKET NUMBER: 39,241
REFERENCE/DOCKET NUMBER: 39,241
REFERENCE/DOCKET NUMBER: 39,241
REGISTRATION NUMBER: 39,241-8697
INFORMATION FOR SEQ ID NO: 961:
SEQUENCE CHARACTERISTICS:
LENGTH: 718 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
STRANDEDENESS: single
TOPOLOGY: linear
MANIET TYPE: DNA (Genomic)
                                                                                                                                                                                                          64.0%; Score 16; DB 3; I ilarity 79.2%; Pred. No. 4.7e+02; Conservative 0; Mismatches 5;
                 PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 133356
LENGTH: 601
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US-08-998-416-961/c
US-08-998-416-961, Application US/08998416
Patent No. 6239264
GENERAL INFORMATION:
APPLICANT: Philippsen, Peter
APPLICANT: Philippsen, Peter
POHJMANN: Rainer
PRIOR APPLICATION NUMBER: 60/231,498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Philippsen, Peter
Pohlmann, Rainer
Steiner, Sabine
Mohr, Christine
Wendland, Jurgen
Knechtle, Philipp
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Best Local Similarity
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Best Local Similarity
Matches 19; Conserv
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ORIGINAL SOURCE:
                                                                                                                                                                   US-09-949-016-133356
                                                                                                                              TYPE: DNA
ORGANISM: Human
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APPLICANT:
APPLICANT:
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APPLICANT:
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                                             APPLICANT: Rey, Michael W.
APPLICANT: Golightly, Blizabet J.
APPLICANT: Golightly, Blizabet J.
TILLE OF INVENTION: Polypeptides Having Lipsee Activity And
TITLE OF INVENTION: Nucleic Acids Encoding Same
FILE REFERENCE: 10052.000-US
CURRENT APPLICATION NUMBER: US/09/703,416
CURRENT FILING DATE: 2000-10-31
NUMBER OF SEQ ID NOS: 10
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                              Length 2940;
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APPLICANT: Rey, Michael W.
APPLICANT: Golightly, Elizabet J.
TITLE OF INVENTION: Polypeptides Having Lipase Activity And
TITLE OF INVENTION: Nucleic Acids Encoding Same
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Parent No. 6558715
GENERAL INFORMATION:
APPLICANT: Rey, Michael W.
APPLICANT: Spendler, Tina
TILLE OF INVENTION: Methods For Using Lipases In Baking
TILLE REFERENCE: 10074.000-US
CURRENT APPLICATION NUMBER: US/09/703,414
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3. 5.7e+02;
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Pred. No. 5.7e+02
0; Mismatches
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FastSEQ for Windows Version 4.0
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CURRENT APPLICATION NUMBER: US/10/171,229
CURRENT FILING DATE: 2002-06-12
PRIOR APPLICATION NUMBER: US/09/703,416
PRIOR FILING DATE: 2000-10-31
NUMBER OF SEQ ID NOS: 10
SOFTWARE: FastSEQ for Windows Version 4.0
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Patent No. 6558715
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Patent No. 6686189
                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 79.2%;
Matches 19; Conservative (
                                                                                                                                                                                                                                                                                        ; TYPE: DNA; ORGANISM: Fusarium venenatum US-09-703-416-1
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SOFTWARE: FastSEQ for
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LENGTH: 2940
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LENGTH: 2940
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LENGTH: 2940
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Pred. No. 5.2e+02;
0; Mismatches 5; Indels
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US-09-489-039A-2930/c
; Sequence 2930, Application US/09489039A
; Sequent No. 6610836
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
; TITLE OF INVENTION: PREUMONIAE FOR DIAGNOSTICS AND THERAPE
                                                                                                                                5; Indels
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5.1e+02;
                                                                                                                                   0; Mismatches
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CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 2930
                                                                                        Score 16;
Pred. No. 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/891,735 CURRENT FILING DATE: 2001-06-06 NUMBER OF SEQ ID NOS: 7 SOFTWARE: Patentin version 3.1
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Pred. No.
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Patent No. 6511837
GENERAL INPORMATION:
APPLICANT: No. 651183702ymes A/S
APPLICANT: TSUTEUMI, No. 65118371ko
TITLE OF INVENTION: Lipolytic Bizymes
FILE REFERENCE: 10057.200-US
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US-09-703-416-1
; Sequence 1, Application US/09703416
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                                                                                   Query Match
Best Local Similarity 79.2%;
Matches 19; Conservative
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Best Local Similarity 79.2%;
Matches 19; Conservative
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Best Local Similarity 79.2%;
Matches 19; Conservative
                    ; ORGANISM: Eucalyptus grandis
US-09-640-211A-154
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US-09-891-735-1
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TYPE: DNA
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Sequence 1239, Application US/09949016
; Sequence 1239, Application US/09949016
; Patent No. 681239
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
; FILE REPERBENCE: CLOOD-01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR PILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR APPLICATION NUMBER: 60/237,468
; RIGH APPLICATION NUMBER: 60/237,468
; RIGH APPLICATION NUMBER: 60/231,498
; NUMBER OF SEQ ID NOS: 207012
; SOUTHARE: FREEE FREEESEQ for Windows Version 4.0
; SQU ID NO 12389
; LENGTH: 36274
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR PILING DATE: 2000-10-20
PRIOR PILING DATE: 2000-01-0-30
PRIOR PILING DATE: 2000-01-0-30
PRIOR PILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FRANKED FRANKED
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US-09-949-016-17230/c
is Sequence 17230, Application US/09949016
is Patent No. 6812339
igeneral information:
is Application Craig et al.
is TITLE OF INVENTION:
is TITLE OF INVENTION WINGER:
is CURRENT APPLICATION NUMBER:
is CORRENT FILING DATE:
is 2000-04-14
is PRIOR APPLICATION NUMBER: 60/241,755
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Best Local Similarity 79.2%; Pred. No. 7.6e+02;
Matches 19; Conservative 0; Mismatches 5; Indels
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Best Local Similarity
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ORGANISM: Human
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US-09-949-016-12389
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Pred. No. 5.7e+02;
0; Mismatches 5; Indels
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US-09-949-016-13876
; Sequence 13876, Application US/09949016
; Patent No. 681239;
; Patent No. 681239;
; APPLICANT: VENTER, J. Craig et al.
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
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US-10-429-398-1

| Sequence 1, Application US/10429398
| Patent No. 6730346
| GENERAL INFORMATION:
| APPLICANT: Rey, Michael W. APPLICANT: Spendler, Tina |
| TITLE OF INVENTION: Methods For Using Lipases In Baking |
| FILE REFERENCE: 10074.000-US |
| CURRENT APPLICATION NUMBER: US/10/429,398 |
| CURRENT FILING DATE: 2003-05-05 |
| PRIOR FILING DATE: 2000-10-31 |
| NUMBER OF SEQ ID NOS: 10 |
| SEQ ID NO 1 |
| LEAST FILING LOS: 10 |
| SEQ ID NO 1 |
| LEAST FILING LOS: 10 |
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Best Local Similarity 79.2%; Pred. No. 6.4e+02;
Matches 19; Conservative 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                       5; Indels
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                                                                                                                                                                                                            Score 16; DB 3; Pred. No. 5.7e+
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/312,641
FILING DATE: 17-FEB-1989
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                                                                                                                                                                                                                                                                                                                                                                                                 2 CCGCTGCAGAGTTGCCCGTTACGA 25
                                                                                                                                                                                                            Query Match
Best Local Similarity 79.2%;
Matches 19; Conservative C
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Best Local Similarity 79.2%;
Matches 19; Conservative (
                       ; TYPE: DNA
; ORGANISM: Fusarium venenatum
US-10-171-229-1
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5175383-1
;Patent No. 5175383
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Gaps

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; TYPE: DNA
; ORGANISM: Rhizobium
US-09-214-808-1
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                                                                                                                                                                                                                  ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 536165
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                                                                                                                                                                                                TYPE: DNA
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SEQ ID NO 1
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i Sequence 15494, Application US/09949016

i Sequence 15494, Application US/09949016

j Patent No. 6812339

i GENERAL INFORMATION:

i APPLICANT: VENTER, J. Craig et al.

i TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

i TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

i TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

i TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

i CURRENT APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20

i PRIOR PILING DATE: 2000-10-03

i PRIOR PILING DATE: 2000-00-08

i WUMBER OF SEQ ID NOS: 207012

i SOFTWARE: FastEEQ for Windows Version 4.0

i LENGTH: 183770
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APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
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                                                                                                                                                                                                                                                                                                                Length 90776;
                                                                                                                                                                                                                                                                                                                                                          5; Indels
                                                                                                                                                                                                                                                                                                           Score 16; DB 3; I
Pred. No. 8.4e+02;
0; Mismatches 5,
                   PRIOR APPLICATION NUMBER: 60/237,768
PRIOR PILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-09-08
PRIOR PILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 90776
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CURRENT FILING DATE: 2000-04-14
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PRIOR FILING DATE: 2000-10-20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; NAME/KEY: misc_feature
; LOCATION: (1)...(183770);
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-15494
                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 79.2%;
Matches 19; Conservative
PRIOR FILING DATE: 2000-10-20
                                                                                                                                                                                                             ; TYPE: DNA
; ORGANISM: Human
US-09-949-016-17230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Human
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US-09-949-016-13418
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Sequence 1, Application US/09214808A

Sequence 1, Application US/09214808A

Batent No. 6475793

GENERAL INFORMATION:

APPLICANT: Resenthal, Andre

APPLICANT: Freiberg, Christoph

APPLICANT: Perret, Xavier Philippe

APPLICANT: Percet, Xavier Philippe

APPLICANT: Parcet, Xavier Philippe

TITLE OF INVENTION: Genomic Sequence of Rhizobium SP. NGR 234 Symbiotic

Patent No. 6475793

TITLE OF INVENTION: Plasmid

TITLE REFRENCE: CARPO068

CURRENT FILING DATE: 1999-06-22

PRIOR PRILICATION NUMBER: US/09/214,808A

PRIOR FILING DATE: 1997-07-10

NUMBER OF SEQ ID NOS: 1
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Patent No. 6783961

GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Duclert, A.
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
Patent No. 6783961
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Best Local Similarity 79.2%; Pred. No. 9.1e+02;
Matches 19; Conservative 0; Mismatches 5
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CURRENT APPLICATION NUMBER: US/09/513,999C
CURRENT FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/122,487
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: PSESEQ for Windows Version 4.0
LENGTH: 236474
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                                                                                                                                                                                                                                                        | FEATURE: | NAME/KEY: misc feature | LOCATION: (1)...(236474) | OTHER INFORMATION: n = A,T,C or G US-09-949-016-13418
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Best Local Similarity 79.2
Matches 19; Conservative
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GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
CURRENT APPLICATION NUMBER: USO9/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FREESEQ for Windows Version 4.0
ILENGTH: 7620
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Pred. No. 7.9e+02;
0; Mismatches 2; Indels 0;
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  Indels
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US-09-196-196G-74495

Sequence 74495. Application US/09396196G

Patent No. 682174

GENERAL INFORMATION:
APPLICANT: Michael Mittmann
APPLICANT: David Lockhart
APPLICANTION WELDOR of Genetic Analysis
CURRENT APPLICATION NUMBER: US/09/396,196G
CURRENT FILING DATE: 1998-09-15

PRIOR FILING DATE: 1998-09-17

NUMBER OF SEQ ID NOS: 127806

SEQ ID NO 74495

LEANTH: 25

LEANTH: 25
0; Mismatches
                                                                                                                                                                                                    Sequence 14973, Application US/09949016 Patent No. 6812339
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                                              4 GCTGCAGAGTTGCCCGTTA 22
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Best Local Similarity 89.5
Matches 17; Conservative
  17; Conservative
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US-09-396-196G-74495
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  Matches
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Sequence 10, Application US/09953318

Batent No. 6710174

GENERAL INFORMATION:
APPLICANT: C. Frank Bennett
APPLICANT: Andrew T. Watt
TITLE OF INVENTION: ANTISENSE MODULATION OF VASCULAR ENDOTHELIAL GROWTH FACTOR RECEPTITIES OF INVENTION: BEXPRESSION
FILE REPERENCE: RTS-0232
CURRENT APPLICATION NUMBER: US/09/953,318
NUMBER OF SEQ ID NOS: 154
SEQ ID NO 10
ILENGTH: 6055
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US-09-953-318-100/c
Sequence 100, Application US/09953318
Patent No. 6710174
GENERAL INFORMATION:
APPLICANT: C. Frank Bennett
APPLICANT: Andrew T. Watt
TITLE OF INVENTION: EXPRESSION
TITLE OF INVENTION: EXPRESSION
TITLE OF INVENTION: EXPRESSION
TITLE OF INVENTION: EXPRESSION
CURRENT APPLICATION NUMBER: US/09/953,318
CURRENT PILING DATE: 2001-09-13
NUMBER OF SEQ ID NOS: 154
SEQ ID NO 100
LENGTH: 3394
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Pred. No. 7.2e+02;
0; Mismatches 2; Indels 0;
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                                                                                                                                                                                 63.2%; Score 15.8; DB 3; Length 290; ilarity 89.5%; Pred. No. 5.3e+02; Conservative 0; Mismatches
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89.5%;
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89.5%;
PRIOR FILING DATE: 1999-02-26
                  NUMBER OF SEQ ID NOS: 36681
SOFTWARE: Patent.pm
SEQ ID NO 30616
LENGTH: 290
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Matches 17; Conservative
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; LOCATION: (252)...(2318)
US-09-953-318-100
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; LOCATION: (27)...(4028)
US-09-953-318-10
                                                                                                                                ; ORGANISM: Homo sapiens
US-09-513-999C-30616
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Best Local Similarity
                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 17; Conserv
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US-09-953-318-10/c
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                                                                                                              TYPE: DNA
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GENERAL INFORMATION:
APPLICANT: GARY BRETON
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABIL.
TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.1002-001
CURRENT APPLICATION NUMBER: 0.909/543,681A
CURRENT FILING DATE: 2000-04-05
PRIOR APPLICATION NUMBER: US 60/128,706
NUMBER OF SEQ ID NOS: 8344
SEQ ID NO 1424
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 1059;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 5, Application US/08106981
Patent No. 5731419
GENERAL INFORMATION:
APPLICANT: STRUAN, Pathey
APPLICANT: LALIBERT , Jean-Fran ois
APPLICANT: LALIBERT , Jean-Fran ois
TITLE OF INVENTION: TOLERANCE PROTEINS IN GRAMINEAE
NUMBER OF SEQUENCES: 11
CORRESPONDENCES: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
PLICATION WINDER: US/08/106,981
FILING DATE: 16-AUG-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 15.6; DB 3;
Pred. No. 7.7e+02;
0; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/106,981
FILING DATE: 16-740G-1993
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: WILSON, MARY J.
REGISTRATION NUMBER: 32,955
REPERENCE/DOCKET NUMBER: 163-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; MOLECULE TYPE: CDNA to mRNA
; ORIGINAL SOURCE: Triticum Aestivum L.
US-08-106-981-5
124, Application US/09543681A
6605709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: NIXON & VANDERHYE P.C. STREET: 1100 NORTH GLEBE ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             124 rccccrccrcarrracccccri 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 TCCGCTGCAGAGTTGCCCGTTA 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 62.4%;
Best Local Similarity 81.8%;
Matches 18; Conservative
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ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                           ; TYPE: DNA
; ORGANISM: Proteus mirabilis
US-09-543-681A-1424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (703) 816-4100
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                             Sequence 305, Application US/09976594

Patent No. 6673549

GENERAL INFORMATION:
APPLICANT: Furness, Michael
APPLICANT: Buchbinder, Jenny
TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
FILE REFERENCE: PA-0041 US
CURRENT APPLICATION NUMBER: US/09/976,594

FRIOR APPLICATION NUMBER: 60/240,409

PRIOR FILING DATE: 2000-10-12

NUMBER OF SEQ ID NOS: 1143
SOFTWARE: PERL PROGram
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81.8%; Pred. No. 7e+02;
iive 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               62.4%; Score 15.6; DB 3; Length 685; 81.8%; Pred. No. 7.3e+02; ive 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:

APPLICANT: Randy M. Berka
APPLICANT: Michael W. Re.
APPLICANT: Jeffrey R. Shuster
APPLICANT: Sakari Kauppinen
APPLICANT: 15 Groth Clausen
APPLICANT: B Groth Clausen
APPLICANT: B TOTH Clausen
APPLICANT: PETER Bjarke Olsen
TITLE OF INVENTION: Expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No. 6673549 1329120.10
NAME/KEY: unsure
LOCATION: 299
OTHER INFORMATION: a, t, c, g, or other
US-09-976-594-305
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CURRENT PEDLICATION NUMBER: US/99/533,559
CURRENT FILING DATE: 2000-03-22
BARLIER APPLICATION NUMBER: 09/273,623
BARLIER FILING DATE: 1999-03-22
NUMBER OF SEQ ID NOS: 7860
SOFTWARE: PSELSEQ FOR Windows Version 4.0
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Patent No. 6902887
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TYPE: DNA; ORGANISM: Aspergillus oryzae
US-09-533-559-4705
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Best Local Similarity 81.8
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 81.8
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Homo sapiens
                                 US-09-976-594-305/c
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US-09-543-681A-1424
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LENGTH: 685
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LENGTH: 452
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                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Chandy, Kanianthara G.
APPLICANT: Chandy, Michael D.
APPLICANT: Chalan, Michael D.
APPLICANT: Grissmer, Stephan
APPLICANT: Grissmer, Stephan
APPLICANT: Godin, Alan L.
APPLICANT: Gutman, George A.
TITLE OF INVENTION: Assay, Methods and Products Based On n
TITLE OF INVENTION: K+ Channel Expression
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Attn: Hohbach, Test, Albritton & Herbert,
ADDRESSEE: Attn: H. H. Dreger
STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/527,152
FILING DATE: UNROWN
CLASSIFICATION NATA:
APPLICATION NUMBER: US 08/170,418
FILING DATE: 20-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/558,568
FILING DATE: 27-JUL-1990
ATTORNEY/AGENT INFORMATION:
NAME: DAEGET: Walter H.
REGISTRATION NUMBER: 24,100
   Best Local Similarity 81.8%; Pred. No. 8.2e+02; Matches 18; Conservative 0; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: A-54444-2/WHD TELECOMMUNICATION INFORMATION:
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                                                                                                                                                             180 GCTGCAGAGTTTTCCATTATGA 159
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                                                                                                                                                                                                                                                                                                                     Sequence 1, Application US/08527152
Patent No. 5827655
GENERAL INFORMATION:
                                                                                                  4 GCTGCAGAGTTGCCCGTTACGA
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LENGTH: 1994 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: California
COUNTRY: United States
ZIP: 94111-4187
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INFORMATION FOR SEQ ID NO:
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150..1736
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear FEATURE:
                                                                                                                                                                                                                                                                                              JS-08-527-152-1/c
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; LOCATION:
US-08-527-152-1
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Fatent No. 6576243
GENERAL INFORMATION:
APPLICANT: Merial Ltd.
APPLICANT: Baudu, Annabelle
APPLICANT: Baudu, Philippe
APPLICANT: Bouchardon, Annabelle
APPLICANT: Bouchardon, Philippe
APPLICANT: Riviere, Michael
TITLE OF INVENTION: Respiratory Pathologies
TITLE OF INVENTION NUMBER: US/09/784,984B
CURRENT APPLICATION NUMBER: PS 96/09338
PRIOR PLING DATE: 1996-07-19
PRIOR APPLICATION NUMBER: PCT/FR97/01313
PRIOR PLING DATE: 1907-07-15
PRIOR FILING DATE: 2001-03-27
NUMBER OF SEQ ID NOS: 54
SOFTWARE: PatentIn version 3.1
SEQ ID NO 11
TAVE: NUMBER OF PATENTION NUMBER: PATENTION 
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                                       Gaps
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APPLICANT: AUDONNET et al.
TITLE OF INVENTION:
POLYNCLEOTIDE VACCINE FORMULA AGAINST PORCINE
TITLE OF INVENTION: POLYNUCLEOTIDE VACCINE FORMULA AGAINST PORCINE
TITLE OF INVENTION: REPRODUCTIVE AND RESPIRATORY PATHOLOGIES
FILE REFERENCE: 454313-2230
CURRENT APPLICATION NUMBER: US/09/232,468A
CURRENT PILLING DATE: 1999-01-05
NUMBER OF SEQ ID NOS: 54
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 13
LENGTH: 1701
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81.8%; Pred. No. 8.2e+02;
iive 0; Mismatches 4; Indels 0
                                    4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA ORGANISM: Porcine Flu Virus (SIV, H1N1 "SW" Strain)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA ORGANISM: Porcine Flu Virus (SIV, H1N1 "SW" Strain
      81.8%; Pred. No. 7.8e+02;
                                    0; Mismatches
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                                                                                               3 CGCTGCAGAGTTGCCCGTTACG 24
Best Local Similarity 81.8
Matches 18; Conservative
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Matches 18; Conservative
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LOCATION: (1)..(1698)
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US-09-784-984B-11
                                                                                                                                                                                                                                                                                              US-09-232-468A-13/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -09-784-984B-11/c
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LOCATION: (1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-232-468A-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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Perna, Nicole T.
Plunkett, Guy
Welch, Rod
TITLE OF INVENTION: No. 6855814el Sequences of E. coli O157
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 62.4%; Score 15.6; DB 3; Length 25165; llarity 81.8%; Pred. No. 1.1e+03; Conservative 0; Mismatches 4; Indels 0;
                                                                                                                                    Length 25165;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 53701-2113
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch. 1.44Mb storage
                                                                                                                                                                                4; Indels
                                                                                                                                    Score 15.6; DB 3;
Pred. No. 1.1e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 960296.95017
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARR: Word Perfect 8.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/114,170
FILING DATE: 01-Apr-2002
CLASSIPICATION NUMBER: 09/453,702
FILING DATE: 03-DEC-1999
APPLICATION NUMBER: 60/110,955
FILING DATE: 04-DEC-1998
                                                                                                               62.4%; Scor.
81.8%; Pred. No. ...
0; Mismatches
                  TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 39:
US-09-453-7028-39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Quarles & Brady
STREET: 1 South Pinckney Street
CITY: Madison
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

SEQUENCE DESCRIPTION: SEQ ID NO: 39:
US-10-114-170-39
                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Blattner, Frederick R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17400 rececrecaserrrececerra 17379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Seay, Nicholas J. REGISTRATION NUMBER: 27386
                                                                                                                                                                                                                       1 TCCGCTGCAGAGTTGCCCGTTA 22
                                                                                                                                                                                                                                                                                                                                                                              Sequence 39, Application US/10114170 Patent No. 6855814 GENERAL INFORMATION:
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STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: double
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                                                                                                                      Ouery Match
Best Local Similarity 81.84
Matches 18; Conservative
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INFORMATION FOR SEO ID NO:
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Best Local Similarity
Matches 18; Conserv
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Perna, Nicole T.
Plunkett, Guy
Welch, Rod
TITLE OF INVENTION: No. 6365723el Sequences of E. coli O157
CORRESPONDENCE 265
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62.4%; Score 15.6; DB 3; Length 5276; 81.8%; Pred. No. 9.4e+02; Live 0; Mismatches 4; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 53701-2113
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch. 1.44Mb storage
                                                                                            GENERAL INFORMATION:
APPLICANT: Plowman, Gregory
APPLICANT: Plowman, Gregory
APPLICANT: Plowman, Gregory
TITLE OF INVENTION: HUMAN ORTHOLOGUES OF WART
FILE REFERENCE: 239/251;
CURRENT APPLICATION NUMBER: US/09/233,857;
CURRENT PILING DATE: 1999-01-20
EARLIER APPLICATION NUMBER: USSN 60/072,023
EARLIER PILING DATE: 1998-01-21
NUMBER: OF SEQ ID NOS: 18
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Seay, Nicholas J.
REGISTRATION NUMBER: 27386
REFERENCE/DOCKET NUMBER: 960296.95017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/09/453,702B
FILING DATE: 03-Dec-1999
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Quarles & Brady
STREET: 1 South Pinckney Street
CITY: Madison
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Word Perfect 8.0 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 60/110,955
FILING DATE: 04-DEC-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Blattner, Frederick R. Burland, Valerie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        663 cagcrecagaegrececarre 642
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 39, Application US/09453702B Patent No. 6365723 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
                                                     Sequence 2, Application US/09233857
Patent No. 6495353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 62.4
Best Local Similarity 81.8
Matches 18; Conservative
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US-09-233-857-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -09-453-702B-39/c
                                                                                                                                                                                                                                                                                                                                                SEO ID NO 2
LENGTH: 5276
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                                                             APPLICANT: Tavigian, Sean V.
APPLICANT: Tavigian, Sean V.
APPLICANT: Tavigian, Sean V.
APPLICANT: Tavigues
APPLICANT: Romans. Johanna M.
APPLICANT: Rommens, Johanna M.
APPLICANT: Myriad Genetics, Inc.
TITLE OF INVENTION: Chromosome 17p-Linked Prostate Cancer Susceptibility
TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes
TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes
FILE REFERENCE: 2318-258
CURRENT APPLICATION NUMBER: US 60/107,468
PRIOR APPLICATION NUMBER: US 60/107,468
PRIOR APPLICATION NUMBER: 09/4134,382
PRIOR FILING DATE: 1998-11-05
NUMBER OF SEQ ID NOS: 240
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 28
LENGTH: 26664
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                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Tartigian, Sean V.
APPLICANT: Tartigian, Sean V.
APPLICANT: Teng, David H.F.
APPLICANT: Simard, Jacques
APPLICANT: Nommens, Johanna M.
APPLICANT: Myriad Genetics, Inc.
TITLE OF INVENTION: Chromosome 17q-Linked Prostate Cancer Susceptibility
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          62.4%; Score 15.6; DB 3; Length 26664; 81.8%; Pred. No. 1.1e+03; ive 0; Mismatches 4; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24888 GCTACGGAGGTGCCCGTTAAGA 24909
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; Sequence 28, Application US/09434382
; Patent No. 6844189
; GENERAL INFORMATION:
              ; Sequence 28, Application US/09564805; Patent No. 6333403; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
US-09-564-805-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-564-805-28
                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
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| Sequence 15607, Application US/09949016
| Sequence 15607, Application US/09949016
| Patent No. 6812339
| GENERAL INFORMATION:
| APPLICANT: VEYTER, USTER, 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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NAME/KEY: misc_feature
LOCATION: (23045)..(26452)
OTHER INFORMATION: exon 19: 23045-23154; exon 20: 23795-23895; exon
OTHER INFORMATION: 21: 23973-24093; exon 22: 24354-24432; exon 23:
OTHER INFORMATION: 25026-25170; exon 24: 25812-26036; polyadenylation
OTHER INFORMATION: signal: 26447-26452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
NAME/KEY: variation
LOCATION: (826)..(23879)
OTHER INFORMATION: s at positions 826 and 23180 is G or C; y at
OTHER INFORMATION: positions 1914, 5568, 7165, 16431, 1857 and 20486
OTHER INFORMATION: is C or T; n at position 13128 is t or tgat; r at
OTHER INFORMATION: positions 22211 and 23879 is A or G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KET: misc feature
LOCATION: (910)...(13104)

OTHER INFORMATION: exon 1: 910-1154; exon 2: 1736-1786; exon 3:
OTHER INFORMATION: 1925-1995; exon 4: 3025-3089; exon 5: 4361-4418;
OTHER INFORMATION: exon 6: 5582-5650; exon 7: 7075-7194; exon 8:
OTHER INFORMATION: 8186-8244; exon 9: 12878-12936; exon 10:
OTHER INFORMATION: 13032-13104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PEATURE:
NAME/KEY: misc_feature
NAME/KEY: misc_feature

COCATION: (13756)..(22917)

OTHER INFORMATION: exon 11: 13756-13868; exon 12: 15283-15378; exon OTHER INFORMATION: 13: 16278-16416; exon 14: 16498-16583; exon 15: OTHER INFORMATION: 18589-18701; exon 16: 20349-20445; exon 17: OTHER INFORMATION: 22172-22310; exon 18: 22879-22917
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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81.8%; Pred. No. 1.1e+03;
tive 0; Mismatches 4; Indels 0;
FILE REFERENCE: HPC2 Gene
CURRENT PEDLICATION NUMBER: US/09/434,382
CURRENT FILING DATE: 1999-11-05
EARLIER APPLICATION NUMBER: US 60/107,468
BARLIER FILING DATE: 1999-11-06
NUMBER OF SEQ ID NOS: 213
SOFTWARE: PATENTIN Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24888 GCTACGGAGGTGCCCGTTAAGA 24909
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Best Local Similarity. 81.8'
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 26664
                                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO 28
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APPLICANT: Lalgudi, Raghunath V.
APPLICANT: Ito, Laura Y.
APPLICANT: Sherman, Bradley K.
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR
FILE REPERENCE: PL-0017 US
CURRENT APPLICATION NUMBER: US/09/313,294A
CURRENT TILING DATE: 1999-05-14
NUMBER OF SEQ ID NOS: 7600
SOFTWARE: PERL PROGRAM
SEQ ID NO 5359
SEQ ID NO 5359
SEQ ID NO 5359
SEQ ID NO 5359
                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:

APPLICANT: Lalgudi, Raghunath V.

APPLICANT: Lalgudi, Raghunath V.

APPLICANT: Ito, Laura Y.

TITLE OF INVENTION: Bradley K.

TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR FILE REFERENCE: PL-0017 US

CURRENT APPLICATION NUMBER: US/09/313,294A

CURRENT FILING DATE: 1999-05-14

NUMBER OF SEQ ID NOS: 7600

SOFTWARE: PERL PLOGRAM
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           Length 267;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61.6%; Score 15.4; DB 3; Length 268; llarity 76.0%; Pred. No. 8.1e+02; Conservative 0; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61.6%; Score 15.4; DB 3; Length 282; 76.0%; Pred. No. 8.2e+02; tive 0; Mismatches 6; Indels
                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No. 6476212 700552775H1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No. 6476212 700350024H1
         Score 15.4; DB 3;
Pred. No. 8.1e+02;
0; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: unsure

LOCATION: 26, 132, 191, 211, 239, 245, 266-267

CTHER INFORMATION: a, t, c, g, or other

US-09-313-294A-2207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; LOCATION: 44, 150, 262, 267
; OTHER INFORMATION: a, t, c, g, or other
US-09-313-294A-5359
                                                                                                                                                 180 TCTCCTGCAAGTGGCCTGTGACGA 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               164 rcecrecaaacriercecracra 140
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                                                                                                                                                                                                                                  US-09-313-294A-2507/c
; Sequence 2507, Application US/09313294A
; Patent No. 6476212
         ch 61.6%;
1 Similarity 76.0%;
19; Conservative
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Best Local Similarity 76.0
Matches 19; Conservative
       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 19; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Zea mays FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: unsure
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LENGTH: 268
                                 Best Loc
Matches
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Sequence 12.00, Application 09/03949010

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REPERENCE: CLOO1307

CURRENT APPLICATION NUMBER: 06/241,755

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR PLING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR PLING DATE: 2000-10-03

PRIOR PLING DATE: 2000-10-03

PRIOR PLING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SEQ ID NO 12966

LENGTH: 222452
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GENERAL INPORMATION:
GENERAL INPORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Duclert, A.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
FILE REFERENCE: 59.US2.REG
CURRENT APPLICATION NUMBER: US/09/513,999C
CURRENT APPLICATION NUMBER: US 60/122,487
PRIOR FILING DATE: 1999-02-26
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                                                                                             Query Match 62.4%; Score 15.6; DB 3; Length 29558; Best Local Similarity 81.8%; Pred. No. 1.1e+03; Matches 18; Conservative 0; Mismatches 4; Indels 0;
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Pred. No. 1.4e+03;
0; Mismatches 4;
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                                                                                                                                                                                       4 GCTGCAGAGTTGCCCGTTACGA 25
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Best Local Similarity 81.8
Matches 18; Conservative
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SOFTWARE: Patent.pm
SEQ ID NO 3441
LENGTH: 267
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US-09-513-999C-3441
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-15607
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ORGANISM: Human
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APPLICANT: Remain, Jane
APPLICANT: Mannion, Jane
APPLICANT: Fan, Lidun
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.4786212
CURRENT APPLICATION NUMBER: US/09/671,325
CURRENT FILING DATE: 2000-09-26
NUMBER OF SEQ ID NOS: 1825
SOFTWARE: FREISEG FOR WINGOWS VEFSION 3.0
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
TITLE OF INVENTION: COMPOSITIONS OF LUNG CANCER
FILE REPERENCE: 210121 478C9
CURRENT APPLICATION NUMBER: US/09/614,124B
CURRENT FILING DATE: 2001-07-11
NUMBER: PSEGID NOS: 1668
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 1202
LENGTH: 325
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1 TCCGCTGCAGAGTTGCCCGTTACGA 25
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; Sequence 1202, Application US/09614124B
; Patent No. 6630574
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Bangur, Chaitanya S.
Lodes, Michael A.
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76.0%;
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APPLICANT: Fanger, Gary
APPLICANT: Vedvick, Tom
APPLICANT: Carter, Darrick
APPLICANT: Retter, Marc
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Best Local Similarity 76.0
Matches 19; Conservative
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APPLICANT: Wang, Tongtong
APPLICANT: Bangur, Chaite
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CORGANISM: Homo sapien
US-09-614-124B-1202
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Best Local Similarity
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APPLICANT: Retter, Marc
APPLICANT: Retter, Marc
APPLICANT: Retter, Marc
APPLICANT: Mannion, Jane
APPLICANT: Fan, Ligun
APPLICANT: Wang, Aijun
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
FILE REPERENCE: 210121.478C15
CURRENT APPLICATION NUMBER: US/09/736,457
CURRENT PILING DATE: 2000-12-13
NUMBER OF SEQ ID NOS: 1864
SOFTWARE: FastSEQ for Windows Version 3.0
TENGTH: 325
                                                                                                                                                                                                                                                                                                          APPLICANT: Wang, Tongtong
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Lodes, Michael A.
APPLICANT: Lodes, Michael A.
APPLICANT: Vedvick, Tom
APPLICANT: Vedvick, Tom
APPLICANT: Retter, Marc
APPLICANT: Mannion, Jane
APPLICANT: Mannion, Jane
APPLICANT: Marc

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1 TCCGCTGCAGAGTTGCCCGTTACGA 25
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Patent No. 6509448
PAPERAL INFORMATION:
APPLICANT: Wang, Tongtong
                                                                                                                                                                                                                       Sequence 1202, Application US/09702705 Patent No. 6504010
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Bangur, Chaitanya S.
Lodes, Michael A.
Fanger, Gary
Vedvick, Tom
Carter, Darrick
Retter, Marc
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Best Local Similarity 76.0
Matches 19; Conservative
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Matches 19; Conservative
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US-09-702-705-1202
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APPLICANT: Mannion, Jane
APPLICANT: Fan, Liqun
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.478C10
CURRENT APPLICATION NUMBER: US/09/651,563
CURRENT FILING DATE: 2000-08-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 325;
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; Sequence 25, Application US/09700820C
; Patent No. 6610465
; GENERAL INFORMATION:
; APPLICANT: TSUCIO, Mikiyoshi
; APPLICANT: Saito, Mikiyoshi
; APPLICANT: Ohtomo, Toshihiko
; TITLE OF INVENTION: NOVEL METHOD FOR GENE CLONING
; FILE REFERENCE: 06501-070001
; CURRENT FILING DATE: 2000-11-20
; CURRENT FILING DATE: 1999-04-30
; PRIOR PILING DATE: 1999-04-30
; PRIOR PILING DATE: 1999-04-30
; PRIOR FILING DATE: 1999-04-30
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: JP 10/138652
; PRIOR FILING DATE: 1999-05-20
; RIGH APPLICATION NUMBER: JP 10/279876
; NUMBER OF SEQ ID NOS: 39
; SEQ ID NO S: 39
; LENGHT: 363
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SOFTWARE: FastSEQ for Windows Version 3.0
             1 TCCGCTGCAGAGTTGCCCGTTACGA 25
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                                                                                                                                                        Sequence 1202, Application US/09651563
Patent No. 6914132
GENERAL INFORMATION:
                                                                                                                                                                                                                         Wang, Tongtong
Bangur, Chaitanya S.
Lodes, Michael A.
                                                                                                                                                                                                                                                                                          Fanger,
Vedvick, Tom
Carter, Darrick
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; ORGANISM: Homo sapien
US-09-651-563-1202
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; LOCATION: (1)..(363)
US-09-700-820C-25
                                                                                                                RESULT 92
US-09-651-563-1202/c
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LENGTH: 325
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CURRENT FILING DATE: 2000-09-08
CURRENT FILING DATE: 1788
SOFTWARE: FastSEQ for Windows Version 3 Changes of SEQ ID NOS: 1788
LENGTH: 325
TYPE: NO.
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Pred. No. 8.3e+02;
0; Mismatches 6; Indels
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REPERENCE: 210121.478C18
CURRENT APPLICATION NUMBER: US/10/017,754
CURRENT FILING DATE: 2001-10-29
NUMBER OF SEQ ID NOS: 2004
SOFTWARE: PRELSEQ for Windows Version 4.0
59 TCCGCGGGAGAGAGCCGTCACCA 35
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Patent No. 6746846
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Patent No. 6858204
PERERAL INFORMATION:
APPLICANT: Henderson, Robert A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Marnerakis, Margarita
Carter, Darrick
Fanger, Gary R.
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Bangur, Chaitanya S.
Lodes, Michael A.
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Bangur, Chaitanya S.
McNabb, Andria
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Watanabe, Yoshihiro
Johnson, Jeffrey C.
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Carter, Darrick
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Best Local Similarity 76.0
Matches 19; Conservative
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; ORGANISM: Homo sapiens
US-10-017-754-1202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; ORGANISM: Homo sapien
US-09-658-824-1202
                                                                                                                US-09-658-824-1202/c
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APPLICANT:
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Query Match 61.6%; Score 15.4; DB 3; Length 582; Best Local Similarity 76.0%; Pred. No. 8.9e+02; Matches 19; Conservative 0; Mismatches 6; Indels (
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US-09-533-559-1903/C

Sequence 1903. Application US/09533559

Patent No. 6902897

GENERAL INFORMATION:
APPLICANT: Michael W. Rey
APPLICANT: Michael W. Rey
APPLICANT: Michael W. Rey
APPLICANT: Defrey R.Shuster
APPLICANT: Defrey R.Shuster
APPLICANT: Defrey R.Shuster
APPLICANT: Defrey R.Shuster
APPLICANT: Defrey S.Shuster
APPLICANT: Defrey Gausen
TITLE OF INVENTION: Methods For Monitoring Multiple Gene
TITLE OF INVENTION: Expression
FILE OF INVENTION: Expression
FILE REPRENCE: 5464.200-US
CURRENT FILING DATE: 1999-03-22
EARLIER PILING DATE: 1999-03-22
MUMBER: OF INVENTION NUMBER: 09/273,623
EARLIER FILING DATE: 1999-03-22
MUMBER: OF SEQ ID NOS: 7860
SOFTWARE: FRAISEQ for Windows Version 4.0
SEQ ID NO 1903
LENGTH: S82
                   COMPUTER KEALALE FORM:
COMPUTER: FLORDY disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,655
FILING DATE:
CLASSIPICATION NUMBER:
FILING DATE:
CLASSIPICATION NUMBER:
FILING DATE:
CLASSIPICATION:
APPLICATION NUMBER:
FILING DATE:
CLASSIPICATION:
ATTORNEY/AGTE INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0001 US
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPAX: (650) 845-055
TELECOMMUNICATION INFORMATION:
SEQUENCE CHARACTERISTICS:
TELEPAX: (650) 845-1166
SEQUENCE CHARACTERISTICS:
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; OTHER INFORMATION: n = A,T,C or G
US-09-533-559-1903
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Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 540 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc_feature
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; CLONE: 938405_2
US-09-023-655-1384
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IMMEDIATE SOURCE
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| Sequence 1384, Application US/09023655
| Patent No. 6607970:
| GENERAL INFORMATION:
| APPLICANT: Cocks, Benjamin G. APPLICANT: Jeffrey J. Seilhamer
| APPLICANT: Jeffrey J. Seilhamer
| TITLE OF INVENTION: EXPRESSION | TITLE OF INVENTION: EXPRESSION | NUMBER OF SEQUENCES: 1508 | CORRESPONDENCE ADDRESSE: INCTTE PHARMACEUTICALS, INC. |
| STREET: 3174 PORTER DRIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61.6%; Score 15.4; DB 3; Length 515; 76.0%; Pred. No. 8.8e+02; tive 0; Mismatches 6; Indels
                                                                                                                                                                                                          US-08-754-477A-119/C

Sequence 119, Application US/08754477A

Sequence 119, Application US/08754477A

Fatent No. 6518411

GENERAL INFORMATION:

APPLICANT: Murray, Jeffrey

APPLICANT: Semina, Blena

TITLE OF INVENTION: RIEG COMPOSITIONS AND THERAPEUTIC

TITLE OF INVENTION: AND DIAGNOSTIC USES THEREFOR

NUMBER OF SEQUENCES: 139

CORRESPONDENCE ADDRESS:

ADDRESSEE: FOLEY, HOAG & ELIOT LLP

STREET: One Post Office Square
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE:
COUNTRY: USA
ZIP: 02109-2170
ZIP: 02109-2170
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/754,477A
APPLICATION NUMBER: 105/08/754,477A
TILING DATE: 22-NOV-1996
ATTORNEY/AGENT INFORMATION:
NAME: Arnold, Beth E.
REGISTRATION NUMBER: 35,430
REFERENCE/DOCKET NUMBER: 35,430
REFERENCE/DOCKET NUMBER: 315,430
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFOR
                                                                        110 TCCGCGGGGGGGAGCCCCGTCACCA 86
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 119: SEQUENCE CHARACTERISTICS: LENGTH: 515 base pairs TYPE: nucleic acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
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Best Local Similarity
Matches 19; Conserva
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STATE: CALIFORNIA
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Application US/09949016
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76.0%;
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Best Local Similarity 76.0
Matches 19; Conservative
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Best Local Similarity 76.0
Matches 19; Conservative
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Job time: 131.903 secs
                        JS-09-949-016-47430/c
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US-09-949-016-47430
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US-09-949-002-1736
                                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID NO 47430
                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
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GENERAL INFORMATION:

APPLICANT: VEXTER:

1 TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;

FILE REFREENCE: CL001307

CURRENT PILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR PELING DATE: 2000-10-03

PRIOR PELING DATE: 2000-10-03

PRIOR PELING DATE: 2000-10-03

PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTUM OF APPLICATION NUMBER: 60/231,498

PRIOR PILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SEQ ID NO 47406

LENGTH: 601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
GURENT PILIAGE OF INFORMATION:
GURENT PILIAGE DATE:
GOO-04-14
FRIOR APPLICATION NUMBER:
GO/241,755
FRIOR APPLICATION NUMBER:
GO/237,768
FRIOR APPLICATION NUMBER:
GO/237,768
FRIOR PILIAGE DATE:
ZO00-10-03
FRIOR FILIAGE DATE:
ZO00-09-08
SUPPRESE FASTES OF WINDOWS VETSION 4.0
SEQ ID NO 47418
LENGTH:
GO1
BENERAL FOR FEATURE OF WINDOWS VETSION 4.0
SEQ ID NO 47418
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Pred. No. 9e+02
0; Mismatches
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Pred. No. 9e+02
0; Mismatches
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                                                                                                               US-09-949-016-47406/c
; Sequence 47406, Application US/09949016
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76.0%;
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Best Local Similarity 76.0
Matches 19; Conservative
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Best Local Similarity 76.0
Matches 19; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Human
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US-09-949-016-47418
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Sequence 1736, Application US/09949002

Batent No. 690016

GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: CLOO0790
CURRENT APPLICATION NUMBER: US/09/949,002
CURRENT FILING DATE: 2000-01-28
PRIOR APPLICATION NUMBER: 60/231,401
PRIOR FILING DATE: 2000-09-08
PATENT NO. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF FILE REFERENCE: CLOO1307
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR PILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-04
PRIOR PILING DATE: 2000-10-09
PRIOR FILING DATE: 2000-09-08
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9e+02;
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Pred. No. 9e+02
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 10823
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 1736
LENCTH: 601
                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 207012-
SOFTWARE: FastSEQ for Windows Version 4.0
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US-10-760-048-24
US-10-760-048-25
US-10-760-048-25
US-10-760-048-26
US-10-760-048-29
US-10-760-048-29
US-10-760-048-39
US-10-760-048-31
US-10-760-048-41
US-10-760-048-41
US-10-760-048-41
US-10-760-048-41
US-10-760-048-41
US-10-760-048-41
US-10-760-048-41
US-10-760-048-42
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US-11-097-143-23899 US-10-471-963-378 US-10-719-993-69278 US-10-719-993-6907 US-10-97-143-37162 US-10-10-10-10-10-10-10-10-10-10-10-10-10-	US-10-719-900-799952 US-10-424-15-35434 US-10-422-115-35434 US-09-925-065A-737916 US-09-925-065A-814934 US-09-925-065A-814935 US-09-925-065A-814935 US-09-925-065A-814935 US-09-925-065A-827450 US-09-925-065A-827450 US-09-925-065A-827450 US-10-027-632-19445 US-10-027-632-19445 US-10-027-632-19445 US-10-10-027-632-19445 US-10-10-113-142292 US-10-10-113-143-20834 US-10-446-77-2 US-10-16-49-5 US-10-16-49-3 US-10-16-49-3 US-10-16-49-3 US-10-16-49-3 US-10-16-49-3 US-10-16-49-3 US-10-16-49-3 US-10-16-49-3 US-10-16-49-3 US-10-16-49-3 US-10-16-49-3 US-10-16-49-3 US-10-16-49-3 US-10-36-33-318-10 US-10-36-33-318-10 US-10-36-33-318-10 US-10-446-373-10 US-10-446-373-10 US-10-446-373-10 US-10-446-373-10 US-10-446-373-10 US-10-446-373-10	US-10-77-73-73-74-74-74-74-74-74-74-74-74-74-74-74-74-
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4.0 3807 10 US-11-097-143-23899 4.0 15124 8 US-10-719-993-6907 4.0 14902 10 US-11-097-143-378 4.0 24281 7 US-10-719-993-6907 4.0 24281 7 US-10-915-740A-37 4.0 39051 9 US-10-087-192-559 4.0 73467 3 US-09-740-026-3 4.0 73467 3 US-10-208-3859-3 4.0 73467 10 US-11-084-813-3 4.0 74878 8 US-10-219-993-6863 4.0 56593 3 US-09-997-722-16 4.0 10021 9 US-10-919-964-1 4.0 2242716 9 US-10-915-740A-1068	US-10-719-900-799952 US-10-424-99-8532 US-10-425-115-3434 US-09-925-065A-814934 US-09-925-065A-814935 US-09-925-065A-814935 US-09-925-065A-814935 US-09-925-065A-814935 US-09-925-065A-814935 US-09-925-065A-827450 US-09-925-065A-827450 US-09-925-065A-827450 US-10-027-632-11445 US-10-027-632-11445 US-10-027-632-11445 US-10-425-115-142292 US-10-425-115-142292 US-10-426-432-495 US-10-364-494-5 US-10-364-494-5 US-10-364-373-100 US-10-364-677-18	3.2 109586 5 US-10-719-993-6778 Sequence 3.2 109586 5 US-10-087-192-73 Sequence 3.2 276276 5 US-10-087-192-74 Sequence 3.2 276276 5 US-10-087-192-74 Sequence 3.2 713059 5 US-10-087-632-174581 Sequence 2.4 449 8 US-10-827-632-174585 Sequence 2.4 449 8 US-10-425-115-117462 Sequence 2.4 487 9 US-10-425-115-117462 Sequence 2.4 487 9 US-10-425-115-117462 Sequence 2.4 487 9 US-10-425-115-117462 Sequence 2.4 559 3 US-09-770-152-442 Sequence 2.4 559 3 US-09-770-152-448 Sequence 2.4 599 9 US-10-972-079-12849 Sequence 2.4 600 9 US-10-972-079-12849 Sequence 2.4 623 4 US-09-225-065A-910820 Sequence 2.4 628 6 US-10-072-079-1289 Sequence 2.4 668 6 US-10-072-079-1289 Sequence 2.4 668 6 US-10-072-053-31996 Sequence 2.4 668 6 US-10-072-632-31996 Sequence 2.4 668 6 US-10-072-632-31996 Sequence 2.4 668 6 US-10-073-632-31996 Sequence 2.4 668 6 U
16 64.0 3807 10 US-11-097-143-23899 16 64.0 6125 7 US-10-437-963-82378 16 64.0 13524 8 US-10-719-993-6907 16 64.0 14902 10 US-11-097-143-37162 16 64.0 24281 7 US-10-322-281-639 16 64.0 53359 5 US-10-915-740A-37 16 64.0 73467 3 US-09-740-026-3 16 64.0 73467 5 US-10-087-192-559 16 64.0 73467 5 US-10-203-6863 16 64.0 73467 10 US-11-084-813-3 16 64.0 73467 10 US-11-084-813-3 16 64.0 110021 9 US-10-719-993-6863 16 64.0 110021 9 US-10-91862-83 16 64.0 2242716 9 US-10-915-740A-1068	5.8 (3.2 25 8 US-10-719-900-799952 5.8 (3.2 204 7 US-10-425-91-832 5.8 (3.2 204 7 US-10-425-91-832 5.8 (3.2 517 4 US-09-925-065A-737916 5.8 (3.2 517 4 US-09-925-065A-614935 5.8 (3.2 517 4 US-09-925-065A-614935 5.8 (3.2 595 4 US-09-925-065A-614935 5.8 (3.2 598 4 US-09-925-065A-614935 5.8 (3.2 598 4 US-09-925-065A-614935 5.8 (3.2 663 4 US-09-925-065A-57450 5.8 (3.2 751 6 US-10-925-065A-57450 5.8 (3.2 751 6 US-10-925-065A-57451 5.8 (3.2 1704 7 US-10-425-115-142292 5.8 (3.2 1167 8 US-10-425-115-142292 5.8 (3.2 2235 6 US-10-108-266A-935 5.8 (3.2 2235 6 US-10-108-266A-935 5.8 (3.2 2235 6 US-10-108-266A-935 5.8 (3.2 2335 6 US-10-108-266A-935 5.8 (3.2 2335 6 US-10-108-266A-935 5.8 (3.2 2335 6 US-10-108-26A-935 5.8 (3.2 2335 6 US-10-108-23303 5.8 (3.2 2335 6 US-10-108-26A-935 5.8	8 63.2 85571 8 US-110-719-793-6774 Sequence 63.2 109586 5 US-110-087-192-73 Sequence 63.2 276205 5 US-110-087-192-73 Sequence 63.2 276205 5 US-110-087-192-754 Sequence 62.4 429 108-10-27-632-174581 Sequence 62.4 449 8 US-10-027-632-174581 Sequence 62.4 449 8 US-10-809-189-7495 Sequence 62.4 449 8 US-10-425-115-117462 Sequence 62.4 487 9 US-10-425-115-117462 Sequence 62.4 487 9 US-10-425-115-117462 Sequence 62.4 559 3 US-10-425-115-147890 Sequence 62.4 559 3 US-10-425-115-147890 Sequence 62.4 599 9 US-10-972-079-77881 Sequence 62.4 599 9 US-10-972-079-77881 Sequence 62.4 620 9 US-10-972-079-77881 Sequence 62.4 620 9 US-10-972-079-12849 Sequence 62.4 620 9 US-10-972-079-12850 Seq

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US-10-295-787D-7
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APPLICANT: Berger, Martina M
APPLICANT: Tilles, Jeremiah G
TITLE OF INVENTION: APPARATUS AND METHODS FOR DETECTING A PATHOGEN IN A SAMPLE
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APPLICANT: The Regents of The University of California
                                                               APPLICANT: Genetics & IVF
APPLICANT: MARIANI, Brian D.
TITLE OF INVERTION: ENTEROVIRUS PRIMERS AND PROBES
FILE REPERENCE: 043956-0121
CURRENT APPLICATION NUMBER: US/10/829,474
CURRENT PILING DATE: 2004-04-22
NUMBER OF SEQ ID NOS: 57
SOFTWARE: Patentin version 3.2
SEQ ID NO 46
LENGTH: 26
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APPLICANT: Genetics & IVF
APPLICANT: MARIANI, Brian D.
TITLE OF INVENTION: ENTEROVIRUS PRIMERS AND PROBES
FILE REPERRENCE: 043956-0121
CURRENT APPLICATION NUMBER: US/10/829,474
CURRENT FILING DATE: 2004-04-22
                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 25; DB 9;
Pred. No. 0.042;
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100.0%; Pred. No. 0.0
tive 0; Mismatches
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CURRENT APPLICATION NUMBER: US/10/295,787D
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; Sequence 46, Application US/10829474; Publication No. US20050239055A1; GENERAL INFORMATION:
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US-10-22-474-47
Sequence-47, Application US/10829474
; Publication No. US20050239055A1
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NUMBER OF SEQ ID NOS: 57
SOFTWARE: PatentIn version 3.2
                                                                                                                                                                                                                                                                                                TYPE: DNA ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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Matches 25, Conservative
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LENGTH: 26
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GENERAL INFORMATION:
APPLICANT: The Regents of The University of California
APPLICANT: The Regents of The University of California
APPLICANT: Tilles, Xi Yu
APPLICANT: Tilles, Jeremiah G
TITLE OF INVENTION: APPARATUS AND METHODS FOR DETECTING A PATHOGEN IN A SAMPLE
TILLE REPERENCE: UCINV--015A
CURRENT APPLICATION NUMBER: US/10/295, 787D
CURRENT FILING DATE: 2002-11-15
FRIOR APPLICATION NUMBER: US 60/335,539
FRIOR APPLICATION NUMBER: US 60/335,539
FRIOR PILING DATE: 2001-11-15
NUMBER OF SEQ ID NOS: 113
SOFTWARE: Patentin version 3.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: The Regents of The University of California
APPLICANT: Jia, Xi Yu
APPLICANT: Jia, Xi Yu
APPLICANT: Tilles, Martina M
APPLICANT: Tilles, Jeremiah G
TITLE OF INVENTION: APPARATUS AND METHODS FOR DETECTING A PATHOGEN IN A SAMPLE FILE REFERENCE: UCIVN--015A
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                                                                                                                                                                                                                                                         ; Score 25; DB 9;
; Pred. No. 0.041;
0; Mismatches
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                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100.0%;
Matches 25; Conservative 0
                                                  NUMBER OF SEQ ID NOS: 113
SOFTWARE: Patentin version 3.3
SEQ ID NO 27
LENGTH: 69
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SOFTWARE: Patentin version 3.3
SEQ ID NO 6
LENGTH: 70
PRIOR APPLICATION NUMBER: US (PRIOR FILING DATE: 2001-11-15
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; ORGANISM: echovirus 30
US-10-295-787D-6
                                                                                                                                                      TYPE: DNA
CORGANISM: Echovirus 7
US-10-295-787D-27
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Best Local Similarity
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US-10-295-787D-7

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TYPE: DNA ORGANISM: Coxsackie Virus B5
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Best Local Similarity
Matches 25; Conserv
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Sequence 12, Application US/10295787D

Publication No. US2005020414A1

GENERAL INFORMATION:
APPLICANT: The Regents of The University of California
APPLICANT: Jia, Xi Yu

APPLICANT: Jia, Xi

TILLE OF INVENTION APPRATUS AND METHODS FOR DETECTING A PATHOGEN IN A SAMPLE

CURRENT APPLICATION NUMBER: US/10/295,787D

CURRENT APPLICATION NUMBER: US 60/335,539

PRIOR FILING DATE: 2001-11-15

PRIOR FILING DATE: 2001-11-15

NUMBER OF SEQ ID NOS: 113

SOFTWARE: PatentIn version 3.3

SEQ ID NO 12

LENGTH: 70
                                                                                                                                                                                                                                                                                                                                                     APPLICANT: The Regents of The University of California
APPLICANT: The Regents of The University of California
APPLICANT: Dia, Xi Yu
APPLICANT: Berger, Martina M
APPLICANT: Tilles, Jeremiah G
TITLE OF INVENTION: APPARATUS AND METHODS FOR DETECTING A PATHOGEN IN A SAMPLE FILE REPERENCE: UCIVN--015A
CURRENT APPLICANTION NUMBER: US 10/295, 787D
CURRENT FILING DATE: 2002-11-15
PRIOR APPLICATION NUMBER: US 60/335,539
PRIOR FILING DATE: 2001-11-15
NUMBER OF SEQ ID NOS: 113
SOFTWARE: Patentin version 3.3
SEQ ID NO 9
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100.0%; Score 25; DB 9; Length 70; 100.0%; Pred. No. 0.041;
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100.0%; Score 25; DB 9; Length 70;
Best Local Similarity 100.0%; Pred. No. 0.041;
Matches 25; Conservative 0; Mismatches 0; Indels
                                                      0; Indels
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US-10-295-787D-9
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US-10-295-787D-12
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Matches 25; Conserv
Query Match
Best Local Similarity
Matches 25; Conserv
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Score 25; DB 9; Length 70; Pred. No. 0.041;
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Pred. No. 0.041;
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Mismatches
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Pred. No. 0
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PRIOR FILING DATE: 2001-11-15
WUMBER OF SEQ ID NOS: 113
SOFTWARR: Patentin version 3.3
SEQ ID NO 35
                                                                                                                                                                                                                                                                                         1 rececrecadaerrececerracea 25
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Matches 25; Conservative 0;
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ilarity 100.0%;
Conservative 0
  SOFTWARE: Patentin version 3.3
SEQ ID NO 20
LENGTH: 70
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PatentIn version 3.3
                                                                 ; TYPE: DNA
; ORGANISM: Ev Stuttgart Virus
US-10-295-787D-20
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Best Local Similarity
Matches 25; Conserv
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ORGANISM: Coxeackie
US-10-295-787D-22
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SOFTWARE: Pa
SEQ ID NO 22
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Publication No. US20050202414A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: The Regents of The University of California
APPLICANT: Jia, Xi Yu
APPLICANT: Berger, Martina M
APPLICANT: Herger, Martina M
APPLICANT: APPRARATUS AND METHODS FOR DETECTING A PATHOGEN IN A SAMPLE
FILE OF INVENTION: APPRARATUS AND METHODS FOR DETECTING A PATHOGEN IN A SAMPLE
CURRENT APPLICATION NUMBER: US/10/295, 787D
CURRENT FILING DATE: 2002-11-15
PRIOR FILING DATE: 2001-11-15
APPLICANT: Berger, Martina M
APPLICANT: Tilles, Jeremlah G
TITLE OF INVENTION: APPARATUS AND METHODS FOR DETECTING A PATHOGEN IN A SAMPLE
FILE REFERENCE: UCIVN--015A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Jia, Xi Yu
APPLICANT: Berger, Martina M
APPLICANT: Tilles, Jeremiah G
TITLE OF INVENTION: APPARATUS AND METHODS FOR DETECTING A PATHOGEN IN A SAMPLE
FILE REPREMENT: UCINV-015A
CURRENT APPLICATION NUMBER: US/10/295,787D
CURRENT FILING DATE: 2002-11-15
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Pred. No. 0.041;
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Publication No. US20050202414A1
GENERAL INFORMATION:
APPLICANT: The Regents of The University of California
                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 25; DB 9;
100.0%; Pred. No. 0.041;
iive 0; Mismatches 0
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                                                                             CURRENT APPLICATION NUMBER: US/10/295,787D
CURRENT FILING DATE: 2002-11-15
PRIOR APPLICATION NUMBER: US 60/335,539
PRIOR FILING DATE: 2001-11-15
NUMBER OF SEQ ID NOS: 113
SOFTWARE: Patentin version 3.3
SEQ ID NO 18
LENGTH: 70
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PRIOR APPLICATION NUMBER: US 60/335,539
PRIOR FILING DATE: 2001-11-15
NUMBER OF SEQ ID NOS: 113
SOFTWARE: PatentIn version 3.3
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US-10-295-787D-18
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Best Local Similarity 100.
Matches 25; Conservative
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APPLICANT: The Regents of The University of California
APPLICANT: The Regents of The University of California
APPLICANT: Jia, Xi Yu
APPLICANT: Berger, Martina M
APPLICANT: Tilles, Jernemiah G
TITLE OF INVENTION: APPRATUS AND METHODS FOR DETECTING A PATHOGEN IN A SAMPLE
FILE REPERENCE: UCIVN--015A
CURRENT APPLICATION NUMBER: US/10/295,787D
CURRENT FILING DATE: 2002-11-15
PRIOR FILING DATE: 2001-11-15
PRIOR FILING DATE: 2001-11-15
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APPLICANT: The Regerts wartina M
APPLICANT: Berger, Martina M
APPLICANT: Tilles, Jermiah G
TITLE OF INVENTION: APPARATUS AND METHODS FOR DETECTING A PATHOGEN IN A SAMPLE
FILE REPRENCE: UCINV--015A
CURRENT PERILOGICATION UNBERS: 105/10/295,787D
CURRENT FILING DATE: 2002-11-15
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Query Match
Best Local Similarity
Matches 25; Conserv
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; Publication No. US20050158710A1
; GENERAL INFORMATION:
; APPLICANT: TSANG, SHIRLEY
; APPLICANT: PRICE, JAMES A.
; TILLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID
; TILLE OF INVENTION: DETECTION OF SHIRLEY
; CURRENT APPLICATION NUMBER: US/10/760,048
; CURRENT PILING DATE: 2004-01-16
; NUMBER OF SEQ ID NOS: 67
; SOFTHARE: Patentin Ver. 3.2
; SOFTHARE: 126
                                                                                                                                                           Sequence 53, Application US/10760048
Publication No. US20050158710A1
GENERAL INFORMATION:
APPLICANT: TSANG, SHIRLEY
APPLICANT: PRICE, JAMES A.
TITLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID
FILE REFERENCE: 020187.0187PUS
CURRENT APPLICATION NUMBER: US/10/760,048
CURRENT FILING DATE: 2004-01-16
NUMBER OF SEQ ID NOS: 67
SOFTHARE: Patentin Ver. 3.2
SEQ ID NO 53
LENGTH: 107
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Best Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Unknown Organism
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25; Conservative
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RESULT 18 US-10-760-048-32/C

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Publication No. US20050158710A1

GENERAL INPORMATION:

APPLICANT: TSANG, SHIRLEY

APPLICANT: PRICE, JAMES A.

TITLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID

FILE REFERENCE: 020187.0187FUS

CURRENT APPLICATION NUMBER: US/10/760,048

CURRENT FILING DATE: 2004-01-16

NUMBER OF SEQ ID NOS: 67

SEQ ID NO 13

LENGTH: 238
Sequence 32, Application US/10760048
Publication No. US20050158710A1
GENERAL INFORMATION:
APPLICANT: TSANG, SHIRLEY
APPLICANT: TSANG, SHIRLEY
APPLICANT: HELLYER, TOBIN J.
TITLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID
FILE REFERENCE: 020187.0187PTUS
CURRENT APPLICATION UNBER: US/10/760,048
CURRENT PILLING DATE: 2004-01-16
NUMBER OF SEQ ID NOS: 67
SOCTHARRE: Patentin Ver: 3.2
SEQ ID NO 32
LENGTH: 237
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APPLICANT: PRICE, JAMES A.
APPLICANT: HELLYER, TOBIN J.
FITLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID
FILE REFERENCE: 0.20187.0187PTUS
CURRENT APPLICATION NUMBER: US/10/760,048
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ilarity 100.0%; Pred. No. 0.04;
Conservative 0; Mismatches
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; Sequence 14, Application US/10760048
; Publication No. US20050158710A1
; GENERAL INFORMATION:
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ORGANISM: Unknown Organism
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ORGANISM: Unknown Organism
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                                                                                  Length 238;
       ; OTHER INFORMATION: 5'untranslated polynucleotide sequence US-10-760-048-19
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APPLICANT: HELLYER, TOBIN J.
TITLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID
TITLE OF INVENTION: DETECTION.
TITLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID
TITLE OF INVENTION: 020197.0197PTUS.
CURRENT APPLICATION NUMBER: US/10/760,048
CURRENT FILING DATE: 2004-01-16
NUMBER OF SEQ ID NOS: 67
SOFTWARE: PALENTIN Ver. 3.2
LENGTH: 238
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APPLICANT: TRICE, JAMES A.
APPLICANT: FRICE, JAMES A.
APPLICANT: HILLYER, TOBIN J.
TITLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID
FILE REFERENCE: 020187.0187PTUS
CURRENT APPLICATION NUMBER: US/10/760,048
CURRENT FILING DATE: 2004-01-16
NUMBER OF SEQ ID NOS: 67
SEQ ID NOS: 67
SEQ ID NO 24
LENGTH: 238
                                                                               Score 25; DB 9;
Pred. No. 0.04;
); Mismatches 0
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100.0%; Score 25; DB 9;
Best Local Similarity 100.0%; Pred. No. 0.04;
Matches 25; Conservative 0; Mismatches 0
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Publication No. US20050158710A1
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Publication No. US20050158710A1
GENERAL INFORMATION:
                                                                             Query Match 100.0%; S. Best Local Similarity 100.0%; P. Matches 25; Conservative 0;
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APPLICANT: PRICE, JAMES A.
APPLICANT: HELLYER, TOBIN J.
TITLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID
FILE REFERENCE: 020187.0187PTUS
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APPLICANT: TSANG, SHIRLEY
APPLICANT: PRICE, JAMES A.
APPLICANT: HELLYSEN, TOBIN J.
TITLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID
FILE REFERENCE: 020187.01877US
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100.0%; Pred. No. 0.04;
tive 0; Mismatches
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CURRENT FILING DATE: 2004-01-16
NUMBER OF SEQ ID NOS: 67
SOFTWARE: Patentin Ver. 3.2
SEQ ID NO 15
LENGTH: 238
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Publication No. US20050158710A1
GENERAL INFORMATION:
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Publication No. US20050158710A1
CURRENT FILING DATE: 2004-0
NUMBER OF SEQ ID NOS: 67
SOFTWARE: PALENLIN VEY. 3.2
SEQ ID NO 14
LENGTH: 238
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ORGANISM: Unknown Organism
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Matches 25; Conserv
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LENGTH: 238
                                                                                                                            TYPE: DNA
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ORGANISM: Unknown Organism
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Best Local Similarity 100.
Matches 25; Conservative
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ORGANISM: Unknown Organism
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Best Local Similarity 100.
Matches 25; Conservative
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US-10-760-048-26/C
; Sequence 26, Application US/10760048
; Publication No. US20050158710A1
; GENERAL INFORMATION:
; APPLICANT: TSANG, SHIRLEY
; APPLICANT: HELLER, TOBIN J.
; TITLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID
; FILE REPRENCE: 0201877.0187PTUS
; CURRENT APPLICATION NUMBER: US/10/760,048
; CURRENT FILING DATE: 2004-01-16
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: Patentin Ver. 3.2
; SEQ ID NO 26
; LENGTH: 238
                                                                                                Sequence 25, Application US/10760048

Publication No. US20050158710A1

GENERAL INFORMATION:

APPLICANT: TSANG, SHIRLEY

APPLICANT: PRICE, JAMES A.

APPLICANT: PRICE, JAMES A.

TITLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID

FILE REFREENCE: 020187.0187PUS

CURRENT PILING DATE: 2004-01-16

NUMBER OF SEQ ID NOS: 67

SOFTHARE: Patentin Ver. 3.2

SEQ ID NO 25

LENGTH: 238
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75 TCCGCTGCAGAGTTGCCCGTTACGA 51
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Best Local Similarity
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US-10-760-048-25/c
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US-10-760-048-27/c
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Pred. No. 0.04;
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Pred. No. 0.04;
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APPLICANT: FRICE, JAMES A.

APPLICANT: HELLYER, TOBLIN J.

TITLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID
FILE REFERENCE: 020187.0187PTUS
CURRENT APPLICATION NUMBER: US/10/760,048

CURRENT FILING DATE: 2004-01-16
NUMBER OF SEQ ID NOS: 67
SEQ ID NOS: 67
SEQ ID NO 27
LENGTH: 238
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Sequence 43, Application US/10760048

Publication No. US20050158710A1

GENERAL INFORMATION:
APPLICANT: TSANG, SHIRLEY
APPLICANT: FRICE, JAMES A.
TITLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID
FILE REFERENCE: 020187.0187PHUS
CURRENT APPLICATION NUMBER: US/10/760,048

CURRENT FILING DATE: 2004-01-16
NUMBER OF SEQ ID NOS: 67
SOFTWARE: Patentin Ver. 3.2
SOFTWARE: Patentin Ver. 3.2
LENGTH: 238
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                          Indels
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APPLICANT: PRICE, JAMES A.
APPLICANT: PRICE, JAMES A.
APPLICANT: HELLYEN TOBIN J.
TITLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID
FILE REPREBNCE: 020187.0187PTUS
CURRENT APPLICATION NUMBER: US/10/760,048
CURRENT FILING DATE: 2004-01-16
NUMBER OF SEQ ID NOS: 67
SEQ ID NOS: 67
SEQ ID NO 42
LENGTH: 238
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    Pred. No. 0.04;
                          Mismatches
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    100.001
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ORGANISM: Unknown Organism
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                          Conservative
Best Local Similarity
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                                                                                                                                                                                        Length 238;
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; Publication No. US20050159710A1
; GENERAL INFORMATION:
; APPLICANT: TSANG, SHIKLEY
; APPLICANT: PRICE, JAMES A.
; APPLICANT: PRICE, JAMES A.
; TITLE OF INVERTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID
; FILE REPERENCE: 020187.0189FUS
; CURRENT APPLICATION NUMBER: US/10/760,048
; CURRENT FILING DATE: 2004-01-16
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: Patentin Ver. 3.2
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100.0%; Score 25; DB 9; Length 238;
Best Local Similarity 100.0%; Pred. No. 0.04;
Matches 25; Conservative 0; Mismatches 0; Indels
                                                                                       OTHER INFORMATION: Description of Unknown Organism: Viral; OTHER INFORMATION: 5'untranslated polynucleotide sequence US-10-760-048-29
                                                                                                                                                                                                                                      0; Indels
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APPLICANT: TSANG, SHIRLEY
APPLICANT: PRICE, JAMES A.
APPLICANT: HELLYER, TOBIN J.
TITLE OF INVENTION: DFFECTION OF ENTEROVIRUS NUCLEIC ACID
FILE REFERENCE: 020187.0187PTUS
                                                                                                                                                                                 DB 9;
0.04;
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100.0%; Score 25; DB
Best Local Similarity 100.0%; Pred. No. 0.0
Matches 25; Conservative 0; Mismatches
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CURRENT FILING DATE: 2004-01-16
NUMBER OF SEQ ID NOS: 67
SOFTWARE: Patentin Ver. 3.2
SEQ ID.NO 31
LENGTH: 238
                                                                                                                                                                                                                                                                                  1 TCCGCTGCAGAGTTGCCCGTTACGA 25
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Publication No. US20050158710A1
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ORGANISM: Unknown Organism
                                         ORGANISM: Unknown Organism
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ORGANISM: Unknown Organism
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; OTHER INFORMATION:
US-10-760-048-30
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LENGTH: 238
LENGTH: 238
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CURRENT APPLICATION NUMBER: US/10/760,048
CURRENT FILING DATE: 2004-01-16
NUMBER OF SEQ ID NOS: 67
SEQ ID NO 48
LENGTH: 238
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COKBACKIEVINE B3
US-10-760-048-67
                                                                                                                                     TYPE: DNA
ORGANISM: Unknown Organism
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ORGANISM: Unknown Organism
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Matches 25; Conservative
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US-10-760-048-67/c
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US-10-760-048-54/c
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US-10-760-048-46/c

; Sequence 46, Application US/10760048
; Publication Wo. US20050158710A1
; GENERAL INFORMATION:
; APPLICANT: TSANG, SHIRLEY
; APPLICANT: HELLYER, JAMES A.;
; APPLICANT: HELLYER, TOBIN J.
; TITLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID
; FILE REFERENCE: 020187.0187PTUS
; CURRENT APPLICATION NUMBER: US/10/760,048
; CURRENT FILING DATES: 2004-01-16
; NUMBER OF SEQ ID MOS: 67
; SOFTWARE: PatentIn Ver. 3.2
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APPLICANT: TSANG, SHIRLEY
APPLICANT: PRICE, JAMES A.
APPLICANT: HELLYER, TOBIN OF
TITLE OF INVENTION: DETECTION OF
FILE REFERENCE: 020187.0187FUG
CURRENT PILING DATE: 2004-01-16
NUMBER OF SEQ ID NOS: 67
SOFTWARE: Patentin Ver. 3.2
SEQ ID NO 47
LENGTH: 238
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| Sequence 48, Application US/10760048
| Publication No. US20050158710A1
| GENERAL INFORMATION:
| APPLICANT: TSANG, SHIRLEY
| APPLICANT: FRICE, JAMES A.
| FILE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID
| FILE REFERENCE: 020187.0187PTUS
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Best Local Similarity 100.0
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ORGANISM: Unknown Organism
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Best Local Similarity 100.
Matches 25; Conservative
                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Unknown Organism
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                                                                                                                                                                                                                                                                                           SEQ ID NO 46
LENGTH: 238
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Sequence 54, Application US/10760048

Publication No. US20050158710A1

GENERAL INFORMATION:

APPLICANT: PRICE, JAMES A.

APPLICANT: PRICE, JAMES A.

TITLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID

FILE REFERENCE: 020187.0187PTUS

CURRENT APPLICATION NUMBER: US/10/760,048

CURRENT APPLICATION NUMBER: US/10/760,048

CURRENT PILING DATE: 2004-01-16

NUMBER OF SEQ ID NOS: 67

SOFTWARE: Patentin Ver. 3.2

SEQ ID NO 54

LENGTH: 238
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| Publication No. US20050158710A1
| GENERAL INPORMATION:
| APPLICANT: TSANG, SHIRLEY
| APPLICANT: TSANG, SHIRLEY
| APPLICANT: PRICE, JAMES A.
| TITLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID
| TITLE REFERENCE: 020107.0187PTUS
| CURRENT PILING DATE: 2004-01-16
| NUMBER OF SEQ ID NOS: 67
| SOFTWARE: Patentin Ver. 3.2
| SEQ ID NO 67
| LENGTH: 660
                                                                                                                Query Match 100.0%; Score 25; DB 9; Length 238; Best Local Similarity 100.0%; Pred. No. 0.04; Matches 25; Conservative 0; Mismatches 0; Indels
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; OTHER INFORMATION: 5'untranslated polynucleotide sequence US-10-760-048-48
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APPLICANT: The Regents of The University of California
APPLICANT: Jia, Xi Yu
APPLICANT: Berger, Martina M
APPLICANT: Tilles, Jeremiah G
TITLE OP INVENTION: APPARATUS AND METHODS FOR DETECTING A PATHOGEN IN A SAMPLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; FEATURE:
; OTHER INFORMATION: Chemically synthesizec probe for enteroviral RNA
US-10-829-474-43
                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: Chemically synthesized probe for enteroviral RNA
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                                                                           APPLICANT: Generics & IVF
APPLICANT: MARIANI, Bitan D.
TITLE OF INVENTION: ENTEROVIRUS PRIMERS AND PROBES
FILE REFERENCE: 043956-0121
CURRENT APPLICATION NUMBER: US/10/829,474
CURRENT FILING DATE: 2004-04-22
NUMBER OF SEQ ID NOS: 57
SEQ ID NOS: 57
SEQ ID NO 42
LENGTH: 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Genetics & IVF
APPLICANT: Genetics & IVF
APPLICANT: MARIANI, Brian D.
TITLE OF INVENTION: ENTEROVIRUS PRIMERS AND PROBES
FILE REPERENCE: 043956-0121
CURRENT APPLICATION NUMBER: US/10/829,474
CURRENT FILING DATE: 2004-04-22
NUMBER OF SEQ ID NOS: 57
SOFTWARE: Patentin version 3.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 96.0%; Score 24; DB 9; 100.0%; Pred. No. 0.13;
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CURRENT APPLICATION NUMBER: US/10/295,787D
CURRENT FILING DATE: 2002-11-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 CCGCTGCAGAGTTGCCCGTTACGA 25
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     Sequence 42, Application US/10829474
Publication No. US20050239055A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 43, Application US/10829474
Publication No. US20050239055A1
                                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA ORGANISM: Artificial Sequence
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Best Local Similarity 100.0
Matches 24; Conservative
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US-10-829-474-43
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Sequence 7, Application US/10136819

Publication No. US20030166593A1

GENERAL INFORMATION:

APPLICANT: Chien, Kenneth

APPLICANT: Hoshijima, Masahiko

TITLE OF INVENTION: No. US20030166593A1-viral vesicle vector for cardiac specific gen

TITLE OF INVENTION: NO. US20030166593A1-viral vesicle vector for cardiac specific gen

TITLE OF INVENTION: NO. US20030166593A1-viral vesicle vector for cardiac specific gen

TITLE OF INVENTION: NO. US20030166593A1-viral vesicle vector for cardiac specific gen

CURRENT APPLICATION NUMBER: US/10/136,819

RIOR APPLICATION NUMBER: 60/287,423

RIOR APPLICATION OF 18

SOFTWARE OF SEQ ID NOS: 18

SOFTWARE PARENT PARENT OF SEQ ID NOS: 18
                                                                                                                                                                                                                                                                                                                                        APPLICANT: HSU, TSU-AN
APPLICANT: HSU, TSONG-YUAN
APPLICANT: HSU, TZONG-YUAN
APPLICANT: HSU, TZONG-YUAN
TITLE OF INVENTION: EXPRESSION
FILE REPERBURE: 0842.0002-00000
CURRENT APPLICATION NUMBER: 108/10/614,283
CURRENT APPLICATION NUMBER: 60/394,269
PRIOR FILING DATE: 2003-07-08
PRIOR APPLICATION NUMBER: 60/394,269
NUMBER OF SEQ ID NOS: 1
SOFTWARE: Patentin Ver: 3.2
SEQ ID NO 1
LENGTH: 709
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  Score 25; DB 9; Length 660; Pred. No. 0.039;
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Pred. No. 0.039;
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Query Match
100.0%; Score 25; DB
Best Local Similarity 100.0%; Pred. No. 0.0
Matches 25; Conservative 0; Mismatches
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Publication No. US20050112095A1
GENERAL INPORMATION:
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ORGANISM: Coxsackievirus B3
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ORGANISM: Enterovirus 71
                                                                                                                                                                                                                                                   -10-614-283-1/c
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PRIOR APPLICATION NUMBER: US 60/335,539

RESULT 41

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Gaps

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Query Match 96.0%; Score 24; DB 9; Length 70; Best Local Similarity 100.0%; Pred. No. 0.13; Matches 24; Conservative 0; Mismatches 0; Indels
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GENERAL INFORMATION:
APPLICANT: Genetics & IVF
APPLICANT: MARIAN', Brian D.
TITLE OF INVENTION: ENTEROVIRUS PRIMERS AND PROBES
TITLE REFERENCE: 04395-0121
CURRENT APPLICATION NUMBER: US/10/829,474
CURRENT FILING DATE: 2004-04-22
NUMBER OF SEQ ID NOS: 57
SOQ ID NO S: SQ ID NOS: 57
LENGTH: 25
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APPLICANT: Genetics & IVF
TITLE OF INVENTION: Brian D.
TITLE OF INVENTION: BASSEA.
FILE REPERENCE: 043956-0121
CURRENT PELICATION NUMBER: US/10/829,474
CURRENT FILING DATE: 2004-04-22
NUMBER OF SEQ ID NOS: 57
SOFTWARE: Patentin version 3.2
SEQ ID NO 56
LENGTH: 26
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10S-10-829-474-5
Sequence 5, Application US/10829474
Publication No. US20050239055A1
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| LOCATION: (19)..(19)
| OTHER INFORMATION: r = a or g
| US-10-829-474-5
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Best Local Similarity 88.0%;
Matches 22; Conservative
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NAME/KEY: misc feature
LOCATION: (9)...(9)
OTHER INFORMATION: r = a or ()
PEATURE:
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LOCATION: (9)..(9)
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Sequence 4, Application US/10295787D

Bublication No. US20050202414A1

GENERAL INFORMATION:

APPLICANT: The Regents of The University of California

APPLICANT: The Regents of The University of California

APPLICANT: Jia, Xi Yu

APPLICANT: Jiles, Jaremiah G

TITLE OF INVENTION: APPARATUS AND METHODS FOR DETECTING A PATHOGEN IN A SAMPLE

FILE REFERENCE: UGIVN--015A

CURRENT FILING DATE: 2002-11-15

PRIOR APPLICATION NUMBER: US 60/335,539

PRIOR APPLICATION NUMBER: US 60/335,539

PRIOR PILING DATE: 2001-11-15

SOFTWARE: PatentIn version 3.3

SEQ ID NO 8

LENGTH: 70
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APPLICANT: Dia, Xi Yu
APPLICANT: Berger, Martina M
APPLICANT: Berger, Martina M
APPLICANT: Tilles, Jeremiah G
TITLE OF INVENTION: APPARATUS AND METHODS FOR DETECTING A PATHOGEN IN A SAMPLE FILE REFERENCE: UCIVN--015A
CURRENT APPLICATION NUMBER: US/10/295,787D
CURRENT FILING DATE: 2002-11-15
PRIOR FILING DATE: 2001-11-15
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Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 24; Conservative 0; Mismatches
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                        NUMBER OF SEQ ID NOS: 113
SOFTWARE: Patentin version 3.3
SEQ ID NO 28
LENGTH: 66
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SOFWARE: Patentin version 3.3
SEQ ID NO 15
LENGTH: 70
    PRIOR FILING DATE: 2001-11-15
                                                                                                                                                                                                                                                               Conservative
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US-10-295-787D-4
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US-10-295-787D-15
                                                                                                                                             ; ORGANISM: Echovirus 27
US-10-295-787D-28
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nes 24; Conserv
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                                                                                                                         TYPE: DNA
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Best Local
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OTHER INFORMATION: Chemically synthesized probe for enteroviral RNA
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Pred. No. 0.16;
3; Mismatches 0; Indels
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CURRENT APPLICATION NUMBER: US/10/295,787D CURRENT FILING DATE: 2002-11-15
      CURRENT FILING DATE: 2002-11-15
PRIOR APPLICATION NUMBER: US 60/335,539
PRIOR FILING DATE: 2001-11-15
NUMBER OF SEQ ID NOS: 113
SEQ ID NO 21
LENGTH: 70
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96.0%;
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Best Local Similarity 96.0%;
Matches 24; Conservative
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; ORGANISM: Echovirus 12
US-10-295-787D-21
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Best Local Similarity
Matches 24; Conserv
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US-10-295-787D-23
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APPLICANT: Tilles, Jeremiah G
TITLE OF INVENTION: APPRARATUS AND METHODS FOR DETECTING A PATHOGEN IN A SAMPLE
FILE REFERENCE: UCIVN--015A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Genetics & IVF
APPLICANT: MARIANI, Brian D.
TITLE OF INVENTION: ENTEROVIRUS PRIMERS AND PROBES
FILE REPERENCE: 043956-0121
CURRENT APPLICATION NUMBER: US/10/829,474
CURRENT FILING DATE: 2004-04-22
                                                                                                                                                                                                                                                                          3; Mismatches
                                                                                                                                                                                                                                  Score 23.8;
Pred. No. 0.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 57 SOFTWARE: Patentin version 3.2 SEQ ID NO 57 LENGTH: 26
                                                          COCATION: (15)...(15)
COCATION: (15)...(15)
COTHER INFORMATION: r = a or g
FEATURE:
NAME/KEY: misc_feature
LOCATION: (19)...(19)
COTHER INFORMATION: r = a or g
US-10-829-474-56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; LOCATION: (20)^{-}. (20)
; OTHER INFORMATION: r = a \text{ or } g
US-10-829-474-57
                                                                                                                                                                                                                                Query Match
Best Local Similarity 88.0%;
Matches 22; Conservative
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ORGANISM: Artificial Sequence
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OTHER INFORMATION: r = a or g
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LOCATION: (16)..(16)
OTHER INFORMATION: r = a or
OTHER INFORMATION: r = a or
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                                             NAME/KEY: misc_feature
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APPLICANT: The Regents of The University of California
APPLICANT: The Regents of The University of California
APPLICANT: Jia, Xi Yu
APPLICANT: Berger, Martina M
APPLICANT: Tilles, Jeremiah G
TITLE OF INTERNATION: APPARATUS AND METHODS FOR DETECTING A PATHOGEN IN A SAMPLE FILE REFERENCE: UCIVN--015A
CURRENT APPLICATION NUMBER: US/10/295,787D
CURRENT APPLICATION NUMBER: US 60/335,539
PRIOR APPLICATION NUMBER: US 60/335,539
PRIOR FILING DATE: 2001-11-15
NUMBER OF SEQ ID NOS: 113
SEQ ID NO 23
LENGTH: 70
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APPLICANT: Jia, Xi Yu
APPLICANT: Jia, Xi Yu
APPLICANT: Jiles, Jereniah M
APPLICANT: Tilles, Jereniah M
TITLE OF INVENTION: APPARATUŞ AND METHODS FOR DETECTING A PATHOGEN IN A SAMPLE
TITLE OF INVENTION: APPARATUŞ AND METHODS FOR DETECTING A PATHOGEN IN A SAMPLE
CURRENT APPLICATION NUMBER: US/10/295, 787D
CURRENT FILING DATE: 2002-11-15
PRIOR APPLICATION NUMBER: US 60/335, 539
PRIOR FILING DATE: 2001-11-15
NUMBER OF SEQ ID NOS: 113
SEQ ID NOS: 13
LENGTH: 70
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0.25;
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Pred. No. 0.25
0; Mismatches
Pred. No. 0.25
0; Mismatches
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Sequence 0, Application US/10295787D

Sequence 0, Application US/10295787D

Publication No. US20050202414A1

GENERAL INFORMATION:

APPLICANT: The Regents of The University of California

APPLICANT: Tiles Wartina M

APPLICANT: Tiles Wartina M

TITLE OF INVENTION: APPRARATUS AND METHODS FOR DETECTING A PATHOGEN IN A SAMPLE

CURRENT APPLICATION NUMBER: US/10/295,787D

CURRENT PELING DATE: 2002-11-15

PRIOR APPLICATION NUMBER: US 60/335,539

PRIOR FILING DATE: 2001-11-15

NUMBER OF SEQ ID NOS: 113

SOFTWARE: Patentin version 3.3

SEQ ID NO 8

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Pred. No. 0.25;
0; Mismatches 1; Indels
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Publication No. US20050158710A1
GENERAL INPORMATION:
APPLICANT: TSANG, SHIRLEY
APPLICANT: PRICE, JAMES A.
TILLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID
FILE REFERENCE: 020187.0187PTUS
CURRENT APPLICATION UNBER: US/10/760,048
CURRENT FILING DATE: 2004-01-16
NUMBER OF SEQ ID NOS: 67
SOCTWARRE: Patentin Ver. 3.2
SEQ ID NO 39
LENGTH: 117
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      1 TCCGCTGCAGAGTTACCGTTACGA 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    93.6%;
96.0%;
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Matches 24; Conservative
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Best Local Similarity
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US-10-760-048-40/c
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US-10-760-048-39/c
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US-10-295-787D-8
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publication No. US2000202414A1

GENERAL INFORMATION:

APPLICANT: THE REGENTE Of The University of California

APPLICANT: The Regents of The University of California

APPLICANT: Tiles, Jeremiah G

TILE OF INVENTION: APPARATUS AND METHODS FOR DETECTING A PATHOGEN IN A SAMPLE

FILE REFERENCE: UCIVN--015A

CURRENT APPLICATION NUMBER: US/10/295,787D

CURRENT APPLICATION NUMBER: US/0295,787D

CURRENT APPLICATION NUMBER: US/0335,539

PRIOR PILING DATE: 2001-11-15

NUMBER OF SEQ ID NOS: 113

SOFTWARE: Patentin version 3.3

SEQ ID NO 112

LENGTH: 70
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APPLICANT: Jia, Xi Yu
APPLICANT: Jia, Xi Yu
APPLICANT: Jia, Xi Yu
APPLICANT: Beger, Martina M
APPLICANT: Berger, Martina M
APPLICANT: Berger, Martina M
APPLICANT: Tilles, Jeremiah G
TITLE OF INVENTION: APPARATUS AND METHODS FOR DETECTING A PATHOGEN IN A SAMPLE
TILE REPRENCE: UGINV--015A
CURRENT APPLICATION NUMBER: US/10/295,787D
CURRENT PILING DATE: 2002-11-15
PRIOR PEPLICATION NUMBER: US 60/335,539
PRIOR FILING DATE: 2001-11-15
NUMBER OF SEQ ID NOS: 113
SEQ ID NO 17
LENGTH: 71
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Pred. No. 0.25;
0; Mismatches 1; Indels
                                                                                                ; DB 9; Length 70;
0.25;
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                                                                                                                                                              1; Indels
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                                                                                                93.6%;
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il Similarity 96.0%;
24; Conservative
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US-10-295-787D-112
                                                                Query Match
Best Local Similarity 96.0.
; ORGANISM: Ev sp virus
US-10-295-787D-31
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; ORGANISM: Echovirus
US-10-295-787D-17
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Best Local Similarity
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US-10-295-787D-112
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US-10-295-787D-17
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Length 236;
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                                                                                                     OTHER INFORMATION: 5'untranslated polynucleotide sequence US-10-760-048-49
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: TSANG, SHIRLEY
APPLICANT: TSANG, SHIRLEY
APPLICANT: PRICE, JAMES A.
APPLICANT: HELLYER, TOBIN J.
TITLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID
FILE REFERENCE: 020187.0187PUS
CURRENT APPLICATION NUMBER: US/10/760,048
CURRENT FILING DATE: 2004-01-16
NUMBER OF SEQ ID-NOS: 67
SOFTWARE: PATENTIN Ver. 3.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: PICE, JARGES A. APPLICANT: PICE, JARGES A. APPLICANT: HELLYER, TOBIN J. TITLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID FILE REFERENCE: 020187.0187PTUS CURRENT APPLICATION NUMBER: US/10/760,048
CURRENT PILING DATE: 2004-01-16
NUMBER OF SEQ ID NOS: 67
SOFTWARE: PATENTIN Ver. 3.2
SEQ ID NO 51
ENROFTH: 236
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Publication No. US20050158710A1
GENERAL INFORMATION:
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; Sequence 50, Application US/10760048
; Publication No. US20050158710A1
; GENERAL INFORMATION:
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Best Local Similarity 96.0%;
Matches 24; Conservative
                                                                                                                                                                                                     Query Match
Best Local Similarity 96.0%;
Matches 24; Conservative
                            TYPE: DNA
ORGANISM: Unknown Organism
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ORGANISM: Unknown Organism
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ORGANISM: Unknown Organism
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LENGTH: 236
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Publication No. US20050158710A1
GENERAL INFORMATION:
APPLICANT: TRANG, SHIRLEY
APPLICANT: PRICE, JAMES A.
APPLICANT: PRICE, JAMES A.
TILLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID
FILE REFERENCE: 020187.0187PTUS
CURRENT APPLICATION NUMBER: US/10/760,048
CURRENT FILING DATE: 2004-01-16
NUMBER OF SEQ ID NOS: 67
SOFTWARE: Patentin Ver. 3.2
                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: Description of Unknown Organism: Viral; OTHER INFORMATION: 5'untranslated polynucleotide sequence US-10-760-048-40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: Description of Unknown Organism: Viral OTHER INFORMATION: 5'untranslated polynucleotide sequence US-10-760-048-37
APPLICANT: PRICE, JAMES A.

APPLICANT: HELLYER, TOBIN J.

TITLE OF INVENTION DETECTION OF ENTEROVIRUS NUCLEIC ACID
FILE REFERENCE: 0.20187.0187PTUS
CURRENT APPLICATION NUMBER: US/10/760,048
CURRENT PILING DATE: 2004-01-16
NUMBER OF SEQ ID NOS: 67
SOFTWARE: Patentin Ver. 3.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: TOTAING, SHIRLEY
APPLICANT: PRICE, JAMES A.
APPLICANT: PRICE, JAMES A.
APPLICANT: HELLYSK, TOBIN J.
TITLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID
FILE REFERENCE: 020187.0187PTUS
CURRENT PRILIGE DATE: 2004-01-16
NUMBER OF SEQ ID NOS: 67
SEQ ID NOS: 67
SEQ ID NO 37
LENGTH: 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 TCCGCTGCAGAGTTGCCCGTTACGA 25
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Publication No. US20050158710A1
GENERAL INFORMATION:
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Best Local Similarity 96.0%;
Matches 24; Conservative (
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ORGANISM: Unknown Organism
                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Unknown Organism
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Matches 24; Conservative
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                                                                                                                                                                                                   SEQ ID NO 40
LENGTH: 117
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us-10-829-474-4.rnpbm

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TYPE: DNA
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Publication No. US20050158710A1

GENERAL INFORMATION:

APPLICANT: TSANG, SHIRLEY

APPLICANT: TRANG, JAMES A.

APPLICANT: HELLYER, TOBIN J.

TITLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID

FILE REFERENCE: 020187.0187PTUS

CURRENT APPLICATION NUMBER: US/10/760,048

CURRENT FILING DATE: 2004-01-16

NUMBER OF SEQ ID NOS: 67

SOFTWARE: Patentin Ver. 3.2
                           1; Indels
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                                                                                                                                                                                                                                                                              APPLICANT: TSAME, SHIRLEY
APPLICANT: TSAME, SHIRLEY
APPLICANT: PRICE, JAMES A.
APPLICANT: HELLYER, TOBIN J.
TITLE CAN THELLYER, TOBIN J.
FILE REFERENCE: 020187.0187PUS
CURRENT APPLICATION NUMBER: US/10/760,048
CURRENT FILING DATE: 2004-01-16
NUMBER OF SEQ. ID NOS: 67
SOFTWARE: PATENTIN Ver. 3.2
  96.0%; Pred. No. 0.24;
                        0; Mismatches
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                                                                                            75 TCCGCTGCAGAGTTGCCCATTACGA 51
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                                                                                                                                                                                                                 ; Sequence 44, Application US/10760048; Publication No. US20050158710A1; GENERAL INFORMATION:
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ORGANISM: Unknown Organism
                        24; Conservative
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ORGANISM: Unknown Organism
Best Local Similarity
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US-10-760-048-44/c
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US-10-760-048-45/c
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LENGTH: 237
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LENGTH: 237
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RESULT 63

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GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GUILLOT, Emmanuelle
APPLICANT: GUILLOT, Emmanuelle
APPLICANT: GUILLOT, Emmanuelle
APPLICANT: WAGNIN, Carole
APPLICANT: WARBILAT, GUY
APPLICANT: WARBER, GUY
APPLICANT: WARBER, GUY
APPLICANT: WARBER, GUY
APPLICANT: WARBER, Philippe
ITILE OF INVENTION: MEDIUM AND KIT THEREPOR
ITILE OF INVENTION: MEDIUM AND KIT THEREPOR
ITILE OF INVENTION: WEDIUM AND KIT THEREPOR
ITILE OF INVENTION: WAS 1003-09-24
CURRENT APPLICATION NUMBER: DCT/FR01/02191
PRIOR APPLICATION NUMBER: PCT/FR01/02191
PRIOR APPLICATION NUMBER: FR00-08839
PRIOR FILING DATE: 2000-07-06
PRIOR APPLICATION NUMBER: PCT/FR01/02191
PRIOR APPLICATION NUMBER: PCT/FR01/02191
PRIOR APPLICATION NUMBER: PCT/FR01/02191
PRIOR APPLICATION NUMBER: PCT/FR01/02191
PRIOR FILING DATE: 2000-07-06
NUMBER OF SEQ ID NOS: 108
SOFTWARE: PATENTING DATE: 2000-07-06
NUMBER OF SEQ ID NOS: 108
SOFTWARE: PATENTING DATE: 2000-07-06
NUMBER OF SEQ ID NOS: 108
SOFTWARE: PATENTING DATE: 2000-07-06
NUMBER OF SEQ ID NOS: 108
SOFTWARE: PATENTING DATE: 2000-07-06
NUMBER OF SEQ ID NOS: 108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           93.6%; Score 23.4; DB 9; Length 238; 96.0%; Pred. No. 0.24;
Sequence 33, Application US/10760048
Publication No. US20050158710A1
GENERAL INFORMATION:
APPLICANT: TSANG, SHIRLEY
APPLICANT: HELLYER, JAMES A.
TITLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID
FILE REFERENCE: 020187. 0187PTUS
CURRENT APPLICATION UNBER: US/10/760,048
CURRENT FILING DATE: 2004-01-16
NUMBER OF SEQ ID NOS: 67
SOFTWARE: Patentin Ver. 3.2
SEQ ID NO 33
LENGTH: 238
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96.0%;
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US-10-332-123-55
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Best Local Similarity 96.04
Matches 24, Conservative
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ORGANISM: Unknown Organism
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Best Local Similarity
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US-10-829-474-38
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ORGANISM: Artificial Sequence FEATURE:
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Tsai, Chuan-Mei
Wang, Yih-Weng
Hsiao, Heiung
Bair, Chi-Horng
Wang, Shin-Hwan
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Best Local Similarity
Matches 23; Conserv
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nes 20; Conserv
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0.4;
                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
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APPLICANT: MARIANI, Brian D.
TITLE OF INVENTION: ENTEROVIRUS PRIMERS AND PROBES FILE REPERENCE: 043956-0121
CURRENT APPLICATION NUMBER: US/10/829,474
CURRENT FILING DATE: 2004-04-22
NUMBER OF SEQ ID NOS: 57
SOFTWARE: Patentin version 3.2
SEQ ID NO 39
LENGTH: 23
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APPLICANT: Genetics & IVF
APPLICANT: MARIANI, Brian D.
TITLE OF INVENTION: ENTEROVIRUS PRIMERS AND PROBES
FILE REPERENCE: 041956-0121
CURRENT APPLICATION NUMBER: US/10/829,474
CURRENT FILING DATE: 2004-04-22
                                                          APPLICANT: MARIANI, Brian D.
TITLE OF INVENTION: ENTEROVIRUS PRIMERS AND PROBES
FILE REPERENCE: 043956-0121
CURRENT APPLICATION NUMBER: US/10/829,474
NUMBER OF SEQ ID NOS: 57
SOFTWARE: Patentin version 3.2
                                                                                                                                                                                                                                                                                                                                                              Query Match 92.0%; Score 23; DB Best Local Similarity 100.0%; Pred. No. 0.4 Matches 23; Conservative 0; Mismatches
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Publication No. US20050239055A1
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Publication No. US20050239055A1
Publication No. US20050239055A1
GENERAL INFORMATION:
APPLICANT: Genetics & IVF
                                                                                                                                                                                                                                          TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Artificial Sequence FEATURE:
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SOFTWARE: Patentin version 3.2
SEQ ID NO 41
LENGTH: 23
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Matches 23; Conserv
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                                                                                                                                                                                                   SEQ ID NO 38
LENGTH: 23
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Gaps
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; OTHER INFORMATION: Chemcially synthesized probe for enteroviral RNA US-10-829-474-41
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OTHER INFORMATION: Chemically synthesized probe for enteroviral RNA
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                                                                        Length 23
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APPLICANT: Genetics & IVF
APPLICANT: MARIANI, Brian D.
TITLE OF INVENTION: ENTEROVIRUS PRIMERS AND PROBES
FILE REPRENCE: 043956-0121
CURRENT APPLICATION NUMBER: 204-04-22
NUMBER OF SEQ ID NOS: 57
SOFTWARE: Patentin version 3.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: BIOMOLECULB-BOUND SUBSTRATES FILE REFERENCE: 12674-002002
CURRENT APPLICATION NUMBER: US/10/408,519
CURRENT FILING DATE: 2003-04-07
PRIOR APPLICATION NUMBER: US 09/522,417
PRIOR FILING DATE: 2000-03-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     92.0%; Score 23; DB 6; ilarity 80.0%; Pred. No. 0.39; Conservative 5; Mismatches
                                                                   Score 23; DB 9;
Pred. No. 0.4;
0; Mismatches
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2.
LENGTH: 58
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                                                                                                                                                                                                                                                                                                                                      Sequence 2, Application US/10408519
Publication No. US20030228683A1
                                                                                              1 Similarity 100.0%; Pi 23; Conservative 0;
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NAME/KEY: misc_feature
LOCATION: (8)..(8)
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Sequence 44, Application US/10829474; Publication No. US20050239055A1; GENERAL INFORMATION:
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                                                                                                                                        TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                OTHER INFORMATION: Probe US-10-366-823-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; ORGANISM: echovirus 2
US-10-295-787D-13
  CURRENT FILING DATE:
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APPLICANT: Hsiung, Chao Agnes
APPLICANT: Lin, Chung-Yen
TITLE OF INVENTION: CROSS-SPECIES NUCLEIC ACID PROBES
FILE REPERENCE: 12563-006001
CURRENT APPLICATION NUMBER: US/10/366,823
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APPLICANT: Genetics & IVF
APPLICANT: Genetics & IVF
APPLICANT: Genetics & IVF
TITLE OF INVENTION: ENTEROVIEUS PRIMERS AND PROBES
FILE REFERENCE: 043956-0121
CURRENT APPLICATION NUMBER: US/10/829,474
CURRENT FILING DATE: 2004-04-22
NUMBER OF SEQ ID NOS: 57
SOFTWARE: Patentin version 3.2
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                                                                                                                                                                                                                                                         3; Mismatches
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Best Local Similarity 87.5%; Pred. No. 0.5
Matches 21; Conservative 3; Mismatches
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US-10-829-474-53
Sequence 53, Application US/10829474
Publication No. US20050239055A1
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LOCATION: (9)...(9)
OTHER INFORMATION: r = a or g
FEATURE:
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                                                                                                                                                       OTHER INFORMATION: r = a or g
US-10-829-474-52
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LOCATION: (15)...(15)
OTHER INFORMATION: r = a or
                                  NAME/KEY: misc_feature
LOCATION: (14)...(14)
OTHER INFORMATION: r = a or
OTHER INFORMATION: r = a
                                                                                                FEATURE:
NAME/KEY: misc_feature
LOCATION: (18)..(18)
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LENGTH: 24
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PRIOR LING DATE: 100.20.20-15

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1 WARREN OF SED ID NOS: 6

2 WARREN INCORPORATION: Probe 1

2 WARREN INCORPORATION: Probe 2

2 WARREN INCORPORATION: Probe 3

3 WARREN INCORPORATION: Probe 4

3 WARREN INCORPORATION: Probe 5

3 WARREN INCORPORATION: Probe 6

3 WARREN INCORPORATION: Probe 6

3 WARREN INCORPORATION: Probe 7

3 WARREN INCORPORATION: Probe 7

4 WARREN INCORPORATION: Probe 7

5 WARREN INCORPORATION: WARREN INCORPORATION AND MATHOOS FOR DETECTING A PARTICION IN A SAMPLE AND INCORPORATION AND WARREN WARR
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Query Match
87.2%; Score 21.8;
Best Local Similarity 87.0%; Pred. No. 1...
Matches 20; Conservative 3; Mismatche
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                      Query Match 87.2%;
Best Local Similarity 87.0%;
Matches 20; Conservative
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OTHER INFORMATION: r = a or g
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ORGANISM: Artificial Sequence
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OTHER INFORMATION: r = a or
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LENGTH: 23
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LENGTH: 23
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US-10-829-474-45
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                                                DB 9; Length 22;
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APPLICANT: Genetics & IVF
TITLE OF INVENTION: BNIEROVIRUS PRIMERS AND PROBES
FILE REFERENCE: 04395-0121
CURRENT APPLICATION NUMBER: US/10/829,474
CURRENT FILING DATE: 2004-04-22
NUMBER OF SEQ ID NOS: 57
SOFTWARE: Patentin version 3.2
SEQ ID NO 48
LENGTH: 23
                                                                                                                                                                                                                                                                                                                                           APPLICANT: Genetics & IVF
APPLICANT: MARLANI, Brian D.
TITLE OF INVENTION: ENTEROVIRUS PRIMERS AND PROBES
FILE REFERENCE: 043956-0121
CURRENT APPLICATION NUMBER: US/10/829,474
CURRENT FILING DATE: 2044-04-22
NUMBER OF SEQ ID NOS: 57
SSOFTWARE: Patentin version 3.2
LENGTH: 22
LENGTH: 22
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100.0%; Pred. No. ...
0; Mismatches
                                        88.0%; Score 22; DB 100.0%; Pred. No. 1.2 :ive 0; Mismatches
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Publication No. US20050239055A1
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; Publication No. US20050239055A1
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LOCATION: (19)...(19)

CTHER INFORMATION: r = a or

US-10-829-474-48
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INFORMATION: r = a or
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Best Local Similarity 100°.
Matches 22; Conservative
                                        Query Match 88.0
Best Local Similarity 100.
Matches 22; Conservative
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LOCATION: (15)..(15)
OTHER INFORMATION: r =
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US-10-829-474-44
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Score 21.8; DB 9; Length 23; Pred. No. 1.5; 3; Mismatches 0; Indels
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Sequence 49, Application US/10829474

Sequence 49, Application US/10829474

PUBLICATION NO. US20050239055A1

GENERAL INFORMATION:
APPLICANT: Genetics & IVF

TITLE OF INTERPOYING FRIMERS AND PROBES

FILE REFERENCE: 043956-0121

CURRENT APPLICATION NUMBER: US/10/829,474

CURRENT FILING ADTE: 2004-04-22

NUMBER OF SEQ ID NOS: 57

SOFTWARE: Patentin version 3.2
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Sequence 51, Application US/10829474

Publication No. US20050239055A1

GENERAL INFORMATION:
APPLICANT: Genetics & IVF

TITLE OF INVENTION: BYTHEROURUS PRIMERS AND PROBES

FILE REFERENCE: 043956-0121

CURRENT APPLICATION NUMBER: US/10/829,474

CURRENT FILING DATE: 2004-04-22

NUMBER OF EXQ ID NOS: 57

SOFTWARE: PatentIn version 3.2
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Pred. No. 1.5;
0; Mismatches 2; Indels
                                                                  Score 21.8; DB 9; Length 70;
Pred. No. 1.5;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                       Sequence 52, Application US/10760048
Publication No. US20050158710A1
GENERAL INFORMATION:
APPLICANT: TSANG, SHIRLEY
APPLICANT: TSANG, SHIRLEY
APPLICANT: TRICE, JAMES A.
TITLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID
FILE REFERENCE: 020187.0187PTUS
CURRENT APPLICATION UNBER: US/10/760,048
CURRENT FILING DATE: 2004-01-16
NUMBER OF SEQ ID NOS: 67
SOUTHARRE: Patentin Ver. 3.2
SEQ ID NO 52
LENGTH: 110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; OTHER INFORMATION: Description of Unknown Organism: Viral; OTHER INFORMATION: 5'untranslated polynucleotide sequence US-10-760-048-52
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APPLICANT: FRICE, JAMES A.
APPLICANT: FRICE, JAMES A.
APPLICANT: HELLYER, TOBIN J.
TITLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID
FILE REFERENCE: 020187.0187PTUS
CURRENT FILING DATE: 2004-01-16
NUMBER OF SEQ ID NOS: 67
SOFTWARE: PATENTIN Ver. 3.2
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Publication No. US20050158710A1
GENERAL INFORMATION:
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Best Local Similarity 92.0%;
Matches 23; Conservative
                                                                    Query Match 87.2%;
Best Local Similarity 92.0%;
Matches 23; Conservative
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ORGANISM: Unknown Organism
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  ; ORGANISM: Echovirus
US-10-295-787D-29
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LENGTH: 235
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**Publication No. US20050202414A1

**Publication No. US20050202414A1

**GENERAL INFORMATION:

**APPLICANT: The Regents of The University of California

**APPLICANT: Dis, Xi Yu

**APPLICANT: Tiles, Jeremiah G

**TITLE OF INVENTION: APPRATUS AND METHODS FOR DETECTING A PATHOGEN IN A SAMPLE

**FILE REFERENCE: UCIVN--015A

**CURRENT PLING DATE: 2002-11-15

**PRIOR APPLICATION NUMBER: US 60/335,539

**PRIOR APPLICATION NUMBER: US 60/335,539

**PRIOR PILING DATE: 2001-11-15

**NUMBER OF SEQ ID NOS: 113

**SOFTWARE: PatentIn version 3.3

**SOFTWARE: PatentIn version 3.3

**SEQ ID NOS:

**TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: IN CAPACION APPLICANT: Jia, Xi Yu
APPLICANT: Jia, Xi Yu
APPLICANT: Breger, Martina M
APPLICANT: Breger, Martina M
APPLICANT: Tilles, Jeremiah G
TITLE OF INVENTION: APPARATUS AND METHODS FOR DETECTING A PATHOGEN IN A SAMPLE
FILE REPERENCE: UCIVA-015A
CURRENT APPLICATION NUMBER: US/10/295, 787D
FILE REPERICANT: S002-11-15
PRIOR APPLICATION NUMBER: US 60/335,539
PRIOR PAPLICATION NUMBER: US 60/335,539
PRIOR PAPLICATION NUMBER: US 60/335,539
PRIOR FILING DATE: 2001-11-15
NUMBER OF SEQ ID NOS: 113
SSC TWARRE: PARCENTIN VERSION 3.3
SSC TWARRE: PARCENTIN VERSION 3.3
SSC TWARRE: PARCENTIN VERSION 3.3
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                                                                                                                                                                                                                                                                                                                                    0; Indels
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Pred. No. 1.5;
3; Mismatches 0;
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                                         FEATURE:
NAME/KEY: misc feature
LOCATION: (14) - (14)
OTHER INFORMATION: r = a or g
FEATURE:
NAME/KEY: misc feature
LOCATION: (18) - (18)
OTHER INFORMATION: r = a or g
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Best Local Similarity 87.0%;
Matches 20; Conservative
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LOCATION: (8)..(8)
OTHER INFORMATION: r =
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DB 9; Length 238;
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Publication No. US20050158710A1

GENERAL INFORMATION:
APPLICANT: TSANG, SHIRLEY
APPLICANT: FRICK, JAMES A.
APPLICANT: HELLYER, TOBIN J.
TITLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID
FILE REPERSINCE: 020187.0187PTUS
CURRENT APPLICATION NUMBER: US/10/760,048
NUMBER OF SEQ ID NOS: 67
SOFTWARE: PATCHIIN OF: 3.2
SEQ ID NO 36
                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: Description of Unknown Organism: Viral; OTHER INFORMATION: 5'untranslated polynucleotide sequence US-10-760-048-34
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                        APPLICANT: HELLYER, TOBIN J.
TITLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID
FILE REFERENCE: 020187.01877FUG
CURRENT APPLICATION NUMBER: US/10/760,048
CURRENT PILING DATE: 2004-01-16
NUMBER OF SEQ ID NOS: 67
SEQ ID NOS: 67
SEQ ID NO 34
LENGTH: 238
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APPLICANT: HELLYER, TOBIN J.
TITLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID
FILE REPERENCE: 020187.0187PTUS
CURRENT APPLICATION NUMBER: US/10/760,048
CURRENT FILING DATE: 2004-01-16
NUMBER OF SEQ ID NOS: 67
SOFTWARE: Patentin Ver. 3.2
SEQ ID NO 35
LENGTH: 238
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Pred. No. 1.4;
0; Mismatches
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Publication No. US20050158710A1
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Best Local Similarity 92.0%;
Matches 23; Conservative
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GENERAL INFORMATION:
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ORGANISM: Unknown Organism
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Matches 23; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Description of Unknown Organism: Viral 5'untranslated polynucleotide sequence
                                                                                                                                                                                                   APPLICANT: PRICE, JAMES A.
APPLICANT: HELLYER, TOBIN J.
TITLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID FILE REPRENDENCE: 0.2019/10.137PTUS
CURRENT APPLICATION NUMBER: US/10/760,048
CURRENT FILING DATE: 2004-01-16
NUMBER OF SEQ ID NOS: 67
SOFTWARE: Patentin Ver. 3.2
SEQ ID NO 21
LENGTH: 237
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APPLICANT: TSANG, SHIRLEY
APPLICANT: PRICE'S
APPLICANT: PRICE'S
APPLICANT: HELLYER, TOBIN J.
TITLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID
FILE REFERENCE: 020187.0187FUS.
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CURRENT FILING DATE: 2004-01-16
NUMBER OF SEQ ID NOS: 67
SOFTWARE: Patentin Ver. 3.2
SEQ ID NO 23
LENGTH: 238
TCCGCTGCAGAGTTACCCATTACGA 51
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Publication No. US20050158710A1
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Publication No. US20050158710A1
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ORGANISM: Unknown Organism
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ORGANISM: Unknown Organism
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APPLICANT: TSANG, SHIRLEY
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Best Local Similarity
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Matches 23; Conserv
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OTHER INFORMATION:
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OTHER INFORMATION: r = a
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LENGTH: 22
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US-10-829-474-40
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OTHER INFORMATION: Chemically synthesized probe for enteroviral RNA
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                                                       PEATURE:
CTHER INFORMATION: Description of Unknown Organism: Viral
CTHER INFORMATION: 5'untranslated polynucleotide sequence
US-10-760-048-36
                                                                                                                                                                                        2; Indels
                                                                                                                                                                                                                                                                                                                                                      Sequence 40, Application US/10829474

Publication No. US20050239055A1

GENERAL INPORMATION:
APPLICANT: MARIANI, Brian D.
TITLE OF INVENTION: ENTEROVIRUS PRIMERS AND PROBES
FILE REFERENCE: 043955-0121

CURRENT APPLICATION NUMBER: US/10/829,474

CURRENT FILING DATE: 2004-04-22

NUMBER OF SEQ ID NOS: 57

SOFTWARE: Patentin version 3.2

SEQ ID NO 40

LENGTH: 21
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APPLICANT: MARIANI, Brian D.
TITLE OF INVENTION: ENTEROVIRUS PRIMERS AND PROBES
FILE REPERENCE: 043956-0121
CURRENT APPLICATION NUMBER: US/10/829,474
CURRENT FILING DATE: 2004-04-22
NUMBER OF SEQ ID NOS: 57
SOFTWARE: Patentin version 3.2
SEQ ID NO 54
                                                                                                                                                 87.2%; Score 21.8; DB
92.0%; Pred. No. 1.4;
iive 0; Mismatches
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ORGANISM: Artificial Sequence
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OTHER INFORMATION: r = a or
                   TYPE: DNA
ORGANISM: Unknown Organism
                                                                                                                                                                                        23; Conservative
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Best Local Similarity
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Matches 21; Conserv
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US-10-829-474-40
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LENGTH: 238
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APPLICANT: The Regents of The University of California
APPLICANT: Jia, Xi Yu
APPLICANT: Jia, Xi Yu
APPLICANT: Jia, Xi Yu
APPLICANT: Tilles, Jeremiah G
TITLE OF INVENTION: APPARATUS AND METHODS FOR DETECTING A PATHOGEN IN A SAMPLE
FILE REFERENCE: UCIVN-015A
CURRENT APPLICATION NUMBER: 105/10/295,787D
CURRENT FILING DATE: 2002-11-15
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                                                                                                                                                      Score 20.8; DB 9; Length 22; Pred. No. 4.7; 3; Mismatches 0; Indels.
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Pred. No. 4.7;
3; Mismatches 0; Indels
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APPLICANT: Genetics & IVF
TITLE OF INVENTION: ENTEROVIRUS PRIMERS AND PROBES
TITLE OF INVENTION: ENTEROVIRUS PRIMERS AND PROBES
TILL SPERENCE: 043956-0121
CURRENT APPLICATION NUMBER: US/10/829,474
NUMBER OF SEQ ID NOS: 57
SOFTWARE: Patentin version 3.2
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PRIOR APPLICATION NUMBER: US 60/335,539
PRIOR FILING DATE: 2001-11-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 24, Application US/10295787D; Publication No. US20050202414A1; GENERAL INFORMATION:
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Sequence 55, Application US/10829474
Publication No. US20050239055A1
GENERAL INFORMATION:
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; OTHER INFORMATION: r = a or g
US-10-829-474-55
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Best Local Similarity 86.4%;
Matches 19; Conservative
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Best Local Similarity 86.4%;
Matches 19; Conservative
                                      NAME/KEY: misc_feature
i_CCATION: (17)...(17)
CTHER INFORMATION: r = a or
US-10-829-474-54
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LOCATION: (8)...(8)
OTHER INFORMATION: r = a or
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OTHER INFORMATION: r = a or
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LOCATION: (14)..(14)
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Pred. No. 8.9;
     ilarity 88.0%; Pred. No. 8.9;
Conservative 0; Mismatches
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88.0%;
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88.0%;
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SOFTWARE: Patentin version 3.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Unknown Organism
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Best Local Similarity 88.0
Matches 22; Conservative
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Best Local Similarity 88.0
Matches 22; Conservative
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     Best Local Similarity
Matches 22; Conser
                                                                                                                                                                           US-10-295-787D-111
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US-10-760-048-38
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LENGTH: 238
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GENERAL INFORMATION

GENERAL INFORMATION

APPLICANT: The Regents of The University of California

APPLICANT: The Reger, Martina M

APPLICANT: Tilles, Jeremiah G

TITLE OF INVENTION: APPRARTUS AND METHODS FOR DETECTING A PATHOGEN IN A SAMPLE
TITLE COF INVENTION: APPLICATION NUMBER: US/10/295, 787D

CURRENT APPLICATION NUMBER: US/10/295, 787D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Jia, Xi Yu
APPLICANT: Berger, Martina M
APPLICANT: Tilles, Jeremiah G
TITLE OF INVENTION: APPARATUS AND METHODS FOR DETECTING A PATHOGEN IN A SAMPLE
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                                                                                                                                                         Length 69;
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APPLICANT: The Regents of The University of California
                                                                                                                                                       DB 9;
                                                                                                                                                                                              0; Mismatches
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                                                                                                                                                       Score 20.8;
Pred. No. 4.
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Pred. No. 4
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CURRENT FILING DATE: 2002-11-15
PRIOR PPLICATION NUMBER: US 60/335,539
PRIOR PILING DATE: 2001-11-15
NUMBER OF SEQ ID NOS: 113
SOFTWARE: Patentin version 3.3
SEQ ID NO 11
LENGTH: 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT FILING DATE: 2002-11-15
PRIOR APPLICATION NUMBER: US 60/335,539
PRIOR FILING DATE: 2001-11-15
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NUMBER OF SEQ ID NOS: 113
SOFTWARE: Patentin version 3.3
SEQ ID NO 24
LENGTH: 69
                                                                                                                                                     Query Match 83.2%;
Best Local Similarity 91.7%;
Matches 22; Conservative
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SOFTWARE: Patentin version 3.3
SEQ ID NO 25
LENGTH: 70
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Best Local Similarity 91.7%;
Matches 22; Conservative
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ORGANISM: Porcine ev virus
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US-10-295-787D-11
                                                                             ; TYPE: DNA
; ORGANISM: Echovirus 5
US-10-295-787D-24
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US-10-295-787D-25
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APPLICANT: The Regents of The University of California
APPLICANT: The Regents of The University of California
APPLICANT: Jia, Xi Yu
APPLICANT: Tiles, Jermina M
APPLICANT: Tiles, Jermina M
APPLICANT: Tiles, Jermina G
TITLE OF INVENTION: APPARATUS AND METHODS FOR DETECTING A PATHOGEN IN A SAMPLE
FILE REPERBURG: UCINA-015A
CURRENT APPLICATION NUMBER: 105/295,787D
CURRENT FILING DATE: 2002-11-15
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  Indels
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APPLICANT: FRICE, JAMES A.
APPLICANT: PRICE, JAMES A.
APPLICANT: HELLYER, TOBIN J.
TITLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID
FILE REPERRUCE: 020187, 0187PTUS
CURRENT APPLICATION NUMBER: US/10/760,048
CURRENT APPLICATION NUMBER: 05/10/760,048
NUMBER OF SEQ ID NOS: 67
SOFTWARE: PATENTIN Ver. 3.2
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Pred. No. 8.7;
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Pred. No. 8.
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PRIOR FILING DATE: 2001-11-15
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                                                                                                                                                                                                ; Sequence 111, Application US/10295787D
; Publication No. US20050202414A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 TCCGCTGCAGAGTTGCCCGTTACGA
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RESULT 95

80.8%; Score 20.2; DB 9; Length 70;

Query Match

us-10-829-474-4.rnpbm

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471 TCCGCCACAGACTTGCGCGTTACGA 447
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                                          Sequence 53, Application US/10332123
Publication No. US20040072239A1
GENERAL INFORMATION:
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Best Local Similarity 87.0°
Matches 20; Conservative
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Matches 21; Conservative
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ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                JS-10-425-114-9634/c
                        JS-10-332-123-53/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 96
US-10-760-048-62/C
; Sequence 62, Application US/10760048
; Publication No. US20050158710A1
; GENERAL INFORMATION:
   APPLICANT: PRICE, JAMES A.
; APPLICANT: PRICE, JAMES A.
; APPLICANT: PRICE, TOBIN J.
; TILLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID
; FILE REFREENCE: 020187.0187PUS
; CURRENT APPLICATION NUMBER: US/10/760,048
; CURRENT FILING DATE: 2004-01-16
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: Patentin Ver. 3.2
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                                                                                 APPLICANT: Genetics & IVF
APPLICANT: MARIANI, Brian D.
TITLE OF INVENTION: ENTEROVIRUS PRIMERS AND PROBES
FILE REPERBENCE: 043956-0121
CURRENT APPLICATION NUMBER: US/10/829,474
NUMBER OF SEQ ID NOS: 57
SOFTWARE: Patentin version 3.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       79.2%; Score 19.8;
85.7%; Pred. No. 14
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                    Sequence 50, Application US/10829474 Publication No. US20050239055Al GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: misc feature
LOCATION: (13)...(13)
OTHER INFORMATION: r = a or g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; LOCATION: (17)...(17); OTHER INFORMATION: r = a or g
US-10-829-474-50
                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc_feature
LOCATION: (7)...(7)
OTHER INFORMATION: r = a or g
FEATURE:
                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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ORGANISM: Unknown Organism
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NAME/KEY: misc_feature
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Best Local Similarity
Matches 18; Conserva
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Best Local Similarity
Matches 21; Conserva
US-10-829-474-50
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LENGTH: 238
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Sequence 9634, Application US/10425114

Sequence 9634, Application US/10425114

Publication No. US20040034888A1

GENERAL INFORMATION:

APPLICANT: Liu, Jingdong

APPLICANT: Liu, Jingdong

APPLICANT: APPLICANT: Acrem E

APPLICANT: Cao, Yongwei

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

TITLE OF INVENTION NUMBER: US/10/425,114

CURRENT APPLICATION NUMBER: US/10/425,114

CURRENT FILING DATE: 2003-04-28

SEQ ID NO 9634

SEQ ID NO 9634

LANDER OF SEQ ID NOS: 73128

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87.0%; Pred. No. 78;
tive 0; Mismatches
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US-10-425-114-9634
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Sequence 2070, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With TILE OF INVENTION: Plants and Uses Thereof for Plant Improvement TILE REFERENCE: 38-21 (53223)
FILE REFERENCE: 38-21 (53223)
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 2070
LENGTH: 1645
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: Clone ID: PAT_MRT3847_101874C.1
US-10-424-599-2070
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CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: UP 99/377484
PRIOR FILING DATE: 1999-12-16
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PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE Patentin ver: 3.0
LENGTH: 1182
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Publication No. US20020197605A1
GENERAL INFORMATION:
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; ORGANISM: Corynebacterium glutamicum
US-09-738-626-2740
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APPLICANT: MIZOGUCHI, HIROSHI
APPLICANT: ANDO, SEIKO
APPLICANT: HAYASHI, MIKIRO
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YOKOI, HARUHIKO
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US-10-424-599-2070/c
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                                                                                                                                                                                             sample which comprises a substrate having multiple microbe identification sites, each having a unique address indicative of the position of that microbe identification site on the substrate and groups of muclaic acid probes disposed at the microbe identification sites, each group being complementary to a target nucleic acid to provide a detectable signal at come or more microbe identification sites. The apparatus is useful for detecting the presence of one or more microbe identification sites. The apparatus is useful for detecting the presence of one or more microbe. The apparatus is particularly useful for clinical diagnosis, research, epidemiological surveillance, bioterrorism countermeasures, environmental pathogen surveys, and monitoring food contaminants. Current testing procedures or devices, such as radioimmunoassays and ELISA, are difficult to implement, time consuming, expensive, outdated, and typically rely on the use of agents that recognise and bind to membrane bound proteins or carbohydrates of the pathogen. These further cannot microbes overcomes these disadvantages. The apparatus is compact, sensitive, and quick to detect the presence of any of a number of any pathogens present in a sample. The present sequence is that of an
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                                                                                                                                                                                   invention relates to a novel apparatus for detecting a microbe in a
                                                                                                        New (microarray) apparatus comprising a substrate with attached nucleic acid probes, useful for detecting one or more microbes in a sample.
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                                                                                                                                                     Claim 16; SEQ ID NO 31; 89pp; English.
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                 (REGC ) UNIV CALIFORNIA
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                                              Jia XY, Berger MA,
                                                                            WPI; 2004-449626/42
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Best Local Similarity
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This invention relates to a novel apparatus for detecting a microbe in a sample which comprises a substrate having multiple microbe identification sites, each having a unique address indicative of the position of that microbe identification site on the substrate and groups of nucleic acid probes disposed at the microbe identification sites, each group being complementary to a target nucleic acid to provide a detectable signal at one or more microbe identification sites. The apparatus is useful for detecting the presence of one or more microbes in a sample, such as virus corviral particle, (non-) pathogenic bacteria, or cellular or accellular microbe. The apparatus is particularly useful for clinical diagnosis, research, epidemiological surveillance, bioterrorism countermeasures, convironmental pathogen surveys, and monitoring food contaminants. Current testing procedures or devices, such as radioimmunosassays and BLISA, are difficult to implement, time consuming, expensive, outdated, and contamination or membrane con
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 bound proteins or carbohydrates of the pathogen. These further cannot assay multiple pathogens. The new apparatus or device for detecting microbes overcomes these disadvantages. The apparatus is compact, sensitive, and quick to detect the presence of any of a number of pathogens present in a sample. The present sequence is that of an oligonucleotide probe which is related to the micorbe detection apparatus
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acid probes, useful for detecting one or more microbes in a sample
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chinical diagnosis; research; epidemiological survaillance;
bioterrorism countermeasure; environmental pathogen survey;
food contaminant; radioimmunoassay; ELISA; probe; ss.
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Tilles JG;
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Berger MA,
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Jia XY,
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This invention relates to a novel apparatus for detecting a microbe in a sample which comprises a substrate having multiple microbe identification sites, each having a unique address indicative of the position of that microbe identification site on the substrate and groups of nucleic acid probes disposed at the microbe identification sites, each group being complementary to a target nucleic acid to provide a detectable signal at one or more microbe identification sites. The apparatus is useful for componentary to a target nucleic acid to provide a detectable signal at one or more microbes in a sample, such as virus comporting the presence of one or more microbes in a sample, such as virus or viral particle, (non-)pathogenic bacteria, or cellular or acellular convironmental pathogen surveys, and monitoring food contaminants. Current testing procedures or devices, such as radioimmunoassays and ELISA, are difficult to implement, time consuming, expensive, outdated, and trypically rely on the use of agents that recognise and bind to membrane conductions or carbohydrates of the pathogen. These further cannot miltiple pathogens. The new apparatus or device for detecting microbes overcomes these disadvantages. The apparatus is compact, sensitive, and quick to detect the present sequence if any of a number of an apparatus or appendent of an apparatus or apparatus of an apparatus or apparatus of an apparatus or apparatus or apparatus of an apparatus or apparatus or apparatus of an apparatus or ap
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                                                                           New (microarray) apparatus comprising a substrate with attached nucleic acid probes, useful for detecting one or more microbes in a sample.
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                                                                                                                                                    Claim 16; SEQ ID NO 20; 89pp; English.
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                        WPI; 2004-449626/42.
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WPI; 2004-449626/42

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This invention relates to a novel apparatus for detecting a microbe in a sample which comprises a substrate having multiple microbe identification of that microbe identification sites, each having a unique address indicative of the position of that microbe identification sites of the position of that corposed at the microbe identification sites, each group being probes disposed at the microbe identification sites, each group being complementary to a target nucleic acid to provide a detectable signal at one or more microbe identification sites. The apparatus is useful for cone or more microbes in a sample, such as virus or viral particle, (non-)pathogenic bacteria, or cellular or acellular microbe. The apparatus is particularly useful for clinical diagnosis, research, epidemiological surveilance, bioterrorism countermeasures, creting procedures or devices, such as radioimmunosassays and ELISA, are difficult to implement, time consuming, expensive, outdated, and creating procedures or devices, such as radioimmunosassays and ELISA, are difficult to implement, time consuming, expensive, outdated, and bound proteins or carbohydrates of the pathogen. These further cannot assay multiple pathogens. The new apparatus or device for detecting microbes overcomes these disadvantages. The apparatus is compact, sensitive, and quick to detect the present equence is that of an under of a number of pathogens present in a sample. The present sequence is that of an opporatus
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                 New (microarray) apparatus comprising a substrate with attached nucleic acid probes, useful for detecting one or more microbes in a sample.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 25; DB 12; Length 70; 100.0%; Pred. No. 0.043;
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cilnical diagnosis; research; epidemiological surveillance;
bioterrorism countermeace; environmental pathogen survey;
food contaminant; radioimmnoassay; ELISA; probe; ss.
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                                                                               Claim 16; SEQ ID NO 18; 89pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               of the invention
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This invention relates to a novel apparatus for detecting a microbe in a

Claim 16; SEQ ID NO 9; 89pp; English.

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This invention relates to a novel apparatus for detecting a microbe in a sample which comprises a substrate having multiple microbe identification altes, each having a unique address indicative of the position of that microbe identification site on the substrate and groups of nucleic acid probes disposed at the microbe identification sites, each group being complementary to a target nucleic acid to provide a detectable signal at one or more microbe identification sites. The apparatus is useful for detecting the presence of one or more microbes in a sample, such as virus or viral particle, (non-)pathogenic bacteria, or cellular or acellular microbe. The apparatus is particularly useful for clinical diagnosis, research, epidemiological surveys, and monitoring food contaminants. Current testing procedures or devices, such as radioimmnossasys and ELISA, are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             oligonucleotide probe which is related to the micorbe detection apparatus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  difficult to implement, time consuming, expensive, outdated, and typically rely on the use of agents that recognise and bind to membrane bound proteins or carbohydrates of the pathogen. These further cannot assay multiple pathogens. The new apparatus or device for detecting
acid probes, useful for detecting one or more microbes in a sample.
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                                                         Claim 16; SEQ ID NO 26; 89pp; English.
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 100.0%; Score 25; DB 12; Length 70; 100.0%; Pred. No. 0.043;
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                                                  1 TCGCTGCAGAGTTGCCCGTTACGA
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Novel microbe detection apparatus-related oligonucleotide probe SeqID9. ADP05504 standard; DNA; 70 BP (first entry) 26-AUG-2004 ADP05504; nicrobe Viruses RESULT 6

detection; microbe identification; virus; viral particle; pathogenic bacterium; cellular microbe; acellular microbè; cilinical diagnosis; research; epidemiological surveillance; bioterrorism countermeasure; environmental pathogen survey; food contaminant; radioimmunoassay; ELISA; probe; ss. WO2004045365-A2 03-JUN-2004

Tilles JG; 23-MAY-2003; 2003WO-US016461 15-NOV-2002; 2002US-00295787 (REGC ) UNIV CALIFORNIA. Berger MA, Jia XY,

New (microarray) apparatus comprising a substrate with attached nucleic acid probes, useful for detecting one or more microbes in a sample. WPI; 2004-449626/42

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sample which comprises a substrate having multiple microbe identification sites, each having a unique address indicative of the position of that microbe identification site on the substrate and groups of nucleic acid probes disposed at the microbe identification sites, each group being complementary to a target nucleic acid to provide a detectable signal at one or more microbe identification sites. The apparatus is useful for detecting the presence of one or more microbes in a sample, such as virus or viral particle, (non-)pathogenic bacteria, or cellular or acellular convirumental pathogen surveyly useful for clinical diagnosis, research, epidemiological surveillance, bioterrorism countermeasures, environmental pathogen surveys, and monitoring food contaminants. Current testing procedures or devices, such as radioimmunosassys and ELISA, are difficult to implement, time consuming, expensive, outdated, and typically rely on the use of agents that recognise and bind to membrane bound proteins or carbohydrates of the pathogen. These further cannot
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                            assay multiple pathogens. The new apparatus or device for detecting microbes overcomes these disadvanteses. The apparatus is compact, sensitive, and quick to detect the presence of any of a number of pathogens present in a sample. The present sequence is that of an
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cilnical diagnosis; research; epidemiological surveillance;
bioterrorism countermeasure; environmental pathogen survey;
food contaminant; radioimmunoassay; ELISA; probe; ss.
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Matches 25; Conservative (
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Sample which comprises a substrate having multiple microbe in a sample which comprises a substrate having multiple microbe identification sites, each having a unique address indicative of the position of that microbe identification site on the substrate and groups of nucleic acid probes disposed at the microbe identification sites, each group being complementary to a target nucleic acid to provide a detectable signal at one or more microbe identification sites. The apparatus is useful for one or more microbes in a sample, such as virus or viral particle, (non-)pathogenic bacteria, or cellular or acellular or viral particle, (non-)pathogenic bacteria, or cellular or acellular or viral particle, (non-)pathogenic bacteria, or cellular or acellular cresearch, epidemiological surveillance, bioterrorism countermeasures, environmental pathogen surveys, and monitoring food contaminants. Current creating procedures or devices, such as radioimmunosasays and ELISA, are difficult to implement, time consuming, expensive, outdated, and typically rely on the use of agents that recognise and bind to membrane assay multiple pathogens. The new apparatus or device for detecting microbes overcomes these disadvantages. The apparatus is compact, such as multiple pathogens. The new apparatus is compact, pathogens present in a sample. The present end any of a number of any of an end of an end of an end of an end of a number of an end of oligonucleotide probe which is related to the micorbe detection apparatus the invention \$

Sequence 70 BP; 13 A; 21 C; 19 G; 17 T; 0 U; 0 Other;

100.0%; Score 25; DB 12; Length 70; 100.0%; Pred. No. 0.043; 0; Indels Mismatches 25 1 rccccrccagacrrcccccrracga 25 1 TCCGCTGCAGAGTTGCCCGTTACGA ö Conservative Query Match Best Local Similarity 25; Matches g ò

ADP05517 standard; DNA; 70 26-AUG-2004 ADP05517; RESULT 8

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Novel microbe detection apparatus-related oligonucleotide probe SeqID22. (first entry)

microbe detection; microbe identification; virus; viral particle; pathogenic bacterium; cellular microbe; acellular microbe; cinical diagnosis; research; epidemiological surveillance; bioterrorism countermeasure; environmental pathogen survey; food contaminant; radioimmunoassay; ELISA; probe; ss.

Viruses.

WO2004045365-A2.

03-JUN-2004.

23-MAY-2003; 2003WO-US016461.

15-NOV-2002; 2002US-00295787.

(REGC ) UNIV CALIFORNIA.

Tilles Jia XY, Berger MA,

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WPI; 2004-449626/42

New (microarray) apparatus comprising a substrate with attached nucleic acid probes, useful for detecting one or more microbes in a sample.

Claim 16; SEQ ID NO 22; 89pp; English.

This invention relates to a novel apparatus for detecting a microbe in a sample which comprises a substrate having multiple microbe identification

microbe identification site on the substrate and groups of nucleic acid probe identification sites, each group soft nucleic acid probes disposed at the microbe identification sites, each group being complementary to a target nucleic acid to provide a detectable signal at one or more microbe identification sites. The apparatus is useful for detecting the presence of one or more microbes in a sample, such as virus or viral particle, (non-)pathogenic bacteria, or cellular or acillular microbe. The apparatus is particularly useful for clinical diagnosis, research, epidemiological surveillance, bioterrorism countermeasures, research, epidemiological surveillance, bioterrorism countermeasures, centing procedures or devices, and monitoring food contaminants. Current testing procedures or devices, and monitoring food contaminants. Current testing procedures or devices, such as radioimmunoassays and Elisa, are typically rely on the use of agents that recognise and bind to membrane bound proteins or carbohydrates of the pathogen. These further cannot assert and the consumination of the pathogen. These further cannot assert and the consumination of the pathogen. These further cannot assert and the consumination of the pathogen. oligonucleotide probe which is related to the micorbe detection apparatus of the invention. microbes overcomes these disadvantages. The apparatus is compact, sensitive, and quick to detect the presence of any of a number of pathogens present in a sample. The present sequence is that of an 

Sequence 70 BP; 8 A; 21 C; 23 G; 18 T; 0 U; 0 Other;

Gaps .. 0 100.0%; Score 25; DB 12; Length 70; 100.0%; Pred. No. 0.043; 0; Indels 0; Mismatches 25; Conservative Local Similarity Query Match Matches

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Gaps

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RESULT 9 ADP05534

ВР ADP05534 standard; DNA; 70

ADP05534;

26-AUG-2004 (first entry)

Novel microbe detection apparatus-related oligonucleotide probe SeqID39.

microbe detection, microbe identification; virus; viral particle, pathogenic bacterium; cellular microbe; acellular microbe; colinical diagnosis, research, epidemiological surveillance; bioterrorism countermeasure; environmental pathogen survey; food contaminant; radioimmunoassay; ELISA; probe; ss. 

Viruses

WO2004045365-A2

03-JUN-2004.

23-MAY-2003; 2003WO-US016461.

15-NOV-2002; 2002US-00295787.

(REGC ) UNIV CALIFORNIA,

Jia XY, Berger MA, Tilles JG;

WPI; 2004-449626/42.

New (microarray) apparatus comprising a substrate with attached nucleic acid probes, useful for detecting one or more microbes in a sample.

Claim 16; SEQ ID NO 39; 89pp; English.

sample which comprises a substrate having multiple microbe identification sites, each having a unique address indicative of the position of that microbe identification site on the substrate and groups of nucleic acid This invention relates to a novel apparatus for detecting a microbe in a

probes disposed at the microbe identification sites, each group being complementary to a target nucleic acid to provide a detectable signal at one or more microbe identification sites. The apparatus is useful for detecting the presence of one or more microbes in a sample, such as virus or viral particle, (non-)pathogenic bacteria, or cellular or acellular microbe. The apparatus is particularly useful for clinical diagnosis, research, epidemiological surveillance, bioterrorism countermeasures, environmental pathogen surveys, and monitoring food contaminants. Current testing procedures or devices, such as radioimmunoassays and ELISA, are difficult to implement, time consuming, expensive, outdated, and typically rely on the use of agents that recognise and bind to membrane bound proteins or carbohydrates of the pathogen. These further cannot microbes overcomes these disadvantages. The apparatus is compact, sensitive, and quick to detect the presence of any of a number of pathogens present in a sample. The present sequence is that of an oligonucleotide probe which is related to the micorbe detection apparatus 858888888888888888888888888

Sequence 70 BP; 11 A; 20 C; 20 G; 19 T; 0 U; 0 Other;

Gaps ö 100.0%; Score 25; DB 12; Length 70; 100.0%; Pred. No. 0.043; Live 0; Mismatches 0; Indels 25; Conservative Local Similarity Query Match Matches

TCCGCTGCAGAGTTGCCCGTTACGA 25 1 TCCGCTGCAGAGTTGCCCGTTACGA 25

RESULT 10

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ADP05503 standard; DNA; 70 BP

ADP05503;

(first entry) 26-AUG-2004

Novel microbe detection apparatus-related oligonucleotide probe SeqID8.

microbe detection, microbe identification, virus, viral particle, pathogenic bacterium; cellular microbe; acellular microbe; clinical diagnosis; research; epidemiological surveillance, bioterrorism countermeasure; environmental pathogen survey; food contaminant; radioimmunoassay; ELISA; probe; ss. ADPOSSO3

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Viruses.

WO2004045365-A2.

03-JUN-2004

23-MAY-2003; 2003WO-US016461

15-NOV-2002; 2002US-00295787

(REGC ) UNIV CALIFORNIA.

Tilles JG Jia XY, Berger MA,

WPI; 2004-449626/42.

New (microarray) apparatus comprising a substrate with attached nucleic acid probes, useful for detecting one or more microbes in a sample. Claim 16; SEQ ID NO 8; 89pp; English.

This invention relates to a novel apparatus for detecting a microbe in a sample which comprises a substrate having multiple microbe identification sites, each having a unique address indicative of the position of that microbe identification site on the substrate and groups of nucleic acid probes disposed at the microbe identification sites, each group being complementary to a target nucleic acid to provide a detectable signal at

one or more microbe identification sites. The apparatus is useful for detecting the presence of one or more microbes in a sample, such as virus or viral particle, (non-)pathogenic bacteria, or cellular or acellular microbe. The apparatus is particularly useful for clinical diagnosis, research, epidemiological surveillance, bioterrorism countermeasures, critical pathogen surveys, and monitoring food contaminants. Current testing procedures or devices; such as radioimmunosasays and ELISA, are difficult to implement, time consuming, expensive, outdated, and crypically rely on the use of agents that recognise and bind to membrane bound proteins or carbohydrates of the pathogen. These further cannot assay multiple pathogens. The new apparatus or device for detecting microbes overcomes these disadvantages. The apparatus is compact, sensitive, and quick to detect the present esquence is that of an unber of pathogens present in a sample. The present sequence is that of an original pathogen which is related to the micorbe detection apparatus ö Gaps ô 100.0%; Score 25; DB 12; Length 70; 100.0%; Pred. No. 0.043; ive 0; Mismatches 0; Indels Sequence 70 BP; 12 A; 21 C; 19 G; 18 T; 0 U; 0 Other; 1 TCCGCTGCAGAGTTGCCCGTTACGA 25 25; Conservative Best Local Similarity of the invention. Query Match Matches ઠે

TCCGCTGCAGAGTTGCCCGTTACGA 25 BP. ADP05519 standard; DNA; 70 ADP05519; RESULT 11 ADP05519

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26-AUG-2004 (first entry)

Novel microbe detection apparatus-related oligonucleotide probe SeqID24. microbe detection; microbe identification; virus; viral particle; pathogenic bacterium; cellular microbe; acellular microbè; cinical diagnosis; research; epidemiological surveillance; bioterrorism countermeasure; environmental pathogen survey; food contaminant; radioimmunoassay; ELISA; probe; ss. 

WO2004045365-A2.

03-JUN-2004.

23-MAY-2003; 2003WO-US016461.

15-NOV-2002; 2002US-00295787.

(REGC ) UNIV CALIFORNIA.

Jia XY, Berger MA, Tilles JG;

WPI; 2004-449626/42.

New (microarray) apparatus comprising a substrate with attached nucleic acid probes, useful for detecting one or more microbes in a sample.

Claim 16; SEQ ID NO 24; 89pp; English.

This invention relates to a novel apparatus for detecting a microbe in a sample which comprises a substrate having multiple microbe identification sites, each having a unique address indicative of the position of that microbe identification site on the substrate and groups of nucleic acid probes disposed at the microbe identification sites, each group being complementary to a target nucleic acid to provide a detectable signal at one or more microbe identification sites. The apparatus is useful for detecting the presence of one or more microbes in a sample, such as virus

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or viral particle, (non-)pathogenic bacteria, or cellular or acellular microbe. The apparatus is particularly useful for clinical diagnosis, research, epidemiological surveillance, bioterrorism countermeasures, environmental pathogen surveys, and monitoring food contaminants. Current testing procedures or devices, such as radioimmunoassays and ELISA, are difficult to implement, time consuming, expensive, outdated, and typically rely on the use of agents that recognise and bind to membrane bound proteins or carbohydrates of the pathogen. These further cannot assay multiple pathogens. The new apparatus or device for detecting microbes overcomes these disadvantages. The apparatus is compact,
                                                                                                                                                           sensitive, and quick to detect the presence of any of a number of pathogens present in a sample. The present sequence is that of an oligonuclectide probe which is related to the micorbe detection apparatus
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                                                                                                                                                                                                                                          Sequence 70 BP; 11 A; 20 C; 19 G; 20 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                       1 TCCGCTGCAGAGTTGCCCGTTACGA 25
                                                                                                                                                                                                                                                                                                                                                         1 TCGCTGCAGAGTTGCCCGTTACGA 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADP05518 standard; DNA; 70 BP.
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                                                                                                                                                                                                                                                                                         Local Similarity 100.
Les 25; Conservative
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                                                                                                                                                                                                               the invention.
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                                                                                                                                                                                                                                                                            Query Match
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research, epidemiological surveillance, bioterrorism countermeasures, environmental pathogen surveys, and monitoring food contaminants. Current testing procedures or devices, such as radioimmunoassays and ELISA, are difficult to implement, time consuming, expensive, outdated, and typically rely on the use of agents that recognise and bind to membrane bound proteins or carbohydrates of the pathogen. These further cannot assay multiple pathogens. The new apparatus or device for detecting microbes overcomes these disadvantages. The apparatus is compact, pathogens present in a sample. The present equence is that of an oligonucleotide probe which is related to the microbe detection apparatus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to an oligonucleotide (I) consisting of: (a) the target binding sequence of an oligonucleotide chosen from any one of the 10 sequence of ABB56762 to ABB56771; and (b) a sequence required for selected amplification or detection reaction. Also described: (1) and (2) detecting (M1) an enterovirus target sequence, involving: (a) amplifying the target sequence using first amplification primer having a sequence consisting essentially of target binding sequence of any one of ABB56764 to ABB56771 and optionally a sequence required for selected amplification reaction; and (b) detecting the amplified target sequence. (I), (M1) and (K1) are useful for detecting enterovirus target sequences. (I) specifically and selectively recognizes the enterovirus genome. (I) sensitively and rapidly detects fewer than 500 copies of enteroviral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel oligonucleotide comprising sequences for binding and amplifying or detecting target, useful for detecting enterovirus nucleic acids.
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                                                                                                                                                                                                                                                                                                              100.0%; Score 25; DB 12; Length 70; 100.0%; Pred. No. 0.043;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human echovirus 30 5' untranslated polynucleotide sequence.
                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                    Sequence 70 BP; 12 A; 22 C; 19 G; 17 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA detection; enteroviral detection; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Isang S, Price JA, Hellyer TJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AEB56869 standard; DNA; 105 BP.
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                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100.
Matches 25, Conservative
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(PRIC/) PRICE J A.
(HBLL/) HBLLYER T J.
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This invention relates to a novel apparatus for detecting a microbe in a sample which comprises a substrate having multiple microbe identification sites, each having a unique address indicative of the position of that microbe identification site on the substrate and groups of nucleic acid microbe identification sites on the substrate and groups of nucleic acid sorbes adsposed at the microbe identification sites, each group being complementary to a target nucleic acid to provide a detectable signal at one or more microbe identification sites. The apparatus is useful for detecting the presence of one or more microbes in a sample, such as virus or viral particle, (non-)pathogenic bacteria, or callular or acidlular microbe. The apparatus is particularly useful for clinical diagnosis,

New (microarray) apparatus comprising a substrate with attached nucleic acid probes, useful for detecting one or more microbes in a sample.

Tilles JG;

Berger MA,

Jia XY,

WPI; 2004-449626/42.

Claim 16; SEQ ID NO 23; 89pp; English.

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The invention relates to an oligonucleotide (I) consisting of: (a) the target binding sequence of an oligonucleotide chosen from any one of the 10 sequence of ABB56762 to ABB56771; and (b) a sequence required for selected amplification or detection reaction. Also described: (1) a kit (XI) comprising (II), and one or more container that contains (I); and (2) detecting (MI) an enterovirus target sequence, involving: (a) amplifying the target sequence using first amplification primer having a sequence consisting essentially of target binding sequence of any one of ABB56764 to ABB5671 and optionally a sequence required for selected amplification reaction; and (b) detecting the amplified target sequence. (I), (MI) and (XI) are useful for detecting enterovirus target sequence. (I) section; and selectively recognizes the enterovirus genome. (I) sensitively and rapidly detects fewer than 500 copies of enteroviral genome and allows detection of broad range of enterovirus serotypes. The
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genome and allows detection of broad range of enterovirus serotypes. The present sequence represents a viral 5' untranslated polynucleotide sequence given in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel oligonucleotide comprising sequences for binding and amplifying or detecting target, useful for detecting enterovirus nucleic acids.
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                                                                                                                  Query Match 100.0%; Score 25; DB 14; Length 105; Best Local Similarity 100.0%; Pred. No. 0.045; Matches 25; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Viral 5' untranslated polynucleotide sequence SEQ ID NO:53.
                                                                             Sequence 105 BP; 22 A; 27 C; 27 G; 29 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 107 BP; 22 A; 28 C; 28 G; 29 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA detection; enteroviral detection; ds.
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                                                                                                                                                                                                                                       70 recericeacaciriececerracca 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hellyer TJ;
                                                                                                                                                                                                                                                                                                                                       AEB56814 standard; DNA; 107 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
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(PRIC/) PRICE J A.
(HELL/) HELLYER T J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unidentified
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ID AEB568
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The invention relates to an oligonucleotide (I) consisting of: (a) the target binding sequence of an oligonucleotide chosen from any one of the 10 sequence of ABB56762 to ABB56771; and (b) a sequence required for selected amplification or detection reaction. Also described: (I) a kit (KI) comprising (I), and one or more container that contains (I); and (2) detecting (MI) an enterovirus target sequence, involving: (a) amplifying the target sequence using first amplification primer having a sequence consisting essentially of target binding sequence of any one of ABB56764 to ABB56771 and optionally a sequence required for selected amplification reaction; and (b) detecting the amplified target sequence. (I), (MI) and (MI) are useful for detecting enterovirus target sequences: (I), (MI) and (MI) are sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel oligonucleotide comprising sequences for binding and amplifying or detecting target, useful for detecting enterovirus nucleic acids.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   specifically and selectively recognizes the enterovirus genome. (I) sensitively and rapidly detects fewer than 500 copies of enteroviral genome and allows detection of broad range of enterovirus serotypes.
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                                                                                                                                                                                                                                        Viral 5' untranslated polynucleotide sequence SEQ ID NO:18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 126 BP; 26 A; 36 C; 31 G; 33 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                          DNA detection; enteroviral detection; ds.
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ID AEB56834 standard; DNA; 180 BP
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                                                                                                                            AEB56779 standard; DNA; 126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (TSAN/) TSANG S.
(PRIC/) PRICE J A.
(HELL/) HELLYER I J.
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                                                                                                                                                                                                                                                                                                                 Unidentified.
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25; C
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Gaps

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0; Indels

100.0%; Score 25; DB 14; Length 107; 100.0%; Pred. No. 0.045;

0; Mismatches

Query Match 100. Best Local Similarity 100. Matches 25; Conservative

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The invention relates to an oligonucleotide (I) consisting of: (a) the target binding sequence of an oligonucleotide chosen from any one of the 10 sequence of ABS5672 to ABS5671; and (b) a sequence required for selected amplification or detection reaction. Also described: (I) a kit (KI) comprising (I), and one or more container that contains (I); and (2) detecting (MI) an enterovirus target sequence, involving: (a) amplifying the target sequence using first amplification primer having a sequence consisting essentially of target binding sequence of any one of ABS56764 to ABS56771 and optionally a sequence required for selected amplification reaction; and (D) detecting the amplified target sequence. (I), (MI) and (XI) are useful for detecting enterovirus target sequence. (I) specifically and rapidly detects fewer than 500 copies of enteroviral sensitively and rapidly detects fewer than 500 copies of enteroviral speneme and allows detection of broad range of enterovirus serotypes. The present sequence represents a viral 5' untranslated polymucleotide squence given in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                          Novel oligonucleotide comprising sequences for binding and amplifying or detecting target, useful for detecting enterovirus nucleic acids.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Fig 1A-D; 34pp; English.
                                                                                                                                                                                                                                                                                                   Isang S, Price JA, Hellyer TJ;
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                                                                                                  16-JAN-2004; 2004US-00760048.
                                                                                                                                                 16-JAN-2004; 2004US-00760048.
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1es 25; Conservative
                                                                                                                                                                                             (TSAN/) TSANG S.
(PRIC/) PRICE J A.
(HELL/) HELLYER T J.
                                                                                                                                                                                                                                                                                                                                               WPI; 2005-512251/52
GENBANK; U11709.
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US2005158710-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to an oligonucleotide (1) consisting of: (a) the target binding sequence of an oligonucleotide chosen from any one of the 10 sequence of ABBS6712 to ABBS6713, and (b) a sequence required for selected amplification or detection reaction. Also described: (1) a kit (K1) comprising (1), and one or more container that contains (1); and (2) detecting (M1) an enterovirus target sequence, involving: (a) amplifying the target sequence using first amplification primer having a sequence consisting essentially of target binding sequence of any one of ABBS6764 to ABBS6771 and optionally a sequence required for selected amplification reaction; and (b) detecting enterovirus target sequence. (1), (M1) and (K1) are useful for detecting enterovirus target sequences. (1) specifically and selectively recognizes the enterovirus genome. (1) specifically and rapidly detects fewer than 500 copies of enteroviral genome and allows detection of broad range of enterovirus serotypes. The present sequence represents a viral 5, untranslated polynucleotide
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                                                                      Human coxsackievirus B1 5' untranslated polynucleotide sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sequence given in the exemplification of the present invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 100.0%; Score 25; DB 14; Length 1
Best Local Similarity 100.0%; Pred. No. 0.047;
Matches 25; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Seguence 180 BP; 37 A; 48 C; 47 G; 48 T; 0 U; 0 Other;
                                                                                                                          DNA detection; enteroviral detection; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA detection; enteroviral detection; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  129 TCCGCTGCAGAGTTGCCCGTTACGA 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure, Fig 1A-D; 34pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             rang S, Price JA, Hellyer TJ;
                                                                                                                                                                                                                                                                                                                          16-JAN-2004; 2004US-00760048
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                    22-SEP-2005 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                         Human coxsackievirus Bl
                                                                                                                                                                                                                                                                                                                                                                                                                     (TSAN/) TSANG S.
(PRIC/) PRICE J A.
(HELL/) HELLYER T J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2005-512251/52
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AEB56858/c ID AEB50 RESULT 17

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21-JUL-2005.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
      셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8
                                                                                                                                                                                                                                                                     The invention relates to an oligomucleotide (I) consisting of: (a) the target binding sequence of an oligomucleotide chosen from any one of the C sequence of ABBS672 to ABBS671; and (b) a sequence required for selected amplification or detection. Also described: (I) a kit (XI) comprising (I), and one or more container that contains (I), and (2) detecting (MI) an enterovirus target sequence, involving: (a) amplifying the target sequence using first amplification primer having a sequence consisting essentially of target binding sequence of any one of ABBS6764 or obsisting essentially of target binding sequence of any one of ABBS6764 or obsisting essentially of target binding sequence (I), (MI) and (KI) are useful for detecting enterovirus target sequence. (I) specifically and selectively recognizes the enterovirus genome. (I) specifically and selectively recognizes the enterovirus serotypes. The present sequence represents a viral 5' untranslated polynucleotide
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                                                                                                                                                                              9
                                                                                                                                                                     Novel oligonucleotide comprising sequences for binding and amplifying detecting target, useful for detecting enterovirus nucleic acids.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human coxsackievirus B5 5' untranslated polynucleotide sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequence given in the exemplification of the present invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 198 BP; 41 A; 49 C; 50 G; 58 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA detection; enteroviral.detection; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           91 rccecrecagaerreccerracea 67
                                                                                                                                                                                                                                      Disclosure; Fig 1A-D; 34pp; English.
                                                                Hellyer TJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hellyer TJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AEB56848 standard; DNA; 237 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100.
Matches 25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human coxsackievirus B5
PRICE J A.
HELLYER T J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (TSAN/) TSANG S.
(PRIC/) PRICE J A.
(HELL/) HELLYER T J.
                                                                Price JA,
                                                                                                         WPI; 2005-512251/52
GENBANK; U11705.
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                                                                Tsang S,
(PRIC/)
(HELL/)
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Novel oligonucleotide comprising sequences for binding and amplifying or

GENBANK; AF114383

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The invention relates to an oligonucleotide (I) consisting of: (a) the target binding sequence of an oligonucleotide chosen from any one of the 10 sequence of ABBS671; and (b) a sequence required for selected amplification or detection reaction. Also described: (I) a kit (KI) comprising (I), and one or more container that contains (I); and (2) detecting (MI) an enterovirus target sequence, involving: (a) amplifying the target sequence using first amplification primer having a sequence consisting essentially of target binding sequence of any one of ABBS6764 to ABBS6771 and optionally a sequence required for selected amplification reaction; and (b) detecting the amplified target sequence. (I) (MI) and (XI) are useful for detecting enterovirus target sequence. (I) specifically and selectively recognizes the enterovirus genome. (I) specifically and rapidly detects fewer than 500 copies of enteroviral genome and allows detection of broad range of enterovirus serotypes. The present sequence represents a viral 5' untranslated polymucleotide sequence given in the exemplification of the present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel oligonucleotide comprising sequences for binding and amplifying or detecting target, useful for detecting enterovirus nucleic acids.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
detecting target, useful for detecting enterovirus nucleic acids.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 25; DB 14; Length 237; Pred. No. 0.049;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0, Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 237 BP; 48 A; 52 C; 66 G; 71 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA detection; enteroviral detection; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         131 rccgcrgcagagrrgcccgrracga 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25
                                              Disclosure; Fig 1A-D; 34pp; English.
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les 25; Conservative 0
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ID AEB56862 standard; DNA; 237
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(PRIC/) PRICE J A.
(HELL/) HELLYER T J.
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                   the target sequence using first amplification primer having a sequence consisting essentially of target binding sequence of any one of ABB56764 to ABB56771 and optionally a sequence required for selected amplification reaction; and (b) detecting the amplifier arget sequence. (I), (MI) and (KI) are useful for detecting enterovirus target sequences. (I) sepcifically and selectively recognizes the enterovirus genome. (I) sensitively and rapidly detects fewer than 500 copies of enteroviral genome and allows detection of broad range of enterovirus serotypes. The present sequence represents a viral 5' untranslated polynucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   target binding sequence of an oligonucleotide chosen from any one of the 10 sequence of ABB56771; and (b) a sequence required for sequence contains (1), and one or more contains that contains (1); and one or more contains that contains (1); and (2) detecting (M1) an enterovirus target sequence, involving; (a) amplifying the target sequence using first amplification primer having a sequence onsisting essentially of target binding sequence of any one of ABB5676 to ABB56771 and optionally a sequence required for selected amplification reaction, and (b) detecting the amplification sequence. (I) (M1) and (M1) are useful for detecting enterovirus target sequence. (I) sensitively and selectively recognizes the enterovirus genome. (I) sensitively and rapidly detects fewer than 500 copies of enteroviral genome and allows detection of broad range of enterovirus serotypes. The present sequence represents a viral 5' untranslated polynucleotide.
(a) amplifying
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel oligonucleotide comprising sequences for binding and amplifying or detecting target, useful for detecting enterovirus nucleic acids.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to an oligonucleotide (I) consisting of: (a) the
                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                            sequence given in the exemplification of the present invention
                                                                                                                                                                                                                                                                                              100.0%; Score 25; DB 14; Length 237; 100.0%; Pred. No. 0.049;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Viral 5' untranslated polynucleotide sequence SEQ ID NO:32.
    enterovirus target sequence, involving:
                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                     Sequence 237 BP; 51 A; 55 C; 62 G; 69 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA detection; enteroviral detection; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; SEQ ID NO 32; 34pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                       130 recerrecadadricecedriacea 106
                                                                                                                                                                                                                                                                                                                                                                                  1 TCCGCTGCAGAGTTGCCCGTTACGA 25
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                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100.us,
Lea 25; Conservative (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22-SEP-2005 (first entry)
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(PRIC/) PRICE J A.
(HELL/) HELLYER T J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2005-512251/52
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel oligonucleotide comprising sequences for binding and amplifying or detecting target, useful for detecting enterovirus nucleic acids.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           specifically and selectively recognizes the enterovirus genome. (1) sensitively and rapidly detects fewer than 500 copies of enteroviral genome and allows detection of broad range of enterovirus serotypes.
                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  present sequence represents a viral 5' untranslated polynucleotide sequence given in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                      Human coxsackievirus B3 5' untranslated polynucleotide sequence.
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sequence given in the exemplification of the present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                            0; Indels
                                                                      Score 25; DB 14; Length
Pred. No. 0.049;
                                    Sequence 237 BP; 52 A; 52 C; 59 G; 74 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 238 BP; 50 A; 56 C; 65 G; 67 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                            DNA detection; enteroviral detection; ds.
                                                                                                                                                1 TCCGCTGCAGAGTTGCCCGTTACGA 25
                                                                                                                                                                     75 TCCGCTGCAGAGTTGCCCGTTACGA 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 TCCGCTGCAGAGTTGCCCGTTACGA 25
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                                                                                                                                                                                                                                                                              BP.
                                                                        100.0%;
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                                                                                                                                                                                                                                                                            AEB56840 standard; DNA; 238
                                                                                                                                                                                                                                                                                                                                                    22-SEP-2005 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches 25; Conservative
                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human coxsackievirus B3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (TSAN/) TSANG S.
(PRIC/) PRICE J A.
(HELL/) HELLYER T J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2005-512251/52.
                                                                      Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENBANK; AH008164.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-JUL-2005.
                                                                                                              25;
                                                                                                                                                                                                                                                                                                                  AEB56840;
                                                                                                              Matches
                                                                                                                                                                                                                                           RESULT 22
                                                                                                                                                                                                                                                           AEB56840/
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Human coxsackievirus B4 5' untranslated polynucleotide sequence

(first entry)

22-SEP-2005

DNA detection; enteroviral detection; ds.

Human coxsackievirus B4

US2005158710-A1.

21-JUL-2005.

Tsang S, Price JA, Hellyer TJ;

2005-512251/52

GENBANK; D00149

(TSAN/) TSANG S. (PRIC/) PRICE J A. (HELL/) HELLYER T J.

16-JAN-2004; 2004US-00760048 16-JAN-2004; 2004US-00760048

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The invention relates to an oligonucleotide (I) consisting of: (a) the target binding sequence of an oligonucleotide chosen from any one of the 10 sequence of ABB56762 to ABB5671; and (b) a sequence required for selected amplification or detection reaction. Also described: (I) a kit (KI) comprising (I), and one or more container that contains (I); and (2) detecting (MI) an enterovirus target sequence, involving: (a) amplifying the target sequence using first amplification primer having a sequence consisting essentially of target binding sequence of any one of ABB56764 consisting optionally a sequence required for selected amplification reaction; and (b) detecting the amplified target sequence. (I), (MI) and (MI) are useful for detecting enterovirus target sequences. (I)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel oligonucleotide comprising sequences for binding and amplifying or detecting target, useful for detecting enterovirus nucleic acids.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 specifically and selectively recognizes the enterovirus genome. (I) sensitively and rapidly detects fewer than 500 copies of enteroviral genome and allows detection of broad range of enterovirus serotypes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         untranslated polynucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sequence given in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 14; Length 238;
                                                                                                                                                                                                                                                                           Viral 5' untranslated polynucleotide sequence SEQ ID NO:30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 238 BP; 54 A; 52 C; 58 G; 74 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 25; DB 14
Pred. No. 0.049;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                         DNA detection; enteroviral detection; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; SEQ ID NO 30; 34pp; English.
131 TCCGCTGCAGAGTTGCCCGTTACGA 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         viral 5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               75 TCCGCTGCAGAGTTGCCCGTTACGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hellyer TJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Sc
100.0%; Pr
tive 0;
                                                                                                                                        AEB56791 standard; DNA; 238 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequence represents a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-JAN-2004; 2004US-00760048
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (TSAN/) TSANG S.
(PRIC/) PRICE J A.
(HELL/) HELLYBR T J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 25, Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Price JA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2005-512251/52
                                                                                                                                                                                                                                                                                                                                                                                                                 US2005158710-A1.
                                                                                                                                                                                                                                                                                                                                                                      Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-JUL-2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Teang S,
                                                                                                                                                                                   AEB56791;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         present
                                                                                                                     AEB56791/c
                                                                                             RESULT 23
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target binding sequence of an oligonucleotide chosen from any one of the 10 sequence of ABB56762 to ABB56771; and (b) a sequence required for selected amplification or detection reaction. Also described: (l) a kit (K1) comprising (l), and one or more container that contains (l); and (2) detecting (M1) an enterovirus target sequence, involving: (a) amplifying the target sequence using first amplification primer having a sequence to ABB56771 and optionally a sequence required for selected amplification reaction; and (b) detecting the amplified target sequence. (l), (M1) and (K1) are useful for detecting enterovirus target sequence. (l), (M1) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ange of enterovirus serotypes. The untranslated polynucleotide
                                                                                                                                           Novel oligonucleotide comprising sequences for binding and amplifying or detecting target, useful for detecting enterovirus nucleic acids.
                                                                                                                                                                                                                                                  consisting of: (a) the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sensitively and rapidly detects fewer than 500 copies of enteroviral genome and allows detection of broad range of enterovirus serotypes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human coxsackievirus B4 5' untranslated polynucleotide sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               recognizes the enterovirus genome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sequence given in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 25; DB 14; Length 238; 100.0%; Pred. No. 0.049; Live 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 238 BP; 50 A; 55 C; 65 G; 68 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                  to an oligonucleotide (I)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA detection; enteroviral detection; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     131 TCCGCTGCAGAGTTGCCCGTTACGA 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 TCCGCTGCAGAGTTGCCCGTTACGA 25
                                                                                                                                                                                                     Disclosure; Fig 1A-D; 34pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AEB56847 standard; DNA; 238 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            specifically and selectively
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             represents
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human coxsackievirus B4
                                                                                                                                                                                                                                                  The invention relates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
nes 25; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US2005158710-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             resent
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Matches
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Gaps

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AEBS6846/c ID AEBS6846 standard; DNA; 238 XX AC AEBS6846; XX

RESULT 24

(PRIC/)

(TSAN/)

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The invention relates to an oligonuclectide (I) consisting of: (a) the target binding sequence of an oligonuclectide chosen from any one of the target binding sequence of ABB56771; and (b) a sequence requirated for selected amplification or detection reaction. Also described: (l) a kit (K1) comprising (I), and one or more container that contains (I); and (2) detecting (M1) an enterovirus target sequence, involving: (a) amplifying the target sequence using first amplification primer having a sequence consisting essentially of target binding sequence of any one of ABB56764 to ABB56771 and optionally a sequence required for selected amplification reaction; and (b) detecting the amplified target sequence. (I), (M1) and (K1) are useful for detecting the amplified target sequence. (I) specifically and selectively recognizes the enterovirus genome. (I) sensitively and rapidly detects fewer than 500 copies of enteroviral sensitively and allows detection of broad range of enterovirus serotypes. The present sequence represents a viral 5' untranslated polymuclectide sequence in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel oligonucleotide comprising sequences for binding and amplifying or detecting target, useful for detecting enterovirus nucleic acids.
                                                                                                                                         Novel oligonucleotide comprising sequences for binding and amplifying or detecting target, useful for detecting enterovirus nucleic acids.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 25; DB 14; Length 238; 100.0%; Pred. No. 0.049;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Viral 5' untranslated polynucleotide sequence SEQ ID NO:14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 238 BP; 57 A; 52 C; 58 G; 71 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA detection; enteroviral detection; ds.
                                                                                                                                                                                                           Disclosure; SEQ ID NO 28; 34pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 TCCGCTGCAGAGTTGCCCGTTACGA 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TCCGCTGCAGAGTTGCCCGTTACGA 51
                                                Price JA, Hellyer TJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hellyer TJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AEB56775 standard; DNA; 238 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (TSAN/) TSANG S.
(PRIC/) PRICE J A.
(HELL/) HELLYER T J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Isang S, Price JA,
(HELL/) HELLYER T J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2005-512251/52
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                                                reang S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AEB56775;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 27
AEB56775/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to an oligonucleotide (I) consisting of: (a) the target binding sequence of an oligonucleotide chosen from any one of the 10 sequence of ABBS6782 to ABBS671; and (b) a sequence required for selected amplification or detection reaction. Also described: (I) a kit (K1) comprising (I), and one or more container that contains (I); and (2) detecting (M1) an enterovirus target sequence, involving: (a) amplifying the target sequence using first amplification primer having a sequence consisting essentially of target binding sequence of any one of ABBS6764 to ABBS6771 and optionally a sequence required for selected amplification reaction; and (b) detecting the amplified target sequence. (I), (M1) and (X1) are useful for detecting enterovirus target sequences. (I), (M1) and specifically and selectively recognizes the enterovirus genome. (I) specifically and rapidly detects fewer than 500 copies of enteroviral sensitively and rapidly detects fewer than 500 copies of enteroviral present sequence represents a viral 5 untranslated polymucleotide specifical the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                            Novel oligonucleotide comprising sequences for binding and amplifying or detecting target, useful for detecting enterovirus nucleic acids.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 25; DB 14; Length 238; Pred. No. 0.049;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Viral 5' untranslated polynucleotide sequence SEQ ID NO:28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 238 BP; 50 A; 55 C; 65 G; 68 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Sco...
100.0%; Pred. No. v. 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA detection; enteroviral detection; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        131 TCCGCTGCAGAGTTGCCCGTTACGA 107
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure, Fig 1A-D; 34pp; English.
                                                                                                                                                                                                                                                            Hellyer TJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AEB56789 standard; DNA; 238 BP
                                                                                                                16-JAN-2004; 2004US-00760048.
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                                                                    16-JAN-2004; 2004US-00760048.
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                                                                                                                                                               TSANG S.
PRICE J A.
HELLYER I J.
                                                                                                                                                                                                                                                                                                        WPI; 2005-512251/52.
GENBANK; X05690.
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                                                                                                                                                                                                                                                         Tsang S, Price JA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TSANG S.
PRICE J A.
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                   21-JUL-2005.
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Query Match

Matches

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AEB56789

**AEB56789/** 

(TSAN/) (PRIC/)

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Gaps . 0 ö

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target binding sequence of an objoint learning of the carget binding sequence of ABB5672 to ABB5671; and (b) a sequence required for selected amplification or detection reaction. Also described: (1) a kit (X1) comprising (II), and one or more container that contains (I); and (2) detecting (M1) an enterovirus target sequence, involving: (a) amplifying the target sequence using first amplification primer having a sequence consisting essentially of target binding sequence of any one of ABB5674 to ABB56771 and optionally a sequence required for selected amplification reaction; and (b) detecting the amplified target sequence. (I), (M1) and (X1) are useful for detecting enterovirus target sequences. (I) specifically and selectively recognizes the enterovirus genome. (I) sensitively and rapidly detects fewer than 500 copies of enteroviral sensitively and allows detection of broad range of enterovirus serotypes. The present sequence represents a viral 5 untranslated polymucleotide sequence given in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to an oligonucleotide (I) consisting of: (a) the target binding sequence of an oligonucleotide chosen from any one of the 10 sequence of ABB56762 to ABB56771; and (b) a sequence required for selected amplification or detection reaction. Also described: (I) a kit (K1) comprising (I), and one or more container that contains (I); and (2) detecting (M1) an enterovirus target sequence, involving: (a) amplifying the target sequence using first amplification primer having a sequence consisting essentially of target binding sequence of any one of ABB56764 to ABB56771 and optionally a sequence required for selected amplification
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                        consisting of: (a) the
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                                                                                                                                                                                                                                                                                                                                                                                                     Score 25; DB 14; Length 238;
Pred. No. 0.049;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel oligonucleotide comprising sequences for binding and detecting target, useful for detecting enterovirus nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                                                                             Sequence 238 BP; 56 A; 55 C; 58 G; 69 T; 0 U; 0 Other;
                    invention relates to an oligonucleotide (I)
                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
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AEB56807/c .
ID AEB56807 standard; DNA; 238
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(PRIC/) PRICE J A.
(HELL/) HELLYER T J.
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les 25; Conser
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The invention relates to an oligonucleotide (I) consisting of: (a) the target binding sequence of an oligonucleotide chosen from any one of the consisting of ABBS6762 to ABBS6771; and (b) a sequence required for selected amplification or detection reaction. Also described: (1) a kit (K1) comprising (I), and one or more container that contains (I); and (2) detecting (M1) an enterovirus target sequence, involving: (a) amplifying the target sequence using first amplification primer having a sequence consisting essentially of target binding sequence of any one of ABBS6764 to ABBS6771 and optionally a sequence required for selected amplification reaction, and (b) detecting the amplified target sequence. (I), (M1) and (K1) are useful for detecting enterovirus target sequences. (I) specifically and selectively recognizes the enterovirus genome. (I) specifically and rapidly detects fewer than 500 copies of enteroviral contains and contains and contains a single sequences. (I) sensitively and rapidly detects fewer than 500 copies of enteroviral contains and contains a supercovirus services.
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                                                                                                                                         genome and allows detection of broad range of enterovirus serotypes. present sequence represents a viral 5' untranslated polynucleotide sequence given in the exemplification of the present invention.
reaction, and (b) detecting the amplified target sequence. (1), (M1) (K1) are useful for detecting enterovirus target sequences. (1) specifically and selectively recognizes the enterovirus genome. (1) sensitively and rapidly detects fewer than 500 copies of enteroviral
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                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 25; DB 14; Length 238; 100.0%; Pred. No. 0.049; Indels C. Mismatches O; Indels C
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                                                                                                                                                                                                                                                                                               Sequence 238 BP; 53 A; 53 C; 58 G; 74 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA detection; enteroviral detection; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       75 TCCGCTGCAGAGTTGCCCGTTACGA
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Best Local Similarity 100.
Matches 25; Conservative
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(PRIC/) PRICE J A.
(HELL/) HELLYER T J.
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XX ARBS 5815/

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XX ARBS 5815/

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XX DISC 78
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Seguence 238 BP; 53 A; 53 C; 55 G; 77 T; 0 U; 0 Other;

BP.

us-10-829-474-4.rng

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Human coxsackievirus B3 5' untranslated polynucleotide sequence.
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                                                  AEB56842 standard; DNA; 238
                                                                                                                                               22-SEP-2005 (first entry)
                                                                                                                                                                                                                                                                                          Human coxsackievirus B3
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(PRIC/) PRICE J A.
(HELL/) HELLYER T J.
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     DB 14; Length 238;
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  Score 25; DB 14;
Pred. No. 0.049;
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                                                  Mismatches
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                                                                                                  1 TCCGCTGCAGAGTTGCCCGTTACGA 25
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Query Match 100.0%; Sc
Best Local Similarity 100.0%; Pr
Matches 25; Conservative 0;
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Best Local Similarity 100.
Matches 25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human coxsackievirus B3.
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(PRIC/) PRICE J A.
(HELL/) HELLYER T J.
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GENBANK; AF169665.
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Hellyer TJ;

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The invention relates to an oligomucleotide (I) consisting of: (a) the target binding sequence of an oligomucleotide chosen from any one of the core target binding sequence of an oligomucleotide chosen from any one of the core degrated for a sequence required for selected amplification or detection reaction. Also described: (1) a kit comprising (I), and one or more container that contains (I); and (2) detecting (MI) an enterovirus target sequence, involving: (a) amplifying the target sequence using first amplification primer having a sequence consisting essentially of target binding sequence of any one of ABB5676 to ABB56771 and optionally a sequence required for selected amplification consisting essentially of target binding sequence. (I), (MI) and (XI) are useful for detecting enterovirus target sequences. (I) specifically and selectively recognizes the enterovirus genome. (I) sensitively and rapidly detects fewer than 50 copies of enteroviral common and allows detection of broad range of enterovirus serotypes. The present sequence represents a viral 5' untranslated polynucleotide sequence given in the exemplification of the present invention.
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Novel oligonucleotide comprising sequences for binding and amplifying or detecting target, useful for detecting enterovirus nucleic acids.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 238 BP; 53 A; 57 C; 64 G; 64 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           131 TCCGCTGCAGAGTTGCCCGTTACGA 107
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                                                                                                                                       Disclosure; Fig 1A-D; 34pp; English.
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Best Local Similarity
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The invention relates to an oligonucleotide (I) consisting of: (a) the target binding sequence of an oligonucleotide chosen from any one of the 10 sequence of ABB56762 to ABB5671; and (b) a sequence required for selected amplification or detection. Also described: (I) a kit (KI) comprising (I), and one or more container that contains (I); and (2) detecting (MI) an enterovirus target sequence, involving: (a) amplifying the target sequence using first amplification primer having a sequence consisting essentially of target binding sequence of any one of ABB56764 to ABB56771 and optionally a sequence required for selected amplification reaction; and (b) detecting the amplified target sequence. (I), (MI) and (KI) are useful for detecting enterovirus target sequences. (I), (MI) and
                                                                                                                                                                                                                                                                Novel oligonucleotide comprising sequences for binding and amplifying or detecting target, useful for detecting enterovirus nucleic acids.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         specifically and selectively recognizes the enterovirus genome. (I) sensitively and rapidly detects fewer than 500 copies of enteroviral genome and allows detection of broad range of enterovirus serotypes. Present sequence represents a viral 5' untranslated polymuclectide sequence given in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 25; DB 14; Length 238; 100.0%; Pred. No. 0.049; Live 0; Mismatches 0; Indels 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 238 BP; 53 A; 56 C; 63 G; 66 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 TCCGCTGCAGAGTTGCCCGTTACGA 25
                                                                                                                                                                                                                                                                                                                                Disclosure; Fig 1A-D; 34pp; English.
                                                                                                                                                     Hellyer TJ;
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                  16-JAN-2004; 2004US-00760048
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                           TSANG S.
PRICE J A.
HELLYER T J.
                                                                                                                                                     Price JA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (TSAN/) TSANG S.
(PRIC/) PRICE J A.
(HELL/) HELLYER I J.
                                                                                                                                                                                                 WPI; 2005-512251/52
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les 25; Conserv
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                                                           (TSAN/)
(PRIC/)
(HELL/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to an oligonucleotide (I) consisting of: (a) the target binding sequence of an oligonucleotide chosen from any one of the consisting of ABB56762 to ABB56771; and (b) a sequence required for consequence amplification or detection reaction. Also described: (I) a kit (KI) comprising (II), and one or more container that contains (I); and (2) detecting (MI) an enterovirus target sequence, involving: (a) amplifying the target sequence using first amplification primer having a sequence consisting essentially of target binding sequence of any one of ABB56764 to ABB56771 and optionally a sequence required for selected amplification reaction; and (b) detecting the amplified target sequence. (I), (MI) and (KI) are useful for detecting enterovirus target sequence. (I) specifically and selectively recognizes the enterovirus genome. (I) sensitively and rapidly detects fewer than 500 copies of enteroviral consistively and rapidly detects fewer than 500 copies of enteroviral consisting and consisting a seriotypes. The
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 comprising sequences for binding and amplifying or
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      detecting target, useful for detecting enterovirus nucleic acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human coxsackievirus B1 5' untranslated polynucleotide sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              present sequence represents a viral 5' untranslated polynucleo' sequence given in the exemplification of the present invention
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                  DNA detection; enteroviral detection; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; SEQ ID NO 24; 34pp; English
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AEB56835 standard; DNA; 238 BP.
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nes 25; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel oligonucleotide
                                                                                                                                                                                                                                                                             (TSAN/) TSANG S.
(PRIC/) PRICE J A.
(HELL/) HELLYER T J.
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                                                       Unidentified
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                                                                                    The invention relates to an oligonucleotide (I) consisting of: (a) the target binding sequence of an oligonucleotide chosen from any one of the 10 sequence of ABB56762 to ABB56771, and (b) a sequence required for selected amplification or detection reaction. Also described: (I) a kit (K1) comprising (I), and one or more container that contains (I); and (2) detecting (M1) an enterovirus target sequence, involving: (a) amplifying the target sequence using first amplification primer having a sequence consisting essentially of target binding sequence of any one of ABB5674 to ABB56771 and optionally a sequence required for selected amplification reaction; and (b) detecting the amplified target sequence. (I), (M1) and (K1) are useful for detecting enterovirus target sequences. (I), (M1) and specifically and selecting enterovirus target sequences. (I) specifically and selecting enterovirus target sequence. (I) specifically and selecting enterovirus target sequences. (I) specifically and selection of broad range of enterovirus senoupes. The present sequence represents a viral 5 untranslated polynucleotide present in the exemplification of the present invention.
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                         Novel oligonucleotide comprising sequences for binding and amplifying or detecting target, useful for detecting enterovirus nucleic acids.
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                                                                                                                                                                                                                                                                                                                                        100.0%; Score 25; DB 14; Length 238;
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                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                 Sequence 238 BP; 57 A; 51 C; 58 G; 72 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                     Pred. No. 0.049;
                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
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                                                               Disclosure; SEQ ID NO 19; 34pp; English.
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1es 25; Conservative
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(PRIC/) PRICE J A.
(HELL/) HELLYER T J.
WPI; 2005-512251/52
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                                                                                                                                                                                                                                                                                                                                           Query Match
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                       (KI) comprising (I), and one or more contains that contains (I); and (2) detecting (MI) an enterovirus target sequence, involving; (a) amplifying the target sequence using first amplification primer having a sequence consisting essentially of target binding sequence of any one of ABB5676 to ABB56771 and optionally a sequence required for selected amplification reaction; and (b) detecting the amplified target sequence. (I), (MI) and (KI) are useful for detecting enterovirus target sequences. (I) specifically and selectively recognizes the enterovirus genome. (I) sensitively and rapidly detects fewer than 500 copies of enteroviral
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                                                                                                                                                                                                                                                                                                                                                                              genome and allows detection of broad range of enterovirus serotypes. The present sequence represents a viral 5' untranslated polynucleotide sequence given in the exemplification of the present invention.
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selected amplification or detection reaction. Also described: (1) a kit
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 238 BP; 49 A; 52 C; 60 G; 77 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA detection; enteroviral detection; ds
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(PRIC/) PRICE J A.
(HELL/) HELLYER T J.
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Les 25; Conserv
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genome and allows detection of broad range of enterovirus serotypes. The present sequence represents a consensus viral 5' untranslated polynucleotide sequence given in the exemplification of the present
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human coxsackievirus B3 5' untranslated polynucleotide sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     reaction; and (b) detecting the amplified target sequence. (I), (K1) are useful for detecting enterovirus target sequences. (I) specifically and selectively recognizes the enterovirus genome.
                                                                                                                                                                          ;
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                                                                                                                                 Score 25; DB 14; Length 238; Pred. No. 0.049;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 14; Length 238;
                                                                                                                                                                        0; Indels
                                                                                              . Sequence 238 BP; 51 A; 55 C; 65 G; 67 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 238 BP; 53 A; 58 C; 64 G; 63 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 25; DB 14,
Pred. No. 0.049;
                                                                                                                               th 100.0%; Score 25; DB Similarity 100.0%; Pred. No. 0.0 25; Conservative 0; Mismatches
                                                                                                                                                                                                                                 TCGCTGCAGAGTTGCCCGTTACGA 107
                                                                                                                                                                                                            1 TCGCTGCAGAGTTGCCCGTTACGA 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA detection; enteroviral detection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure, Fig 1A-D; 34pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hellyer TJ;
                                                                                                                                                                                                                                                                                                                                            AEB56843 standard; DNA; 238 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human coxsackievirus B3.
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PRICE J A.
HELLYER T J.
                                                                                                                                                     Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US2005158710-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                        22-SEP-2005
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                                                            invention
                                                                                                                                                                                                                                                 131
                                                                                                                                                                                                                                                                                                                                                                                   AEB56843;
                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (TSAN/) (PRIC/) (HELL/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           reand
                                                                                                                                                                        Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel oligonucleotide comprising sequences for binding and amplifying or detecting target, useful for detecting enterovirus nucleic acids.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             specifically and selectively recognizes the enterovirus genome. (I) sensitively and rapidly detects fewer than 500 copies of enteroviral genome and allows detection of broad range of enterovirus serotypes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ange of enterovirus serotypes. untranslated polynucleotide
                                                                                                                                                                                                                                                        Human coxsackievirus B3 5' untranslated polynucleotide sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 238 BP; 54 A; 57 C; 62 G; 65 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                DNA detection; enteroviral detection; ds.
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                                 131 rcccrccadagrrcccccrracca 107
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25
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1 TCCGCTGCAGAGTTGCCCGTTACGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fang S, Price JA, Hellyer TJ;
                                                                                                                                      BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           16-JAN-2004; 2004US-00760048
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                                                                                                                                    AEB56845 standard; DNA; 238
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les 25; Conservative
                                                                                                                                                                                                                                                                                                                                       Human coxsackievirus B3
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PRICE J A.
HELLYER T J.
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                                                                                                                                                                                                                                                                                                                                                                               US2005158710-A1.
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(PRIC/) I
(HELL/) I
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Matches
                                                                                               RESULT 38
AEB56845/
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RESULT 39 AEB56774/c us-10-829-474-4.rng

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RESULT 41
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                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to an oligonucleotide (1) consisting of: (a) the target binding sequence of an oligonucleotide chosen from any one of the carget binding sequence of ABBS6771; and (b) a sequence required for selected amplification or detection reaction. Also described: (1) a kit (K1) comprising (1), and one or more container that contains (1); and (2) detecting (M1) an enterovirus target sequence, involving: (a) amplifying the target sequence using first amplification primer having a sequence consisting essentially of target binding sequence of any one of ABBS6764 to ABBS6771 and optionally a sequence required for selected amplification reaction; and (b) detecting the amplified target sequence. (1), (M1) and (K1) are useful for detecting enterovirus target sequences. (1) (M1) and specifically and selectively recognizes the enterovirus genome. (1) specifically and selectively recognizes the enterovirus senotypes. The sensitively and rapidly detects fewer than 500 copies of enteroviral sensitively and selection of broad range of enterovirus serotypes. The present sequence represents a viral 5' untranslated polymucleotide sequence given in the exemplification of the present invention.
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                                                                                                                                                                                                                                                                                                                                             Novel oligonucleotide comprising sequences for binding and amplifying or detecting target, useful for detecting enterovirus nucleic acids.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Viral 5' untranslated polynucleotide sequence SEQ ID NO:27.
                                                                      Viral 5' untranslated polynucleotide sequence SEQ ID NO:13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 238 BP; 59 A; 51 C; 54 G; 74 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA detection; enteroviral detection; ds.
                                                                                              DNA detection; enteroviral detection; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 TCCGCTGCAGAGTTGCCCGTTACGA 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   75 rccgcrdcagagrrdcccgrracga 51
                                                                                                                                                                                                                                                                                               Hellyer TJ
BP
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                                                                                                                                                                                                                      16-JAN-2004; 2004US-00760048
AEB56774 standard; DNA; 238
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                                                (first entry)
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nes 25; Conservative
                                                                                                                                                                                                                                            (TSAN/) TSANG S.
(PRIC/) PRICE J A.
(HELL/) HELLYER T J.
                                                                                                                                                                                                                                                                                             Tsang S, Price JA,
                                                                                                                                                                                                                                                                                                                   WPI; 2005-512251/52
                                                                                                                                             JS2005158710-A1.
                                                                                                                     Unidentified
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                                                22-SEP-2005
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                        AEB56774
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Matches
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AEB56788/c
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The invention relates to an oligonucleotide (I) consisting of: (a) the target binding sequence of an oligonucleotide chosen from any one of the 10 sequence of ABBS6771; and (b) a sequence required for selected amplification or detection reaction. Also described: (I) a kit (KI) comprising (I), and one or more container that contains (I); and (2) detecting (MI) an enterovirus target sequence, involving: (a) amplifying the target sequence using first amplification primer having a sequence consisting essentially of target binding sequence of any one of ABBS676 to ABBS6771 and optionally a sequence required for selected amplification reaction; and (b) detecting the amplified target sequence. (I), (MI) and (KI) are useful for detecting energy recognizes the enterovirus genome. (I) specifically and selectively recognizes the enterovirus genome. (I) sensitively and rapidly detects fewer than 500 copies of enteroviral cyneme and allows detection of broad range of enterovirus serotypes. The present sequence represents a viral 5' untranslated polymucleotide sequence con the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel oligonucleotide comprising sequences for binding and amplifying or detecting target, useful for detecting enterovirus nucleic acids.
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Pred. No. 0.049;
; Mismatches 0; Indels (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; SEQ ID NO 27; 34pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fang S, Price JA, Hellyer TJ;
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ID AEB56792 standard; DNA; 238 BP.
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                                                                                                                                                                                                                                                                                                                                                                      (TSAN/) TSANG S.
(PRIC/) PRICE J A.
(HELL/) HELLYER T J.
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                                                                      JS2005158710-A1
Unidentified
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Disclosure; SEQ ID NO 22; 34pp; English.
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                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                             RESULT 43
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                                                                                                                                             The invention relates to an oligonucleotide (I) consisting of: (a) the target binding sequence of an oligonucleotide chosen from any one of the target binding sequence of ABBS6771; and (b) a sequence required for selected amplification or detection reaction. Also described: (1) a kit (K1) comprising (II), and one or more container that contains (I); and (2) detecting (M1) an enterovirus target sequence, involving: (a) amplifying the target sequence using first amplification primer having a sequence consisting essentially of target binding sequence of any one of ABBS6764 to ABBS6771 and optionally a sequence required for selected amplification reaction, and (b) detecting the amplified target sequence. (I), (M1) and (K1) are useful for detecting enterovirus target sequence. (I) specifically and selectively recognizes the enterovirus genome. (I) sensitively and rapidly detects fewer than 500 copies of enteroviral contains and analyse detection of broad range of enterovirus fargetypes. The
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                                                                                          Novel oligonucleotide comprising sequences for binding and amplifying or detecting target, useful for detecting enterovirus nucleic acids.
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                                                                                                                                                                                                                                                                                                              untranslated polynucleotide
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Viral 5' untranslated polynucleotide sequence SEQ ID NO:22
                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                                                                                                                                                Sequence 238 BP; 54 A; 52 C; 58 G; 74 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
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                                                                                                                         Disclosure, SEQ ID NO 31; 34pp; English
                                                                                                                                                                                                                                                                                                              viral 5'
                                                                                                                                                                                                                                                                                                                                                                                                                   25
                                                                                                                                                                                                                                                                                                                                                                                                                                       rcccrccagacrrccccrracga 51
                                                                                                                                                                                                                                                                                                                                                                                                                   1 TCCGCTGCAGAGTTGCCCGTTACGA
                                              Hellyer TJ;
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                                                                                                                                                                                                                                                                                                                                                                      100.0%;
                                                                                                                                                                                                                                                                                                              sequence represents a
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                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100.0
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(TSAN/) TSANG S.
(PRIC/) PRICE J A.
(HELL/) HELLYER T J.
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(PRIC/) PRICE J A.
(HELL/) HELLYER T J.
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                                              Price JA,
                                                                    WPI; 2005,512251/52
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target binding sequence of an oligonuclectide chosen from any one of the lose of ABBS676 to ABBS671; and (b) a sequence required for selected amplification or detection reaction. Also described. (1) a kit (X1) comprising (1), and one or more container that contains (1); and (2) detecting (M1) an enterovirus target sequence, involving: (a) amplifying the target sequence using first amplification primer having a sequence consisting essentially of target binding sequence of any one of ABBS670 to ABBS6771 and optionally a sequence required for selected amplification reaction, and (b) detecting enterovirus target sequence. (1), (M1) and (X1) are useful for detecting enterovirus target sequence. (1), (M1) and (X1) are useful for detecting enterovirus target sequences. (1) specifically and selectively recognizes the enterovirus genome. (1) sensitively and rapidly detects fewer than 500 copies of enteroviral genome and allows detection of broad range of enterovirus recovers. Or present sequence represents a viral S, untranslated polymorlecting enterovirus in the example of a viral S, untranslated polymorlecting enterovirus translated polymorlecting enterovirus translated polymorlecting enterovirus enterovirus enterovirus enterovirus consisting enterovirus than the enterovirus enterovirus than the example of enterovirus enter
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The invention relates to an oligonucleotide (I) consisting of:
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AEB56786 standard; DNA; 238
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(PRIC/) PRICE J A.
(HELL/) HELLYER T J.
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Sequence 238 BP; 57 A; 52 C; 58 G; 71 T; 0 U; 0 Other;

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The invention relates to an oligonucleotide (1) consisting of: (a) the target binding sequence of an oligonucleotide chosen from any one of the consequence of ABB56782 to ABB56771; and (b) a sequence required for selected amplification or detection reaction. Also described: (1) a kit (K1) comprising (1), and one or more container that contains (1); and (2) detecting (M1) an enterovirus target sequence, involving: (a) amplifying the target sequence using first amplification primer having a sequence consisting essentially of target binding sequence of any one of ABB56764 to ABB56771 and optionally a sequence required for selected amplification reaction; and (b) detecting the amplified target sequence. (1), (M1) and (M1) are useful for detecting enterovirus target sequence. (1) specifically and selecting enterovirus target sequence. (1) specifically and selecting enterovirus target sequence. (1) specifically and selectively recognizes the enterovirus genome. (1) sensitively and rapidly detects fewer than 500 copies of enteroviral genome and allows detection of broad range of enterovirus serotypes. The present sequence represents a viral 5' untranslated polymucleotide sequence given in the exemplification of the present invention.
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               to AEB56771 and optionally a sequence required for selected amplification reaction; and (b) detecting the amplified target sequence. (I), (M1) and (K1) are useful for detecting enterovirus target sequences. (I) specifically and selectively recognizes the enterovirus genome. (I) genome and allows detection of broad range of enterovirus genorically and rapidly detects fewer than 500 copies of enteroviral present sequence represents a viral S' untranslated polynuclectide sequence given in the exemplification of the present invention.
consisting essentially of target binding sequence of any one of AEB56764
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                                                                                                                                                                                                                                                             100.0%; Score 25; DB 14; Length 238; 100.0%; Pred. No. 0.049; ive 0; Mismatches 0; Indels (
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                                                                                                                                                                                                                      Sequence 238 BP; 55 A; 53 C; 59 G; 71 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                        1 TCCGCTGCAGAGTTGCCCGTTACGA 25
                                                                                                                                                                                                                                                                                                                                                                                   75 TCCGCTGCAGAGTTGCCCGTTACGA 51
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AEB56787 standard; DNA; 238 BP.
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nes 25; Conservative
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(PRIC/) PRICE J A.
(HELL/) HELLYER T J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sensitively and rapidly detects fewer than 500 copies of enteroviral genome and allows detection of broad range of enterovirus serotypes. present sequence represents a viral 5' untranslated polynucleotide
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100.0%; Score 25; DB 14; Length 238; 100.0%; Pred. No. 0.049;
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              100.0%; Prec. ...
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Conservative 0; Mismatches
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                                         Conservative
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(PRIC/) PRICE J A.
(HELL/) HELLYER T J.
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                    Local Similarity
hes 25; Conserv
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Matches 25; Conserv
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 Query Match
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                                         Matches
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AEB56830;

AEB56830/

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The invention relates to an oligonucleotide (I) consisting of: (a) the target binding sequence of an oligonucleotide chosen from any one of the target binding sequence of ABB56772 to ABB56771; and (b) a sequence required for selected amplification or detection reaction. Also described. (1) a kit (XI) comprising (II), and one or more container that contains (I); and (2) detecting (MI) an enterovirus target sequence, involving: (a) amplifying the target sequence using first amplification primer having a sequence of consisting essentially of target binding sequence of any one of ABB56764 to ABB56771 and optionally a sequence required for selected amplification reaction; and (b) detecting the amplified target sequence. (I), (MI) and (KI) are useful for detecting enterovirus target sequence. (I) specifically and selectively recognizes the enterovirus genome. (I) sensitively and rapidly detects fewer than 500 copies of enteroviral secretypes. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel oligonucleotide comprising sequences for binding and amplifying or detecting target, useful for detecting enterovirus nucleic acids.
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                        Human echovirus 11 5' untranslated polynucleotide sequence.
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                                                                    DNA detection; enteroviral detection; ds.
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                                                                                                                                                                                                                                                                                                                                                  (TSAN/) TSANG S.
(PRIC/) PRICE J A.
(HELL/) HELLYER T J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tsang S, Price JA,
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GENBANK; X80059.
                                                                                                                   Human echovirus 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to an oligonucleotide (I) consisting of: (a) the target binding sequence of an oligonucleotide chosen from any one of the 10 sequence of ABB56762 to ABB5671; and (b) a sequence required for selected amplification or detection reaction. Also described: (I) a kit (KI) comprising (I), and one or more container that contains (I); and (2) detecting (MI) an enterovirus target sequence, involving: (a) amplifying the target sequence using first amplification primer having a sequence consisting essentially of target binding sequence of any one of ABB56764
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        to AEB56771 and optionally a sequence required for selected amplification reaction; and (b) detecting the amplified target sequence. (I), (M1) and (K1) are useful for detecting enterovirus target sequences. (I)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sensitively and rapidly detects fewer than 500 copies of enteroviral genome and allows detection of broad range of enterovirus serotypes. The present sequence represents a viral 5' untranslated polynucleotide sequence given in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel oligonucleotide comprising sequences for binding and amplifying or detecting target, useful for detecting enterovirus nucleic acids.
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                                                                                                                                                                                                                              Human coxsackievirus A9 5' untranslated polynucleotide sequence.
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                                                                                                                                                                                                                                                                             DNA detection; enteroviral detection; ds
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                                                                                     AEB56830 standard; DNA; 238 BP
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PRICE J A.
HELLYER T J.
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AEB56864;

AEB56864/c ID AEB568 XX AC AEB568 XX DT 22-SEP

RESULT 47

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Query Match Best Local S: Matches 25,

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The invention relates to an oligonucleotide (I) consisting of: (a) the target binding sequence of an oligonucleotide chosen from any one of the 10 sequence of ABSS672 to ABSS671; and (b) a sequence required for selected amplification or detection reaction. Also described: (I) a kit (KI) comprising (I), and one or more container that contains (I); and (2) detecting (MI) an enterovirus target sequence, involving: (a) amplifying the target sequence using first amplification primer having a sequence consisting essentially of target binding sequence of any one of ABSS6764 to ABSS6771 and optionally a sequence required for selected amplification reaction; and (b) detecting enterovirus target sequence. (I), (MI) and (XI) are useful for detecting enterovirus target sequences. (I) specifically and selectively recognizes the enterovirus genome. (I) sensitively and rapidly detects fewer than 500 copies of enteroviral genome and allows detection of broad range of enterovirus serotypes. The present sequence represents a viral 5' untranslated polynucleotide
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                                                                                                                    Novel oligonucleotide comprising sequences for binding and amplifying or detecting target, useful for detecting enterovirus nucleic acids.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 238 BP; 58 A; 55 C; 55 G; 70 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
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                                                                                                                                                                                             Disclosure, SEQ ID NO 15; 34pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 TCCGCTGCAGAGTTGCCCGTTACGA 25
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                         Hellyer TJ;
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Best Local Similarity 100.0
Matches 25; Conservative
                         Price JA,
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(PRIC/) PRICE J A.
(HELL/) HELLYER T J.
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                         Isang S,
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AEB56790/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  to AEB56771 and optionally a sequence required for selected amplification reaction; and (b) detecting the amplified target sequence. (I), (M1) and (K1) are useful for detecting enterovirus target sequences. (I)
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AEB56776 standard; DNA; 238
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Best Local Similarity 100.
Matches 25; Conservative
                                                                                                                                          (TSAN/) TSANG S.
(PRIC/) PRICE J A.
(HELL/) HELLYER T J.
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(PRIC/) PRICE J A.
(HELL/) HELLYER I J.
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21-JUL-2005
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**AEB56776/** 

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The invention relates to an oligonucleotide (I) consisting of: (a) the target binding sequence of an oligonucleotide chosen from any one of the 10 sequence of ABBS672 to ABBS6771; and (b) a sequence required for selected amplification or detection. Also described: (1) a kit (X1) comprising (I), and one or more container that contains (I); and (2) detecting (MI) an enterovirus target sequence, involving: (a) amplifying the target sequence using first amplification primer having a sequence consisting essentially of target binding sequence of any one of ABBS6764 consisting essentially of target binding sequence of any one of ABBS6764 consisting and Oblicanally a sequence required for selected amplification reaction; and (b) detecting the amplified target sequences. (I) (X1) are useful for detecting enterovirus target sequences. (I) (X1) are useful for detecting enterovirus target sequences. (I) (X1) and selectively recognizes the enterovirus genome. (I) sensitively and rapidly detects fewer than 500 copies of enteroviral connect represents a viral 5' untranslated polynucleotide
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                                                                                                                                                                                                                                                                                                              sequence given in the exemplification of the present invention
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                                                                                                                                                                                                                                                                                                                                                     Sequence 238 BP; 57 A; 51 C; 57 G; 73 T; 0 U; 0 Other;
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ID AEB56841 standard; DNA; 238
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hes 25; Conservative
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(PRIC/) PRICE J A.
(HELL/) HELLYER T J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      S, Price JA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2005-512251/52
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22-SEP-2005
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                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               to AEB56771 and optionally a sequence required for selected amplification reaction; and (b) detecting the amplified target sequence. (I), (M1) and (K1) are useful for detecting enterovirus target sequences. (I)
        and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel oligonucleotide comprising sequences for binding and amplifying or detecting target, useful for detecting enterovirus nucleic acids.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The
  reaction; and (b) detecting the amplified target sequence. (I), (MI) (XI) are useful for detecting enterovirus target sequences. (I) specifically and selectively recognizes the enterovirus genome. (I) sensitively and rapidly detects fewer than 500 copies of enteroviral genome and allows detection of broad range of enterovirus serotypes. Present sequence represents a viral 5' untranslated polynuclectide sequence given in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       specifically and selectively recognizes the enterovirus genome. (I) sensitively and rapidly detects fewer than 500 copies of enteroviral genome and allows detection of broad range of enterovirus serotypes. present sequence represents a viral 5' untranslated polymucleotide
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                                                                                                                                                                                                  100.0%; Score 25; DB 14; Length 238; 100.0%; Pred. No. 0.049; 100.0%; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Viral 5' untranslated polynucleotide sequence SEQ ID NO:48.
                                                                                                                                                              Sequence 238 BP; 52 A; 58 C; 65 G; 63 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA detection; enteroviral detection; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; SEQ ID NO 48; 34pp; English.
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                                                                                                                                                                                                                                                                                     25
                                                                                                                                                                                                                                                                                     1 TCCGCTGCAGAGTTGCCCGGTTACGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Price JA, Hellyer TJ;
                                                                                                                                                                                                                                                                                                                                                                                                                             BP.
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                                                                                                                                                                                                                                                                                                                                                                                                        AEB56809/c
ID AEB56809 standard; DNA; 238
                                                                                                                                                                                              Query Match
Best Local Similarity 100.'
Matches 25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22-SEP-2005 (first entry)
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(PRIC/) PRICE J A.
(HELL/) HELLYER T J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2005-512251/52
and (b)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unidentified
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AEB56809;
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55 G; 76 T; 0 U; 0 Other;

Sequence 238 BP; 53 A; 54 C;

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RESULT 54
                             AEB56808,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to an oligonucleotide (I) consisting of: (a) the target binding sequence of an oligonucleotide chosen from any one of the 10 sequence of AEBS6702 to AEBS6771; and (b) a sequence required for selected amplification or detection reaction. Also described: (I) a kit (KI) comprising (I), and one or more container that contains (I); and (2) detecting (MI) an enterovirus target sequence, involving: (a) amplifying the target sequence using first amplification primer having a sequence consisting essentially of target binding sequence of any one of AEBS6764 to AEBS671 and optionally a sequence required for selected amplification reaction; and (b) detecting the amplified target sequence. (I) (MI) and selection and the recognizes the enterovirus genome. (I) sensitively and rapidly detects fewer than 500 copies of enteroviral genome and allows detection of broad range of enteroviral
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel oligonucleotide comprising sequences for binding and amplifying or detecting target, useful for detecting enterovirus nucleic acids.
                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                               Human coxsackievirus A16 5' untranslated polynucleotide sequence
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100.0%; Score 25; DB 14; Length 238; 100.0%; Pred. No. 0.049; or Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 14; Length 238;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 238 BP; 51 A; 55 C; 64 G; 68 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 25; DB 14
Pred. No. 0.049;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA detection; enteroviral detection; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              viral 5'
                                                                                                1 TCCGCTGCAGAGTTGCCCGTTACGA 25
                                                                                                                         Disclosure; Fig 1A-D; 34pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hellyer TJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%;
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                                                                                                                                                                                                                                                                  AEB56831 standard; DNA; 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sequence represents
                                                                                                                                                                                                                                                                                                                                                                (first entry)
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Best Local Similarity 100.
Matches 25; Conservative
                                                 25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human coxsackievirus A16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (TSAN/) TSANG S.
(PRIC/) PRICE J A.
(HELL/) HELLYER T J.
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                           Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US2005158710-A1
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Query Match
                                                                                                                                                                                                                     RESULT 53
ABB56811/C
ADB56811/C
A
                                               Matches
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The invention relates to an oligonucleotide (I) consisting of: (a) the target binding sequence of an oligonucleotide chosen from any one of the 10 sequence of ABBS6771; and (b) a sequence required for selected amplification or detection reaction. Also described: (1) a kit (K1) comprising (I), and one or more container that contains (I); and (2) detecting (M1) an enterovirus target sequence, involving: (a) amplifying the target sequence using first amplification primer having a sequence consisting essentially of target binding sequence of any one of ABBS676 to ABBS6771 and optionally a sequence required for selected amplification reaction; and (b) detecting the amplified target sequence. (I), (M1) and (K1) are useful for detecting enterovirus target sequence. (I) specifically and selectively recognizes the enterovirus genome. (I) specifically and rapidly detects fewer than 500 copies of enteroviral genome and allows detection of broad range of enterovirus serotypes. The present sequence represents a viral 5 untranslated polynucleotide sequence given in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel oligonucleotide comprising sequences for binding and amplifying or detecting target, useful for detecting enterovirus nucleic acids.
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                                                                                                                                                                                                        Viral 5' untranslated polynucleotide sequence SEQ ID NO:47.
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Pred. No. 0.049;
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                                                                                                                                                                                                                                                                        DNA detection; enteroviral detection; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; SEQ ID NO 47; 34pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Price JA, Hellyer TJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 55
AEB56844/c
ID AEB56844 standard; DNA; 238 BP.
AEB56808 standard; DNA; 238 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16-JAN-2004; 2004US-00760048.
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                                                                                                                                     (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (TSAN/) TSANG S.
(PRIC/) PRICE J A.
(HELL/) HELLYER T J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2005-512251/52
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                              JS2005158710-A1
                                                                                                                                                                                                                                                                                                                                           Unidentified.
                                                                                                                                     22-SEP-2005
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Gaps

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0; Indels

0; Mismatches

1 TCCGCTGCAGAGTTGCCCGTTACGA 25

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us-10-829-474-4.rng

21-JUL-2005

Tsang S,

WPI;

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target binding sequence of an oligonucleotide chosen from any one of the selected amplification or detection reaction. As degence required for selected amplification or detection reaction. As described: (1) a kit (K1) comprising (1), and one or more contains that contains (1); and (2) detecting (M1) an enterovirus target sequence, involving: (a) amplifying the target sequence using first amplification primer having a sequence consisting essentially of target binding sequence of any one of AEBS6774 to AEBS6771 and optionally a sequence required for selected amplification reaction; and (b) detecting the amplified target sequence. (1), (M1) and (K1) are useful for detecting enterovirus target sequences. (1), (M1) and (K1) are useful for detecting enterovirus target sequences. (1), (M1) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (KI) are useful for detecting enterovirus carge, evacuate the useful for detecting enterovirus genome. (I) specifically and selectively recognizes the enterovirus genomially and rapidly detects fewer than 500 copies of enteroviral genome and allows detection of broad range of enterovirus serotypes. The genome and allows detection of variance of enterovirus detection of broad range of enterovirus serotypes. The genome and allows detection of variance invention.
                                                                                                                                                                                                                                                                          Novel oligonucleotide comprising sequences for binding and amplifying or detecting target, useful for detecting enterovirus nucleic acids.
                                                                                                                                                                                                                                                                                                                                                                                                  to an oligonuclectide (I) consisting of: (a) the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Coxeackie virus strain VD2921; diabetogenic coxeackie B virus-4; strain VD2921; VP1; VP2; VP4; P2A; P2B; P2C; P3A; P3B; P3C; diabetes; diabetogenic enterovirus; beta cell loss; blindness; renal failure; leg amputation; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 25; DB 14; Length 238; 100.0%; Pred. No. 0.049;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Coxsackie B virus 4 (CBV-4) strain VD2921 associated DNA #6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 238 BP; 48 A; 52 C; 60 G; 78 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                               Disclosure; SEQ ID NO 43; 34pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 TCCGCTGCAGAGTTGCCCGTTACGA 25
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                                                                                                                                                                           Tsang S, Price JA, Hellyer TJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABX12451 standard; DNA; 502 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (INNO-) INNOVENTUS PROJECT AB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20-JUN-2001; 2001SE-00002198.
                         16-JAN-2004; 2004US-00760048
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1es 25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates
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                                                                          (TSAN/) TSANG S.
(PRIC/) PRICE J A.
(HELL/) HELLYER I J.
                                                                                                                                                                                                                         WPI; 2005-512251/52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO2002103060-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Coxsackievirus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABX12451;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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ABX12451/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to an oligonucleotide (I) consisting of: (a) the target binding sequence of an oligonucleotide chosen from any one of the 10 sequence of ABB5672 to ABB5671; and (b) a sequence required for selected amplification or detection reaction. Also described: (1) a kit (K1) comprising (I), and one or more container that contains (I); and (2) detecting (M1) an enterovirus target sequence, involving: (a) amplifying the target sequence using first amplification primer having a sequence consisting essentially of target binding sequence of any one of ABB56764 to ABB56771 and optionally a sequence required for selected amplification reaction; and (b) detecting the amplified target sequence. (I), (M1) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel oligonucleotide comprising sequences for binding and amplifying or detecting target, useful for detecting enterovirus nucleic acids.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    reaction, and (b) detecting the amplified target sequence. (I), (M1) (K1) are useful for detecting enterovirus target sequences. (I) specifically and selectively recognizes the enterovirus genome. (I) sensitively and rapidly detects fewer than 500 copies of enteroviral genome and allows detection of broad range of enterovirus serotypes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               untranslated polynucleotide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             present sequence represents a viral 5' untranslated polynucleo sequence given in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 14; Length 238;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Viral 5' untranslated polynucleotide sequence SEQ ID NO:43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 238 BP; 53 A; 57 C; 64 G; 64 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 25; DB 14
Pred. No. 0.049;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Scc.
100.0%; Pred. No. v
0; Mismatches
DNA detection; enteroviral detection; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       131 TCCGCTGCAGAGTTGCCCGTTACGA 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 TCGCTGCAGAGTTGCCCGTTACGA 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Fig 1A-D; 34pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                  Hellyer TJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AEB56804/c
ID AEB56804 standard; DNA; 238 BP.
                                                                                                                                                                                               16-JAN-2004; 2004US-00760048
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                                                Human coxsackievirus B3
                                                                                                                                                                                                                                                                                            (TSAN/) TSANG S.
(PRIC/) PRICE J A.
(HELL/) HELLYER T J.
                                                                                                                                                                                                                                                                                                                                                                                               Price JA,
                                                                                                                                                                                                                                                                                                                                                                                                                                        2005-512251/52
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Gaps

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Indels

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P3D;

22-SEP-2005

AEB56804;

Query Match

Matches

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21-JUL-2005.

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The invention describes a polymerase chain reaction (PCR) and primers for detecting nucleic acids from the diabetogenic coxsackie B virus-4 (CBV-4) strain VD2921, (particularly VP1, VP2, VP3, VP4, P2A, P2B, P2C, P3A, P3B, P3C and P3D nucleic acids). The methods and primers are used for the detection of CBV-4 strain VD2921 which is associated with diabetes detection of chabetogenic enterovirus). Early detection of the diabetes e.g. detection of diabetogenic enteroviral RNA in peripheral mononuclear cells, can improve prognosis by allowing treatment e.g. with antiviral drugs, to prevent further loss of beta cells and severe long term consequences of diabetes including blindness, renal failure and leg amputations. This sequence represents a diabetogenic coxsackie B virus 4
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                                                                       Polymerase chain reaction and primers for detecting nucleic acids from the diabetogenic coxsackie B virus-4 strain VD2921.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 25; DB 8; Length 502; 100.0%; Pred. No. 0.053;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 502 BP; 120 A; 132 C; 128 G; 122 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (CBV-4) strain VD2921 associated polynucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
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                                                                                                                                                                                   Disclosure; Page 73; 79pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19-JUN-2002; 2002WO-IB003278.
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ABX12448 standard; DNA; 548
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WPI; 2003-278229/27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO2002103060-A2.
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ABX12448/c
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The invention describes a polymerase chain reaction (PCR) and primers for detecting nucleic acids from the diabetogenic coxsackie B virus-4 (CBV-4) strain vD2921, (particularly VP1, VP2, VP3, VP4, P2A, P2B, P2C, P3A, P3B, P3C and P3D nucleic acids). The methods and primers are used for the detection of CBV-4 strain VD2921 which is associated with diabetes (diabetogenic enterovirus). Early detection of the diabetes e.g.

Polymerase chain reaction and primers for detecting nucleic acids from the diabetogenic coxsackie B virus-4 strain VD2921.

WPI; 2003-278229/27

Disclosure; Page 72; 79pp; English

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Coxsackie virus strain VD2921; diabetogenic coxsackie B virus-4; CBV-4; strain VD2921; VP1; VP2; VP3; VP4; P2A; P2B; P2C; P3A; P3B; P3C; P3D; diabetes; diabetogenic enterovirus; beta cell loss; blindness; renal failure; leg amputation; ds.
detection of diabetogenic enteroviral RNA in peripheral mononuclear cells, can improve prognosis by allowing treatment e.g. with antiviral drugs, to prevent further loss of beta and severe long term consequences of diabetes including blindness, renal failure and leg amputations. This sequence represents a diabetogenic coxsackie B virus (CBV-4) strain VD2921 associated polynucleotide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Coxsackie B virus 4 (CBV-4) strain VD2921 associated DNA #8.
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                                                                                                                                                                           100.0%; Score 25; DB 8; Length 548; 100.0%; Pred. No. 0.054;
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                                                                                                                                       Sequence 548 BP; 124 A; 145 C; 144 G; 135 T; 0 U; 0 Other;
                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                              TCCGCTGCAGAGTTGCCCGTTACGA 418
                                                                                                                                                                                                                                                        1 TCCGCTGCAGAGTTGCCCGTTACGA 25
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                                                                                                                                                                                                                                                                                                                                                                                             BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19-JUN-2002; 2002WO-IB003278.
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                                                                                                                                                                                               Local Similarity 100.
1es 25; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                               ABX12453;
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                                                                                                                                                                             Query Match
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                                                                                                                                                                                                                                                                                                                                                      RESULT
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ABX12452;

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The invention provides an enterovirus genome (I) for use as a vector or vaccine, modified to produce a virus (VI) having a restricted or altered species or tissue tropism, compared to an equivalent unmodified virus, or modified to produce an attenuated virus (V2), by replacing a part or all of the 5'non-translated region (5'NTR) of (I) with a 5'NTR of an enterovirus genome that encodes VI or V2. (I) is useful as vaccine or vector in targeting genes of interest to specific cells or tissues. (I) is also useful for diagnostic purposes, e.g. to identify virulent, versus nonvirulent strains of an enterovirus. The present sequence represents the 5'NTR (non-translated region) of a non-cardiovirulent enterovirus
                                                                                                                                                                                                                                                                                                                                                                                                                                      Recombinant enterovirus genome for use as vector or vaccine, modified by replacing a part or all of its 5'non-translated region by 5'NTR of enterovirus genome that encodes virus modified in tropism or virulence.
    Coxsackievirus B3 (CVB3)/CO 5' non-translated region (NTR) sequence.
                                          Gene therapy; enterovirus; vaccine; diagnostic; RT-PCR; primer; Coxsackievirus B3; CVB3; NTR; non-translated region; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                           Dunn JJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 2; Page 25; 49pp; English.
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nes 25; Conservative
                                                                                                                                                                                                                                                                                                                                                         Bradrick SS,
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                                                                                                         Coxsackievirus.
                                                                                                                                               WO200104136-A1.
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                                                                                                                                                                                                                                                                                                                                                         Romero JR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AEB56828;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 62
AEB56828/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
    셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Š
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention describes a polymerase chain reaction (PCR) and primers for detecting nucleic acids from the diabetogenic coxsackie B virus-4 (CBV-4) strain VD221, (particularly VP1, VP2, VP3, VP4, P2A, P2B, P2C, P3A, P3B, P3C and P3D nucleic acids). The methods and primers are used for the detection of CBV-4 strain VD291 which is associated with diabetes (diabetogenic enterovirus). Early detection of the diabetes e.g. (diabetogenic enteroviral RNA in peripheral monomuclear cells, can improve prognosis by allowing treatment e.g. with antiviral drugs, to prevent further loss of beta cells and severe long term consequences of diabetes including blindness, renal failure and leg
                                                                                                                                                                                                                                                                                                          Coxeackie virus strain VD2921; diabetogenic coxeackie B virus-4; CBV-4; strain VD2921; VP1; VP2; VP3; VP4; P2A; P2B; P2C; P3A; P3B; P3C; P3D; diabetes; diabetogenic enterovirus; beta cell loss; blindness; renal failure; leg amputation; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Polymerase chain reaction and primers for detecting nucleic acids from the diabetogenic coxsackie B virus-4 strain VD2921.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                 Coxsackie B virus 4 (CBV-4) strain VD2921 associated DNA #7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 25; DB 8; Length 552; 100.0%; Pred. No. 0.054;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 552 BP; 131 A; 143 C; 140 G; 138 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (CBV-4) strain VD2921 associated polynucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             . 0.054;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                       TCCGCTGCAGAGTTGCCCGTTACGA 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  449 TCCGCTGCAGAGTTGCCCGTTACGA 425
25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 TCCGCTGCAGAGTTGCCCGTTACGA 25
TCCGCTGCAGAGTTGCCCGTTACGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 73; 79pp; English.
                                                                                                                                             Ħ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (INNO-) INNOVENTUS PROJECT AB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20-JUN-2001; 2001SE-00002198.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19-JUN-2002; 2002WO-IB003278.
                                                                                                                                         ABX12452 standard; DNA; 552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAC85174 standard; DNA; 660
                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tuvemo HT, Frisk GE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
These 25; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2003-278229/27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO2002103060-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                   Coxsackievirus
                                                                                                                                                                                                                        10-MAY-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      08-MAY-2001
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Gaps

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0; Indels

dв.

AAC85174;

RESULT 61
AAC85174/c
ID AAC8517
XX
AC AAC8517
XX
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XX
XX
XX
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(WUTT/) WU T. (LEEJ/) LEE J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Coxsackievirus
                                       Wu T,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAC85152;
                                       Hsu T,
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                                                                                                                                                                  The invention relates to an oligonucleotide (I) consisting of: (a) the target binding sequence of an oligonucleotide chosen from any one of the 10 sequence of ABB56762 to ABB56771, and (b) a sequence required for selected amplification or detection reaction. Also described: (I) a kit (KI) comprising (I), and one or more container that contains (I); and (2) detecting (MI) an enterovirus target sequence, involving: (a) amplifying the target sequence using fixst amplification primer having a sequence consisting essentially of target binding sequence of any one of ABB56764 to ABB56771 and optionally a sequence required for selected amplification reaction; and (b) detecting the amplified target sequence. (I), (MI) and (MI) are useful for detecting enterovirus target sequences. (I), (MI) and (MI) sequences.
                                                                                                                                                                                                                                                                                                           specifically and selectively recognises the enterovirus genome. (I) sensitively and rapidly detects fewer than 500 copies of enteroviral genome and allows detection of broad range of enterovirus serotypes. The present sequence represents a coxsackie virus B5 polymuclocide sequence, which is given in the exemplification of the present invention. Note: the present sequence is designated as SEQ ID NO:67 in the Sequence Listing. but corresponds with the sequence given in figure 2 designated SEQ ID
                                                                                                      Novel oligonucleotide comprising sequences for binding and amplifying or detecting target, useful for detecting enterovirus nucleic acids.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          internal ribosome entry site; cystic fibrosis; cns-gen.;
respiratory-gen.; factor VIII deficiency; hemostatic; genetic disorder;
factor IX deficiency; Duchenne dystrophy; muscular-gen.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Enterovirus 71 5' untranslated region internal ribosome entry site DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Becker's disease; cancer; cytostatic; neoplasm;
acquired immune deficiency syndrome; anti-hiv; infectious disease;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 25; DB 14; Length 660; 100.0%; Pred. No. 0.055;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 660 BP; 157 A; 170 C; 166 G; 167 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 vector; neurological disease; ds; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                            NO:14 in the description of the drawings.
                                                                                                                                            Disclosure; SEQ ID NO 67; 34pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human enterovirus 71; strain TW/2086/98.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              457 TCCGCTGCAGAGTTGCCCGTTACGA 433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 TCCGCTGCAGAGTTGCCCGTTACGA
                                       Hellyer TJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  08-JUL-2003; 2003US-00614283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            09-JUL-2002; 2002US-0394269P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AEA00424 standard; DNA; 709
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 10v...
Best 25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28-JUL-2005 (first entry)
PRICE J A.
HELLYER T J.
                                       Price JA,
                                                                WPI; 2005-512251/52
                                                                             GENBANK; AF169665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US2005112095-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              antimicrobial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26-MAY-2005,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AEA00424;
                                       Tsang S,
(PRIC/)
(HELL/)
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                                                                                   wew nucleic acid vector for the expression of at least two cistrons comprising a nucleotide sequence comprising an internal ribosome entr site (IRES) e.g. enterovirus 71 (EV71), useful for treating a patient having e.g. AIDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Coxsackievirus B3 (CVB3) 5' non-translated region (NTR) sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gene therapy, enterovirus, vaccine, diagnostic, RT-PCR; primer, Coxsackievirus B3; CVB3; NTR, non-translated region; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  in gene therapy. The present sequence is the enterovirus 71 Suntranslated region (UTR) IRES DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 25; DB 14; Length 709; 100.0%; Pred. No. 0.055; ive 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 709 BP; 165 A; 185 C; 172 G; 187 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 504 TCCGCTGCAGAGTTGCCCGTTACGA 480
                                                                                                                                                                                                                                                             Example 2; SEQ ID NO 1; 23pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 TCCGCTGCAGAGTTGCCCGTTACGA 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
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/*tag= a
/note= "stemloop B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /*tag= b
/note= "stemloop C"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /*tag= c
/note= "stemloop D"
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'note= "Domain III"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2. .b.
/*tag= d
'~+a= "Domain I"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           '*tag= e
'note= "Domain II"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAC85152 standard; RNA; 745 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              08-MAY-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100.
Matches 25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           35. .45
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Lee J;
                                                    WPI; 2005-371616/38.
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241. .444

g "Domain IV"

\*tag= 'note= '

/note= "Domain VII"

WO200104136-A1

524. .644

stem\_loop

\*tag=

08-JUL-2000; 2000WO-US018681.

99US-0143104P

09-JUL-1999;

Dunn JJ;

Bradrick SS,

Romero JR,

WPI; 2001-138310/14.

(UYNE-) UNIV NEBRASKA

Disclosure; Fig 1; 49pp; English.

887. .623 /\*tag= i /note= "Domain VI"

'\*tag= h 'note= "Domain

452. .560 /\*tag= h

stem\_loop

stem\_loop

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The invention relates to a novel method for detecting and/or quantifying Human metapneumovirus (hMPV) in a sample comprising providing at least one probe or primer specific for a nucleic acid sequence of hMPV, contacting the one probe and/or primer with the sample to allow annealing of the probe and/or primer with the nucleic acid sequence and detecting and/or quantifying the nucleic acid sequence using the annealed probe and/or primer. The method of the invention may be useful for detecting and/or quantifying Human metapneumovirus (hMPV) in a sample. The current sequence is that of the Human coxsackievirus Bl complete genomic DNA of the invention.
                                                                                                                                                                                                  Detecting and/or quantifying human, metapneumovirus (hMPV) in a sample comprises contacting the at least one probe and/or primer with the sample to allow annealing of the probe and/or primer with the nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 25; DB 12; Length 810;
Pred. No. 0.056;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Seguence 810 BP; 243 A; 180 C; 190 G; 197 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0.056;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
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/bound_moiety= "p2 probe"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Detection; enterovirus type 71; EV71; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               bound moiety= "pl probe"
                                                                                                                                                                                                                                                                                          Claim 32; SEQ ID NO 137; 158pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 TCCGCTGCAGAGTTGCCCGTTACGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     88 rccccrccagagriccccgrracga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /*tag= a
/note= "fl primer"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     primer"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              primer"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADU47469/c
ID ADU47469 standard; cDNA; 1560 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Enterovirus type 71 (EV71) cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%;
19-DEC-2003; 2003WO-CA001994
                                    19-DEC-2002; 2002CA-02411264.
24-JAN-2003; 2003CA-02418004.
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'note= "f2
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note= "f3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             '*tag= d
'note= "f5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27-JAN-2005 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .266
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                                                                                                                                                                WPI; 2004-500307/47.
                                                                                       (UYLA-) UNIV LAVAL
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                                                                                                                           Boivin G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADU47469;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention provides an enterovirus genome (1) for use as a vector or vaccine, modified to produce a virus (V1) having a restricted or altered species or tissue tropism, compared to an equivalent unmodified virus, or modified to produce an attenuated virus (V2), by replacing a part or all of the 5'non-translated region (5'NTR) of (1) with a 5'NTR of an enterovirus genome that encodes V1 or V2. (1) is useful as vaccine or vector in targeting genes of interest to specific cells or tissues. (1) is also useful for diagnostic purposes, e.g. to identify virulent, versus nonvirulent strains of an enterovirus. The present sequence represents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Recombinant enterovirus genome for use as vector or vaccine, modified by replacing a part or all of its 5'non-translated region by 5'NTR of enterovirus genome that encodes virus modified in tropism or virulence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /irulent strains of an enterovirus. The present sequence represents enterovirus Coxsackievirus B3 (CVB3) 5' NTR (non-translated region)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
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0.056;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human coxsackievirus B1 complete genomic DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 25; DB
100.0%; Pred. No. 0.0
ive 0; Mismatches
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1 TCCGCTGCAGAGTTGCCCGTTACGA

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Query Match 100. Best Local Similarity 100. Matches 25; Conservative

seguence

ADP82873 standard; DNA; 810

ADP82873/c RESULT 65

(first entry)

23-SEP-2004

ADP82873;

Human coxsackievirus Bl

WO2004057021-A2

08-JUL-2004

hMPV detection; ds

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Gaps

CBV-4;

Coxsackie virus strain VD2921; diabetogenic coxsackie B virus-4; CBV--strain VD2921; VP1; VP2; VP3; VP4; P2A; P2B; P2C; P3A; P3B; P3C; P3D; diabetes; diabetogenic enterovirus; beta cell loss; blindness; renal failure; leg amputation; ds.

Coxsackievirus

Diabetogenic coxsackie B virus 4 (CBV-4) strain VD2921 genome

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The invention provides a method and a kit for detecting and differentiating an enterovirus type 71 (8771) in a sample. The method involves contacting nucleic acids in the sample with a pair of primers to form an amplification product; contacting the amplification product with at least one synthetic nucleotide sequence fixed on a solid substrate and detecting hybridisation. The present sequence is the enterovirus type 71 (BV71) cDNN.
                                                                                                                                                                                                                                                                                                                                                                                                                                           New kit comprising a pair of oligonucleotide primers for nucleic acid amplification, useful in detecting and differentiating an enterovirus in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 13; Length 1560;
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has 0; Indels
                                                                                                                                                                          *tag= 1
bound_moiety= "71-2/16-2 probe"
                                                                                                                                                     *tag= m
bound moiety= "71-3 probe"
485. _1504
                                                                                                                                                                                                                                                                                                                                                                                         Wang S;
          *tag= g
bound moiety= "p3 probe"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 25;
Pred. No. 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; SEQ ID NO 16; 14pp; English.
                                                                                                                                                                                                                                                                                                                                                                                       Wang Y,
                                                             27. .645
*tag= i
note= "rl primer"
                                          *tag= h
note= "r2 primer"
                                                                                                           *tag= j
note= "f7 primer"
344. .1373
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'note= "r3 primer"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%;
100.0%;
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                                                                                                                                                                                                                                                                                                                                            28-NOV-2000; 2000US-00724678.
                                                                                                179. .1198
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                              .602
 .574
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ses 25; Conservative
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misc_binding
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The invention describes a polymerase chain reaction (PCR) and primers for detecting nucleic acids from the diabetogenic coxsackie B virus-4 (CBV-4) strain VD2921, (particularly VP1, VP2, VP3, VP4, P2A, P2B, P2C, P3A, P3B, P3C and P3D nucleic acids). The methods and primers are used for the detection of CBV-4 strain VD2921 which is associated with diabetes (diabetogenic enterovirus). Early detection of the diabetes e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Polymerase chain reaction and primers for detecting nucleic acids from the diabetogenic coxsackie B virus-4 strain VD2921.
                                                                                                                                                                                                                                                                                                                                                                                                                                           note = "Specifically claimed in claim 41" (0134, .5029
                                                                                                                                                                                                                                                                                                                                                                                                                         38"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'note = "Specifically claimed in claim 44"
                                                                                                           1. .87
/*tag= a
/note= "Specifically claimed in claim 16"
                                                                                                                                 8. .512
/*tag= b
/note= "Specifically claimed in claim 19"
513. .742
                                                                                                                                                                                                                 *tag= d
'note= "Specifically claimed in claim 25"
(43. .7303
                                                                                                                                                                                                                                                                                 *tag= e
'note= "Specifically claimed in claim 26"
953. .1726
                                                                                                                                                                                                                                                                                                                  *tag= g
note= "Specifically claimed in claim 29"
                                                                                                                                                                                                                                                                                                                                                          'note= "Specifically claimed in claim 32"
                                                                                                                                                                                    *tag≈ c
note= "Specifically claimed in claim
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                                                                                                                                                                                                                                                   *tag= f
product= "Polyprotein"
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                                                                                             Location/Qualifiers
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Gaps

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0; Mismatches

Best Loc Matches

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1 TCGCTGCAGAGTTGCCCGTTACGA 25 TCCGCTGCAGAGTTGCCCGTTACGA

516

540

RESULT 67

ABX12440/c
1D ABX12440 standard; DNA; 7392 BP
XX
AC ABX12440;
XX
DT 10-MAY-2003 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This RNA encodes an enteroviral polypeptide which is used to raise polyor monoclonal antibodies (Abs). These are useful in assays for detecting enterovirus specific antigens, as an indication of enteroviral disease. All 70 serotypes of the enteroviral family can be detected. Diseases such as myocarditis, menin- gitis, encephalitis and pancreatitis can be diagnosed using the Abs. (Updated on 25-MAR-2003 to correct PA field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                myocarditis, myositis, menin- gitis, encephalitis and pancreatitis can diagnosed using the Abs. (Updated on 25-MAR-2003 to correct PA field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Enteroviruses; monoclonal antibodies; myocarditis; myositis; meningitis; encephalitis; pancreatitis; post viral fatigue syndrome; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       for
                        with antiviral
                                                                                                                                                                                                      Gaps
                    cells, can improve prognosis by allowing treafment e.g. with antivix drugs, to prevent further loss of beta cells and severe long term consequences of diabetes including blindness, renal failure and leg amputations. This sequence represents the genome of diabetogenic coxsackie B virus 4 (CBV-4) strain VD2921
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New enteroviral polypeptide for raising group specific antibodies detecting any type of enterovirus in blood or serum, also new DNA encoding it.
                                                                                                                            Sequence 7392 BP; 2095 A; 1724 C; 1809 G; 1764 T; 0 U; 0 Other;
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0
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                                                                                                                                                                 Length 7392;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 100.0%; Score 25; DB 2; Length 7399; Best Local Similarity 100.0%; Pred. No. 0.073; Matches 25; Conservative 0; Mismatches 0; Indels
                                                                                                                                                             ; Score 25; DB 8; Length 73; Pred. No. 0.073; 0; Mismatches 0; Indels
of diabetogenic enteroviral RNA in peripheral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product= "enteroviral polypeptide"
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                                                                                                                                                                                                                                                                       538 rccccrccacacrrcccccrracca 514
                                                                                                                                                                                                                                        1 TCCGCTGCAGAGTTGCCCGTTACGA 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RNA encoding enteroviral polypeptide.
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742. .7299
/*tag= a
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                                                                                                                                                                                                                                                                                                                                                                 AAQ11816 standard; RNA; 7399 BP
                                                                                                                                                             Query Match
Best Local Similarity 100.0%;
Matches 25; Conservative 0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     89DE-03939200
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(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1991-165150/23.
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05-AUG-1991
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The present sequence is that of a coxsackie virus B3 capsid protein VP1 nucleic acid. The invention provides a non-viral vestcle vector for the clivery of nucleic acid to various cardiac cell types. The vestcle vector the cetor contains the hepatitis B virus envelope protein in which at least of a part of the liver targetting sequence is deleted and replaced with a specific cardiac cell targetting sequence. For example, the coxsackie virus B3, VP1 sequence can be used to target the vector to cardiomyocytes. The vesicle vector can be delivered intravenously or intra-arterially rather than by more invasive methods such as direct cardiac injection. It can be used to deliver gene products to replace or enhance expression of proteins for treatment of heart failure, errythmia, reperfusion injury, atherosalerosis, to promote angiogenesis, etc. The vesicles are highly stable and can be produced in large quantities, making them ideal for gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             envelope protein with cardiac targeting sequence, and nucleotide sequence for gene therapy useful for treating, e.g., heart failure, arrhythmia and
                                                                                                                                                                                                                                                                                                                                                                                                   hepatitis B virus; cardiovascular disease; heart; antiarrhythmic; antiarteriosclerotic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel non-viral vector comprises vesicular membrane with hepatitis B
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                                                                                                                                                                                                                                                                                                                                            Coxsackievirus capsid protein VP1 nucleic acid.
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rcccrccadagrrcccccrracga 514
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                                                                                                                                                         ABV76134 standard; DNA; 7399
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                                                                                                                                                                                                                                                                         07-MAR-2003 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      capsid protein; gene; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                   Gene therapy; vector;
cardiant; vasotropic;
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Best Local Similarity
Matches 25; Conserv
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atherosclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200287594-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Coxsackievirus
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538
                                                                                                                                                                                                                ABV76134;
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                                                                                                                            ABV76134/
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Gaps

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(microarray) apparatus comprising a substrate with attached nucleic probes, useful for detecting one or more microbes in a sample.
                    Novel microbe detection apparatus-related oligonucleotide probe SeqID6.
                                                               microbe detection; microbe identification; virus; viral particle;
                                                                                    pathogenic bacterium; cellular microbe; acellular microbe;
chinical diagnosis; research; epidemiological surveillance;
bioterrorism countermeasure; environmental pathogen survey;
food contaminant; radioimmunoassay; ELISA; probe; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 16; SEQ ID NO 6; 89pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Jia XY, Berger MA, Tilles JG
                                                                                                                                                                                                                                                                                                                             23-MAY-2003; 2003WO-US016461.
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                                                                                                                                                                                               Viruses.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This invention relates to a novel apparatus for detecting a microbe in a sample which comprises a substrate having multiple microbe identification sites, each having a unique address indicative of the position of that microbe identification site and groups of nucleic acid probes disposed at the microbe identification sites, each group being complementary to a target nucleic acid to provide a detectable signal at one or more microbe identification sites. The apparatus is useful for detecting the presence of one or more microbes in a sample, such as virus or viral particle, (non-)pathogenic bacteria, or cellular or acellular necessarch, epidemiological surveys, and monitoring food contaminants. Current testing procedures or devices, such as radioimmunossays and ELISA, are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          difficult to implement, time consuming, expensive, outdated, and typically rely on the use of agents that recognise and bind to membrane bound proteins or carbohydrates of the pathogen. These further cannot assay multiple pathogens. The new apparatus or device for detecting microbes overcomes these disadvantages. The apparatus is compact, sensitive, and quick to detect the presence of any of a number of pathogens present in a sample. The present sequence is that of an oligonucleotide probe which is related to the microbe detection apparatus
                                                             Novel microbe detection apparatus-related oligonucleotide probe SeqID32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New (microarray) apparatus comprising a substrate with attached nucleic acid probes, useful for detecting one or more microbes in a sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                      detection; microbe identification; virus; viral particle;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
0
                                                                                                                             pathogenic bacterium; cellular microbe; acellular microbe;
clinical diagnosis; research; epidemiological surveillance;
bioterrorism countermeasure; environmental pathogen survey;
food contaminant; radioimmunoassay; ELISA; probe; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 66 BP; 13 A; 19 C; 19 G; 15 T; 0 U; 0 Other;
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0.13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              96.0%; Score 24; 100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 16; SEQ ID NO 32; 89pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tilles JG;
                                                                                                                                                                                                                                                                                                                                                                        23-MAY-2003; 2003WO-US016461.
                                                                                                                                                                                                                                                                                                                                                                                                                    15-NOV-2002; 2002US-00295787.
                    26-AUG-2004 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          (REGC ) UNIV CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Jia XY, Berger MA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2004-449626/42
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Best Local Similarity
                                                                                                                                                                                                                                                                                    WO2004045365-A2.
                                                                                                                                                                                                                                                                                                                           03-JUN-2004
                                                                                                                                                                                                                                        Viruses.
                                                                                                           microbe
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sample which comprises a substrate having multiple microbe identification sites, each having a unique address indicative of the position of that microbe identification site on the substrate and groups of nucleic acid probes disposed at the microbe identification sites, each group being complementary to a target nucleic acid to provide a detectable signal at come or more microbe identification sites. The apparatus is useful for detecting the presence of ene or more microbes in a sample, such as virus or viral particle, (non-)pathogenic bacteria, or cellular or acellular microbe. The apparatus is particularly useful for clinical diagnosis, research, epidemiological surveillance, bioterrorism countermeasures, environmental pathogen surveys, and monitoring food contaminants. Current testing procedures or devices, such as radioimmunoassays and ELISA, are difficult to implement, time consuming, expensive, outdated, and typically rely on the use of agents that recognise and bind to membrate bound proteins or carbohydrates of the pathogen. These further cannot assay multiple pathogens. The new apparatus is compact, espathogens present in a sample. The presence of any of a number of an enembrate shathogen present in a sample of any and a number of an enembrate of any and any of an any of an any of an enembrate of all and any of any o
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              oligonucleotide probe which is related to the micorbe detection apparatus of the invention.
This invention relates to a novel apparatus for detecting a microbe in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel microbe detection apparatus-related oligonucleotide probe SeqID19.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 70 BP; 13 A; 20 C; 19 G; 18 T; 0 U; 0 Other;
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ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25
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Matches 24; Conservative
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ADP05501 standard; DNA; 70 BP

ADP05501

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26-AUG-2004 (first entry)

ADP05501;

pathogenic bacterium; cellular microbe; acellular microbe; clinical diagnosis; research; epidemiological surveillance; bioterrorism countermeasure; environmental pathogen survey; food contaminant; radioimmunossay; ELISA, probe; se.

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This invention relates to a novel apparatus for detecting a microbe in a sample which comprises a substrate having multiple microbe identification of that sires, each having a unique address indicative of the position of that microbe identification sites of the position of that probes disposed at the microbe identification sites, each group being complementary to a target nucleic acid to provide a detectable signal at cone or more microbe identification sites. The apparatus is useful for detecting the presence of one or more microbes in a sample, such as virus con virtal particle, (non-)pathogenic bacteria, or cellular or accllular microbe. The apparatus is particularly useful for clinical diagnosis, research, epidemiological surveillance, bioterrorism countermeasures, convironmental pathogen surveys, and monitoring food contaminants. Current testing procedures or devices, such as radioimmunoassays and ELISA, are difficult to implement, time consuming, expensive, outdated, and contaminant or carbohydrates of the pathogen. These further cannot convicting assay multiple pathogens. The new apparatus or device for detecting convictives or carbohydrates of the pathogen. These further cannot casesy multiple pathogens. The new apparatus or device for detecting convictives.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence is that of an related to the micorbe detection apparatus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New (microarray) apparatus comprising a substrate with attached nucleic acid probes, useful for detecting one or more microbes in a sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sensitive, and quick to detect the presence of any of a number of pathogens present in a sample. The present sequence is that of an
                                          pathogenic bacterium; cellular microbe; acellular microbe;
cinical diagnosis; research; epidemiological surveillance;
bioterrorism countermeasure; environmental pathogen survey;
food contaminant; radioimmunoassay; ELISA; probe; ss.
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Pred. No. 0.13;
                     microbe identification;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 16; SEQ ID NO 19; 89pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                    Tilles JG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          igonuclectide probe which is
                                                                                                                                                                                                                                                                                                                                          15-NOV-2002; 2002US-00295787.
                                                                                                                                                                                                                                                                                               23-MAY-2003; 2003WO-US016461,
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Jia XY, Berger MA,
                     microbe detection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the invention.
                                                                                                                                                                                                  WO2004045365-A2.
                                                                                                                                                                                                                                                  03-JUN-2004
                                                                                                                                                          Viruses
%XGCCCCCCCCCCCCCCCCCCX8X41XXBX1XXBXXBX8XXBXXBXXBXX
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New (microarray) apparatus comprising a substrate with attached nucleic acid probes, useful for detecting one or more microbes in a sample.

Berger MA, Tilles JG;

Jia XY,

WPI; 2004-449626/42

(REGC ) UNIV CALIFORNIA

23-MAY-2003; 2003WO-US016461 15-NOV-2002; 2002US-00295787

WO2004045365-A2.

Viruses

03-JUN-2004

Claim 16; SEQ ID NO 17; 89pp; English.

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This invention relates to a novel apparatus for detecting a microbe in a sample which comprises a substrate having multiple microbe identification sites, each having a unique address indicative of the position of that microbe identification site on the substrate and groups of nucleic acid probes disposed at the microbe identification sites, each group being complementary to a target nucleic acid to provide a detectable signal at one or more microbe identification sites. The apparatus is useful for detecting the presence of one or more microbes in a sample, such as virus or viral particle, (non-)pathogenic bacteria, or cellular or acellular convironmental pathogenic bacteria, bioterrorism countermeasures, research, epidemiological surveillance, bioterrorism countermeasures, environmental pathogen survey, and monitoring food contaminants. Current testing procedures or devices, such as radioimmunoassays and BLISA, are difficult to implement, time consuming, expensive, undated, and typically rely on the use of agents that recognise and bind to membrane bound proteins or carbohydrates of the pathogen. These further cannot a sasay multiple pathogenen. The new apparatus or device for detecting microbes in a sasay multiple and bind disadvantative or device for detecting and procedures.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  microbes overcomes these disadvantages. The apparatus is compact, sensitive, and quick to detect the presence of any of a number of pathogens present in a sample. The present sequence is that of an oligonucleotide probe which is related to the micorbe detection apparatus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel microbe detection apparatus-related oligonucleotide probe SeqID35.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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Pred. No. 0.25;
0; Mismatches 1; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 70 BP; 9 A; 20 C; 23 G; 18 T; 0 U; 0 Other;
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96.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the invention
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Local St.
24;
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Gaps

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0; Indels

100.0%; Pred. No. 0.1 ive 0; Mismatches

24; Conservative

Matches

2 CCGCTGCAGAGTTGCCCGTTACGA 25

24

1 CCGCTGCAGAGTTGCCCGTTACGA

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ADP05512 standard; DNA; 70 BP

RESULT 73 ADP05512 Novel microbe detection apparatus-related oligonucleotide probe SeqID17.

(first entry)

26-AUG-2004

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ADP05512;

microbe detection; microbe identification; virus; viral particle;

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New (microarray) apparatus comprising a substrate with attached nucleic acid probes, useful for detecting one or more microbes in a sample.
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                                                                                                    23-MAY-2003; 2003WO-US016461.
                                                                                                                                    15-NOV-2002; 2002US-00295787
                                                                                                                                                              (REGC ) UNIV CALIFORNIA
                                                                                                                                                                                                                          WPI; 2004-449626/42
                                           WO2004045365-A2.
                                                                          03-JUN-2004
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               Viruses.
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                                                                                                                                                                                                                                                                                                                                                        This invention relates to a novel apparatus for detecting a microbe in a sample which comprises a substrate having multiple microbe identification sites, each having a unique address indicative of the position of that microbe identification site and groups of mucleic acid probes disposed at the microbe identification sites, each group being complementary to a target nucleic acid to provide a detectable signal at one or more microbe identification sites. The apparatus is useful for detecting the presence of one or more microbes in a sample, such as virus or viral particle, (non-)pathogenic bacteria, or cellular or acellular necessarch, epidemiological surveys, and monitoring food contaminants. Current testing procedures or devices, and monitoring food contaminants. Current esting procedures or devices, such as radioimmunosasys and ELISA, are esting to the contaminants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gonucleotide probe which is related to the micorbe detection apparatus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel microbe detection apparatus-related oligonucleotide probe SeqID11.
                                                                                                                                                                                                                                                                                    New (microarray) apparatus comprising a substrate with attached nucleic acid probes, useful for detecting one or more microbes in a sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      difficult to implement, time consuming, expensive, outdated, and typically rely on the use of agents that recognise and bind to membrane bound proteins or carbohydrates of the pathogen. These further cannot assay multiple pathogens. The new apparatus or device for detecting microbes overcomes these disadvantages. The apparatus is compact.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sensitive, and quick to detect the presence of any of a number of pathogens present in a sample. The present sequence is that of an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             microbe detection; microbe identification; virus; viral particle;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 23.4; DB 12; Length 70;
Pred. No. 0.25;
0; Mismatches 1; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         pathogenic bacterium; cellular microbe; acellular microbe;
cilnical diagnosis; research; epidemiological surveillance;
bioterrorism countermeasure; environmental pathogen survey;
food contaminant; radioimmunoassay; ELISA; probe; se.
bioterrorism countermeasure; environmental pathogen survey; food contaminant; radioimmunoassay; ELISA; probe; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 70 BP; 12 A; 21 C; 21 G; 16 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25
                                                                                                                                                                                                                                                                                                                                 Claim 16; SEQ ID NO 35; 89pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               rccecrecagaerreccearracga 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TCCGCTGCAGAGTTGCCCGTTACGA
                                                                                                                                                                                                                          Tilles JG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADP05506 standard; DNA; 70 BP
                                                                                                                                  23-MAY-2003; 2003WO-US016461.
                                                                                                                                                               15-NOV-2002; 2002US-00295787.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        93.6%;
96.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24; Conservative
                                                                                                                                                                                             (REGC ) UNIV CALIFORNIA.
                                                                                                                                                                                                                         Jia XY, Berger MA,
                                                                                                                                                                                                                                                        WPI; 2004-449626/42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                of the invention.
                                                                        WO2004045365-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26-AUG-2004
                                                                                                      03-JUN-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADP05506;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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This invention relates to a novel apparatus for detecting a microbe in a sample which comprises a substrate having multiple microbe identification lites, each having a unique address indicative of the position of that microbe identification site on the substrate and groups of nucleic acid probes disposed at the microbe identification sites, each group being complementary to a target nucleic acid to provide a detectable signal at one or more microbe identification sites. The apparatus is useful for detecting the presence of one or more microbes in a sample, such as virus or viral particle, (non-)pathogenic bacteria, or cellular or acellular microbe. The apparatus is particularly useful for clinical diagnosis, research, epidemiological surveillance, bloterrorism countermeasures, environmental pathogen surveys, and monitoring food contaminants. Current testing procedures or devices, such as radioimunoassays and ELISA, are difficult to implement, time consuming, expensive, outdated, and typically rely on the use of agents that recognise and bind to membrane bound proteins or carbohydrates of the pathogen. These further cannot assay multiple pathogens. The new apparatus is compact, or analysis of a number of an incrobes overcomes these disadvantages. The apparatus is compact, and apparatus is compact, and apparent or an analysis of a number of an analysis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          igonuclectide probe which is related to the micorbe detection apparatus the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  oathogens present in a sample. The present sequence is that of an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       microbe detection; microbe identification; virus; viral particle;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 23.4; DB 12; Length 70; Pred. No. 0.25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  pathogenic bacterium; cellular microbe; acellular microbe;
cilinical diagnosis; research; epidemiological surveillance;
bioterrorism countermeasure; environmental pathogen survey;
food contaminant; radioimmunoassay; ELISA; probe; se.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 70 BP; 13 A; 20 C; 18 G; 19 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 TCCGCTGCAGAGTTGCCCGTTACGA 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 TCCGCTGCAGAGTTACCCGTTACGA 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADP05522 standard; DNA; 70 BP
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Best Local Similarity
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This invention relates to a novel apparatus for detecting a microbe in a sample which comprises a substrate having multiple microbe identification sites, each having a unique address indicative of the position of that microbe identification site on the substrate and groups of nucleic acid probes disposed at the microbe identification sites, each group being complementary to a target nucleic acid to provide a detectable signal at one or more microbe identification sites. The apparatus is useful for detecting the presence of one or more microbes in a sample, such as virus or viral particle, (non-)pathogenic bacteria, or callular or accillular microbe. The apparatus is particularly useful for clinical diagnosis, research, epidemiological surveillance, bioterrorism countermeasures,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         environmental pathogen surveys, and monitoring food contaminants. Current testing procedures or devices, such as radioimmunoassays and ELISA, are difficult to implement, time consuming, expensive, outdated, and typically rely on the use of agents that recognise and bind to membrane bound proteins or carbohydrates of the pathogen. These further cannot assay multiple pathogens. The new apparatus or device for detecting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 chogens present in a sample. The present sequence is that of an igonucleotide probe which is related to the micorbe detection apparatus
                                                                                                                                                                                                                                                                                                                                                New (microarray) apparatus comprising a substrate with attached nucleic acid probes, useful for detecting one or more microbes in a sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   overcomes these disadvantages. The apparatus is compact, and quick to detect the presence of any of a number of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 70 BP; 13 A; 20 C; 18 G; 19 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sensitive, and quick to detect the presence of
                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 16; SEQ ID NO 27; 89pp; English
                                                                                                                                                                                                                                                         Tilles JG;
                                                                                                               23-MAY-2003; 2003WO-US016461
                                                                                                                                                             15-NOV-2002; 2002US-00295787
                                                                                                                                                                                                         (REGC ) UNIV CALIFORNIA
                                                                                                                                                                                                                                                       Jia XY, Berger MA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       of the invention.
                     WO2004045365-A2
                                                                   03-JUN-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      pathogens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           microbes
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ö Score 23.4; DB 12; Length 70; Pred. No. 0.25; 0; Mismatches 1; Indels C Match 93.6%; Local Similarity 96.0%; les 24; Conservative Query Match Matches

1 TCCGCTGCAGAGTTGCCCGTTACGA 25 rccecrecadarracceerracea 25

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ADP05520 standard; DNA; 70 BP ADP05520; RESULT 77 ADP05520 

(first entry) 26-AUG-2004

Novel microbe detection apparatus-related oligonucleotide probe SeqID25.

microbe detection; microbe identification; virus; viral particle; pathogenic bacterium; cellular microbe; clinical diagnosis; research; epidemiological surveillance; bioterrorism countermeasure; environmental pathogen survey; food contaminant; radioimmunoassay; ELISA; probe; ss.

Viruses

WO2004045365-A2.

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This invention relates to a novel apparatus for detecting a microbe in a sample which comprises a substrate having multiple microbe identification of states, each having a unique address indicative of the position of that microbe identification site on the substrate and groups of nucleic acid probes disposed at the microbe identification sites, each group being complementary to a target nucleic acid to provide a detectable signal at come or more microbe identification sites. The apparatus is useful for detecting the presence of one or more microbes in a sample, such as virus or viral particle, (non-) pathogenic bacteria, or callular or acellular concore. The apparatus is particularly useful for clinical diagnosis, research, epidemiological surveillance, bioterrorism countermeasures, convironmental pathogen surveys, and monitoring food contaminates. Current testing procedures or devices, such as radioinmunosassay and ELISA, are difficult to implement, time consuming, expensive, outdated, and contaminates or devices, such as radioinmunosassay and ELISA, are difficult to implement, time consuming, expensive, outdated, and contaminates or carbohydrates of the pathogen. These further cannot assay multiple pathogens. The new apparatus or device for detecting microbes overcomes these disadvantages. The apparatus is compact, sensitive, and quick to detect the present eapparatus is compact, or invarior. The invarior paparatus is related to the micorbe detection apparatus
                                                                                                                                                                                                                                                                                                                    New (microarray) apparatus comprising a substrate with attached nucleic acid probes, useful for detecting one or more microbes in a sample.
                                                                                                                                                                                                                                                                                                                                                                                        Claim 16; SEQ ID NO 25; 89pp; English.
                                                                                                                                                                                                                     Berger MA, Tilles JG,
                                                                  23-MAY-2003; 2003WO-US016461.
                                                                                                                15-NOV-2002; 2002US-00295787
                                                                                                                                                                  (REGC ) UNIV CALIFORNIA.
                                                                                                                                                                                                                                                                 WPI; 2004-449626/42.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the invention.
                      03-JUN-2004
                                                                                                                                                                                                                   Jia XY,
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Sequence 70 BP; 14 A; 21 C; 18 G; 17 T; 0 U; 0 Other;

Gaps ö Score 23.4; DB 12; Length 70; Pred. No. 0.25; 0; Mismatches 1; Indels ( ö 93.6%; ilarity 96.0%; Conservative ( Similarity 24; Query Match Best Local ( **datches** 

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Gaps

ADP05516 standard; DNA; 71 BP ADP05516; RESULT 78

(first entry) 26-AUG-2004 Novel microbe detection apparatus-related oligonucleotide probe SeqID21.

microbe detection, microbe identification, virus, viral particle, pathogenic bacterium; cellular microbe; acellular microbe; clinical diagnosis, research; epidemiological surveillance; bioterrorism countermeasure; environmental pathogen survey; food contaminant; radioimmunoassay; ELISA; probe; ss. 

Viruses.

WO2004045365-A2

03-JUN-2004.

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                                                                                                                                                                                                       This invention relates to a novel apparatus for detecting a microbe in a sample which comprises a substrate having multiple microbe identification of that acts having a unique address indicative of the position of that microbe identification site on the substrate and groups of nucleic acid probes disposed at the microbe identification sites, each group being complementary to a target nucleic acid to provide a detectable signal at one or more microbe identification sites. The apparatus is useful for detecting the presence of one or more microbes in a sample, such as virus or viral particle, (non-)pathogenic bacteria, or cellular or accllular microbe. The apparatus is particularly useful for clinical diagnosis, research, epidemiological surveillance, bioterrorism countermeasures, convironmental pathogen surveys, and monitoring food contaminants. Current testing procedures or devices, such as radioimmunoassays and ELISA, are difficult to implement, time consuming, expensive, outdated, and contaminants or carbohydrates of the pathogen. These further cannot assay multiple pathogens. The new apparatus or device for detecting microbes overcomes these disadvantages. The apparatus is compact, sensitive, and quick to detect the presence of any of a number of sensitive, and quick to detect the presence of any of a number of sensitive, and quick to detect the presence of any of a number of colligonuleotide probe which is related to the microbe detection apparatus
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                                                                                                                                            New (microarray) apparatus comprising a substrate with attached nucleic acid probes, useful for detecting one or more microbes in a sample.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          93.6%; Score 23.4; DB 12; Length 71; 96.0%; Pred. No. 0.25; 1; Indels (ive 0). Mismatches 1; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Viral 5' untranslated polynucleotide sequence SEQ ID NO:39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 71 BP; 11 A; 20 C; 21 G; 19 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA detection; enteroviral detection; ds.
                                                                                                                                                                                  Claim 16; SEQ ID NO 21; 89pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 TCCGCTGCAGAGTTGCCCGTTACGA 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TCCGCTGCAGAGTTACCCGTTACGA
                                                                                           Tilles JG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AEB56800 standard; DNA; 117 BP
             23-MAY-2003; 2003WO-US016461.
                                       15-NOV-2002; 2002US-00295787.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-JAN-2004; 2004US-00760048.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22-SEP-2005 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 96.0
Marches 24; Conservative
                                                                (REGC ) UNIV CALIFORNIA
                                                                                           Jia XY, Berger MA,
                                                                                                                   WPI; 2004-449626/42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unidentified
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AEB56800/
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target binding sequence of an oligomiclectide chosen from any one of the losequence of ABB5672; and (b) a sequence required for selected amplification or detection reaction. Also described: (1) an kit (XI) comprising (I), and one or more container that contains (I); and (2) detecting (MI) an enterovirus target sequence, involving: (a) amplifying the target sequence using first amplification primer having a sequence consisting essentially of target binding sequence of any one of ABB5674 to ABB56771 and optionally a sequence required for selected amplification reaction; and (b) detecting the amplified target sequence. (I), (MI) and (XI) are useful for detecting enterovirus target sequence. (I) are useful for detecting enterovirus target sequence. (I) specifically and selectively recognizes the enterovirus genome. (I) sensitively and rapidly detects fewer than 500 copies of enteroviral consistively and rapidly detects fewer than 500 copies of enteroviral present sequence represents a viral 5' untranslated polymuclectide sequence given in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                    Novel oligonucleotide comprising sequences for binding and amplifying or detecting target, useful for detecting enterovirus nucleic acids.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel oligonucleotide comprising sequences for binding and amplifying or detecting target, useful for detecting enterovirus nucleic acids.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to an oligonucleotide (I) consisting of: (a) the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ch 93.6%; Score 23.4; DB 14; Length 117; Similarity 96.0%; Pred. No. 0.27; 24; Conservative 0; Mismatches 1; Indels 0:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Viral 5' untranslated polynucleotide sequence SEQ ID NO:40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 117 BP; 25 A; 32 C; 28 G; 32 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; SEQ ID NO 39; 34pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 TCCGCTGCAGAGTTGCCCGTTACGA 25
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                                                                                                                            Price JA, Hellyer TJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Isang S, Price JA, Hellyer TJ;
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(PRIC/) PRICE J A.
(HELL/) HELLYER T J.
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(PRIC/) PRICE J A. (HELL/) HELLYER T J.
                                                                                                                                                                                                  WPI; 2005-512251/52
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                                                                                                                            Isang S,
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AEB56801/c
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The invention relates to an oligonucleotide (I) consisting of: (a) the target binding sequence of an oligonucleotide chosen from any one of the 10 sequence of ABB5672 to ABB56771; and (b) a sequence required for selected amplification or detection reaction. Also described: (1) a kit (K1) comprising (I), and one or more container that contains (I); and (2) detecting (M1) an enterovirus target sequence, involving: (a) amplifying the target sequence using first amplification primer having a sequence consisting essentially of target binding sequence of any one of ABB5674 to ABB56771 and optionally a sequence required for selected amplification reaction; and (b) detecting the amplified target sequence. (I), (M1) and (K1) are useful for detecting enterovirus target sequences. (I), (M1) and (M2) are applied target arget sequences.
                                                                                                                                                                                                                                                                                                                                                      specifically and selectively recognizes the enterovirus genome. (I) sensitively and rapidly detects fewer than 500 copies of enteroviral genome and allows detection of broad range of enterovirus serotypes. The
                                                                                                                                                                                                                                                                                                                                                                                                                                             present sequence represents a viral 5' untranslated polynucleotide sequence given in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 14; Length 117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 117 BP; 25 A; 33 C; 28 G; 31 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23.4; DB
No. 0.27;
Disclosure; SEQ ID NO 40; 34pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score Pred. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          93.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 24; Conserv
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25 5 75 TCCGCTGCAGAGTTGCCCATTACGA 1 TCGGCTGCAGAGTTGCCCGTTACGA ò 셤

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Gaps

. 0

Indels

1;

0; Mismatches

24; Conservative

AEB56856 standard; DNA; 173 22-SEP-2005 AEB56856; RESULT 81 **AEB56856**/ 

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Human echovirus 5 5' untranslated polynucleotide sequence. DNA detection; enteroviral detection; ds (first entry)

Human echovirus 5. US2005158710-A1.

16-JAN-2004; 2004US-00760048. 21-JUL-2005.

16-JAN-2004; 2004US-00760048. (TSAN/) TSANG S. (PRIC/) PRICE J A. (HELL/) HELLYER T J. Hellyer TJ; Tsang S, Price JA,

WPI; 2005-512251/52. GENBANK; AF188359.

Novel oligonucleotide comprising sequences for binding and amplifying or detecting target, useful for detecting enterovirus nucleic acids. Disclosure; Fig 1A-D; 34pp; English.

The invention relates to an oligonucleotide (I) consisting of: (a) the target binding sequence of an oligonucleotide chosen from any one of the 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for selected amplification or detection reaction. Also described: (I) a kit (XI) comprising (I), and one or more container that contains (I); and detecting (MI) an enterovirus target sequence, involving: (a) amplifying the target sequence using first amplification primer having a sequence

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                to AEBS6771 and optionally a sequence required for selected amplification seaction; and (b) detecting the amplified target sequence. (I), (MI) and (KI) are useful for detecting enterovirus target sequences. (I) specifically and selectively recognizes the enterovirus genome. (I) sensitively and rapidly detects fewer than 500 copies of enteroviral genome and allows detection of broad range of enterovirus serotypes. The present sequence represents a viral 5' untranslated polynucleotide sequence given in the exemplification of the present invention.
essentially of target binding sequence of any one of AEB56764
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                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (K1) are useful for detecting enterovirus target sequences. (1) specifically and selectively recognizes the enterovirus genome. (1) sensitively and rapidly detects fewer than 500 copies of enteroviral genome and allows detection of broad range of enterovirus serotypes. Present sequence represents a viral 5' untranslated polynucleotide sequence given in the exemplification of the present invention.
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                                                                                                                                                                                                                                           Score 23.4; DB 14; Length 173;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human echovirus 5 5' untranslated polynucleotide sequence.
                                                                                                                                                                                                                                                                                   1; Indels
                                                                                                                                                                                                     Sequence 173 BP; 36 A; 44 C; 45 G; 48 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                            0.28;
                                                                                                                                                                                                                                                                96.0%; Pred. No. 0.28
live 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA detection; enteroviral detection; ds.
                                                                                                                                                                                                                                                                                                                                                                  rcccrccacacirccccarracca 107
                                                                                                                                                                                                                                                                                                                            1 TCGCTGCAGAGTTGCCCGTTACGA 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Fig 1A-D; 34pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BP
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                                                                                                                                                                                                                                             93.68;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AEB56855 standard; DNA; 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22-SEP-2005 (first entry)
                                                                                                                                                                                                                                                                                   24; Conservative
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(PRIC/) PRICE J A.
(HELL/) HELLYER T J.
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                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human echovirus 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENBANK; AF188358
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  consisting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AEB56855;
                                                                                                                                                                                                                                                                                                                                                                    131
                                                                                                                                                                                                                                             Query Match
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TCCGCTGCAGAGTTGCCCATTACGA 67

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Novel oligonucleotide comprising sequences for binding and amplifying or detecting target, useful for detecting enterovirus nucleic acids.
                                                                                                                                          Human echovirus 2 5' untranslated polynucleotide sequence.
                                                                                                                                                                     DNA detection; enteroviral detection; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Fig 1A-D; 34pp; English
                                                        AEB56853 standard; DNA; 198 BP.
                                                                                                                                                                                                                                                                                                               16-JAN-2004; 2004US-00760048.
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                                                                                                              22-SEP-2005 (first entry)
                                                                                                                                                                                                                                                                                                                                        (TSAN/) TSANG S.
(PRIC/) PRICE J A.
(HELL/) HELLYER T J.
                                                                                                                                                                                                                                                                                                                                                                                                   reang S, Price JA,
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                                                                                                                                                                                                 Human echovirus 2.
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                                                                                    AEB56853;
                                         AEB56853,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to an oligonucleotide (I) consisting of: (a) the target binding sequence of an oligonucleotide chosen from any one of the sequence of AEBS6772 to AEBS6771; and (b) a sequence required for selected amplification or detection reaction. Also described: (I) a kit (KI) comprising (I), and one or more container that contains (I); and (2) detecting (MI) an enterovirus target sequence, involving: (a) amplifying the target sequence using first amplification primer having a sequence consisting essentially of target binding sequence of any one of AEBS670 to AEBS6771 and optionally a sequence required for selected amplification reaction, and (b) detecting the amplified target sequence. (I), (MI) and (KI) are useful for detecting enterovirus target sequences. (I) (MI) and selectively recognizes the enterovirus genome. (I)
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                                                         Gaps
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                         Score 23.4; DB 14; Length 173;
Pred. No. 0.28;
0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                    Human echovirus 12 5' untranslated polynucleotide sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 198 BP; 41 A; 49 C; 50 G; 58 T; 0 U; 0 Other;
Sequence 173 BP; 36 A; 45 C; 45 G; 47 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                DNA detection; enteroviral detection; ds.
                                                                                                 1 TCCGCTGCAGAGTTGCCCGTTACGA 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Fig 1A-D; 34pp; English.
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                                                                                                                                                 16-JAN-2004; 2004US-00760048.
                         93.6%;
ilarity 96.0%;
Conservative
             Query Match
Best Local Similarity
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Hellyer TJ;

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The invention relates to an oligonuclectide (I) consisting of: (a) the target binding sequence of an oligonuclectide chosen from any one of the target binding sequence of ABBS6771; and (b) a sequence required for selected amplification or detection reaction. Also described: (I) a kit (KI) comprising (I), and one or more container that contains (I); and (2) detecting (MI) an enterovirus target sequence, involving: (a) amplifying the target sequence using first amplification primer having a sequence consisting essentially of target binding sequence of any one of AEBS676; to AEBS6771 and optionally a sequence required for selected amplification reaction; and (b) detecting enterovirus target sequence. (I), (MI) and (KI) are useful for detecting enterovirus target sequence. (I) specifically and selectively recognizes the enterovirus genome. (I) sensitively and rapidly detects fewer than 500 copies of enteroviral genome and allows detection of broad range of enterovirus the correspondence represents a viral 5, untranslated polymuclectide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 198 BP; 42 A; 53 C; 51 G; 52 T; 0 U; 0 Other;
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AEB56860/c
ID AEB56860 standard; DNA; 198 BP.
XX
AC AEB56860;
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Gaps ö

1 TCCGCTGCAGAGTTGCCCGTTACGA 25

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target binding sequence of an oligonucleotide chosen from any one of the 10 sequence of AEBS6762 to AEBS6771; and (b) a sequence required for selected amplification or detection reaction. Also described: (1) a kit (K1) comprising (I), and one or more contains that contains (I); and (2) detecting (M1) an enterovirus target sequence, involving: (a) amplifying the target sequence using first amplification primer having a sequence consisting essentially of target binding sequence of any one of AEBS6774 to AEBS6771 and optionally a sequence required for selected amplification reaction; and (b) detecting the amplified target sequence. (I), (M1) and (M2) are useful for detecting enterovirus target sequences. (I), (M1) and (M2) are useful for detecting enterovirus target sequences. (I), (M3) and (M3) 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel oligonucleotide comprising sequences for binding and amplifying or detecting target, useful for detecting enterovirus nucleic acids.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               invention relates to an oligonucleotide (I) consisting of: (a) the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             specifically and selectively recognizes the enterovirus genome. (1) sensitively and rapidly detects fewer than 500 copies of enteroviral
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; SEQ ID NO 50; 34pp; English
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ID AEB56810 standard; DNA; 236
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                                                                                                                                                                                                                                                    (TSAN/) TSANG S.
(PRIC/) PRICE J A.
(HELL/) HELLYER T J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2005-512251/52
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PRICE J A.
HELLYER I
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                                        21-JUL-2005.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (TSAN/)
(PRIC/)
(HELL/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     target binding.sequence of an oligonucleotide chosen from any one of the 10 sequence of AEB5672 to AEB56771; and (D) a sequence required for selected amplification or detection reaction. Also described: (1) a kit (K1) comprising (I), and one or more container that contains (I); and detecting (M1) an enterovirus target sequence, involving: (a) amplifying the target sequence using first amplification primer having a sequence consisting essentially of target binding sequence of any one of AEB56764 to AEB56771 and optionally a sequence required for selected amplification reaction; and (b) detecting the amplified target sequence. (I), (M1) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         specifically and selectively recognizes the enterovirus genome. (1) sensitively and rapidly detects fewer than 500 copies of enteroviral genome and allows detection of broad range of enterovirus serotypes. The present sequence represents a viral 5' untranslated polymuclectide sequence given in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel oligonuclectide comprising sequences for binding and amplifying or detecting target, useful for detecting enterovirus nucleic acids.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to an oligonucleotide (I) consisting of: (a) the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 93.6%; Score 23.4; DB 14; Length 198; Best Local Similarity 96.0%; Pred. No. 0.29; Matches 24; Conservative 0; Mismatches 1: Indels 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        for detecting enterovirus target sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Viral 5' untranslated polynucleotide sequence SEQ ID NO:50.
                                                                      Human echovirus 9 5' untranslated polynucleotide sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 198 BP; 39 A; 49 C; 52 G; 58 T; 0 U; 0 Other;
                                                                                                                                            DNA detection; enteroviral detection; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA detection; enteroviral detection; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           91 rccecrecedaerrecccerracea 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Fig 1A-D; 34pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hellyer TJ;
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ID AEB56811 standard; DNA; 236 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (K1) are useful for detecting specifically and selectively
                                                                                                                                                                                                                                                                                                                                                                                                                                  16-JAN-2004; 2004US-00760048
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16-JAN-2004; 2004US-00760048
(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (TSAN/) TSANG S.
(PRIC/) PRICE J A.
(HELL/) HELLYER T J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tsang S, Price JA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2005-512251/52
                                                                                                                                                                                                                      Human echovirus 9.
                                                                                                                                                                                                                                                                                     US2005158710-A1.
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22-SEP-2005
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AEB56811;

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RESULT 86

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Gaps

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                                                                                                            The invention relates to an oligonucleotide (I) consisting of: (a) the target binding sequence of an oligonucleotide chosen from any one of the 10 sequence of AEBS6775 to AEBS6771; and (b) a sequence required for selected amplification or detection reaction. Also described: (I) a kit (K1) comprising (I), and one or more container that contains (I); and (2) detecting (M1) an enterovitus target sequence, involving: (a) amplifying the target sequence using first amplification primer having a sequence consisting essentially of target binding sequence of any one of AEBS6764 to AEBS6771 and optionally a sequence required for selected amplification reaction; and (b) detecting the amplified target sequence. (I), (M1) and (M1) are useful for detecting enterovirus target sequences. (I) specifically and selectively recognizes the enterovirus genome. (I) specifically and rapidly detects fewer than 500 copies of enteroviral genome and allows detection of broad range of enterovirus serotypes. The present sequence represents a viral 5, untranslated polymorleotide
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                                                      comprising sequences for binding and amplifying or ful for detecting enterovirus nucleic acids.
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                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                            sequence given in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                        Score 23.4; DB 14; Length 236; Pred. No. 0.29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Viral 5' untranslated polynucleotide sequence SEQ ID NO:51.
                                                                                                                                                                                                                                                                                                                                                               1; Indels
                                                                                                                                                                                                                                                                                                                 Sequence 236 BP; 60 A; 52 C; 51 G; 73 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA detection; enteroviral detection; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; SEQ ID NO 51; 34pp; English
                                                                                          Disclosure; SEQ ID NO 49; 34pp; English
                                                                                                                                                                                                                                                                                                                                                                                      1 TCCGCTGCAGAGTTGCCCGTTACGA 25
                                                                                                                                                                                                                                                                                                                                                                                                   Hellyer TJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hellyer TJ
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                                                                                                                                                                                                                                                                                                                                        93.6%;
96.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22-SEP-2005 (first entry)
                                                                                                                                                                                                                                                                                                                                                               24; Conservative
                                                                   detecting target, useful
                                                        Novel oligonucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (TSAN/) TSANG S.
(PRIC/) PRICE J A.
(HELL/) HELLYER T J.
          Price JA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    reang S, Price JA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2005-512251/52.
                                WPI; 2005-512251/52
                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unidentified
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            Isang S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AEB56812;
                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 88
AEB56812/
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The invention relates to an oligonucleotide (I) consisting of: (a) the target binding sequence of an oligonucleotide chosen from any one of the 10 sequence of ABB56772 to ABB56771; and (b) a sequence required for selected amplification or detection. Also described: (I) a kit (KI) comprising (I), and one or more container that contains (I); and (2) detecting (MI) an enterovirus target sequence, involving: (a) amplifying the target sequence using first amplification primer having a sequence consisting essentially of target binding sequence of any one of ABB56764 to ABB56771 and optionally a sequence required for selected amplification reaction, and (b) detecting the amplified target sequence. (I), (MI) and (KI) are useful for detecting enterovirus target sequences. (I) specifically and selectively recognizes the enterovirus genome. (I) sensitively and rapidly detects fewer than 500 copies of enteroviral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (K1) comprising (I), and one or more container that contains (I), and (2) detecting (M1) an enterovirus target sequence, involving: (a) amplifying the target sequence using first amplification primer having a sequence consisting essentially of target binding sequence of any one of ARBS576 to ARBS5771 and optionally a sequence required for selected amplification reaction, and (b) detecting the amplified target sequence. (I), (M1) and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       genome and allows detection of broad range of enterovirus serotypes present sequence represents a viral 5' untranslated polynucleotide sequence given in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   93.6%; Score 23.4; DB 14; Length 236; 96.0%; Pred. No. 0.29;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 236 BP; 60 A; 52 C; 51 G; 73 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hellyer TJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AEB56798 standard; DNA; 236 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16-JAN-2004; 2004US-00760048.
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nes 24; Conservative
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(PRIC/) PRICE J A.
(HELL/) HELLYER T J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2005-512251/52.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 JS2005158710-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21-JUL-2005
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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AEB56798/c
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96.04;

Best Local Similarity

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               specifically and selectively recognizes the enterovirus general. (1) sensitively and rapidly detects fewer than 500 copies of enteroviral genome and allows detection of broad range of enterovirus serctypes. The present sequence represents a viral 5' untranslated polymucleotide sequence given in the exemplification of the present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel oligonucleotide comprising sequences for binding and amplifying detecting target, useful for detecting enterovirus nucleic acids.
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                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           specifically and selectively recognizes the enterovirus genome.
                                                                                                                                                                   93.6%; Score 23.4; DB 14; Length 236; 96.0%; Pred. No. 0.29; 1. Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Viral 5' untranslated polynucleotide sequence SEQ ID NO:44.
                                                                                                                               Sequence 236 BP; 52 A; 58 C; 57 G; 69 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 237 BP; 54 A; 53 C; 56 G; 74 T; 0 U; 0 Other;
useful for detecting enterovirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA detection; enteroviral detection; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; SEQ ID NO 44; 34pp; English.
                                                                                                                                                                                                                                               1 TCCGCTGCAGAGTTGCCCGTTACGA 25
                                                                                                                                                                                                                                                                       TCGCTGCAGAGTTGCCCATTACGA 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hellyer TJ;
                                                                                                                                                                                                                                                                                                                                                                                 AEB56805 standard; DNA; 237 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                 Query Match
Best Local Similarity 96.v
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(PRIC/) PRICE J A.
(HELL/) HELLYER T J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unidentified
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                                                                                                                                                                                                                                                                                                                                            RESULT 90
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel oligonucleotide comprising sequences for binding and amplifying or detecting target, useful for detecting enterovirus nucleic acids.
                  Gaps
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Pred. No. 0.29;
0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                          Viral 5' untranslated polynucleotide sequence SEQ ID NO:45.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sensitively and rapidly detects fewer than 500 copies of
genome and allows detection of broad range of enterovirus
                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 237 BP; 54 A; 53 C; 56 G; 74 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              viral 5' untranslated
Pred. No. 0.29;
); Mismatches
                                                                                                                                                                                                                                                                                        DNA detection; enteroviral detection; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; SEQ ID NO 45; 34pp; English.
                                              25
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                                              1 TCGCTGCAGAGTTGCCCGTTACGA
                                                                         75 TCCGCTGCGGAGTTGCCCGTTACGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Price JA, Hellyer TJ;
                                                                                                                                                             AEB56806 standard; DNA; 237 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              represents a
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96.0%;
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Matches 24; Conservative
               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (TSAN/) TSANG S.
(PRIC/) PRICE J A.
(HELL/) HELLYER T J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2005-512251/52.
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                                                                                                                                                                                                                                                                                                                        Unidentified
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               24;
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                Matches
                                                                                                                             RESULT 91
AEB56806/c
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AEB56861/c

93.6%; Score 23.4; DB 14; Length 237;

Query Match

RESULT 92

Hellyer TJ;

Price JA,

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Novel oligonucleotide comprising sequences for binding and amplifying or detecting target, useful for detecting enterovirus nucleic acids.
                                                                                                                                                                                                                                                                                        Disclosure, Fig 1A-D; 34pp; English
                                                                                      16-JAN-2004; 2004US-00760048
                                                                                                             16-JAN-2004; 2004US-00760048
           Human coxsackievirus B5.
                                                                                                                                                                                                               WPI; 2005-512251/52
                                                                                                                                      TSANG S.
PRICE J A.
HELLYER T
                                    US2005158710-A1
                                                                                                                                                                                                                            GENBANK; X67706
                                                             21-JUL-2005
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                                                                                                                                      (TSAN/)
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                      target binding sequence of an objoint of the chosen from any one of the losequence of ABB5672; and (b) a sequence required for selected amplification or detection reaction. Also described: (1) at kit (K1) comprising (1), and one or more container that contains (1); and (2) detecting (M1) an enterovirus target sequence, involving: (a) amplifying the target sequence using first amplification primer having a sequence consisting essentially of target binding sequence of any one of ABB5674 to ABB56771 and optionally a sequence required for selected amplification reaction; and (b) detecting the amplified target sequences. (1), (M1) and (K1) are useful for detecting enterovirus target sequences. (1) specifically and selectively recognizes the enterovirus genome. (1) specifically and selectively recognizes the enterovirus genome. (1) sensitively and rapidly detects fewer than 500 copies of enteroviral common and allows detection of broad range of enterovirus serotypes. The present sequence represents a viral 5 untranslated polymucleotide sequence given in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                Novel oligonucleotide comprising sequences for binding and amplifying or detecting target, useful for detecting enterovirus nucleic acids.
                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to an oligonucleotide (I) consisting of: (a) the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human coxsackievirus B5 5' untranslated polynucleotide sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     93.6%; Score 23.4; DB 14; Length 237; 96.0%; Pred. No. 0.29;
                                                                         Human echovirus 9 5' untranslated polynucleotide sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 237 BP; 48 A; 54 C; 65 G; 70 T; 0 U; 0 Other;
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                                                                                                NNA detection; enteroviral detection; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA detection; enteroviral detection; ds
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                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure, Fig 1A-D; 34pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 TCCGCTGCAGAGTTGCCCGTTACGA
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В
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ID AEB56849 standard; DNA; 238
AEB56861 standard; DNA; 237
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                                                (first entry)
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                                                                                                                                                                                                                                                 (TSAN/) TSANG S.
(PRIC/) PRICE J A.
(HELL/) HELLYER T J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                    Isang S, Price JA,
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                                                                                                                          Human echovirus 9.
                                                                                                                                                   US2005158710-A1.
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                                                 22-SEP-2005
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                       AEB56861
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The invention relates to an oligonucleotide (I) consisting of: (a) the target binding sequence of an oligonucleotide chosen from any one of the 10 sequence of ABB56762 to ABB56771; and (b) a sequence required for selected amplification or detection. Also described: (1) a kit (K1) comprising (I), and one or more container that contains (I); and (2) detecting (M1) an enterovirus target sequence, involving: (a) amplifying the target sequence using first amplification primer having a sequence consisting essentially of target binding sequence of any one of ABB56764 reaction; and (b) detecting the amplified target sequence. (I), (M1) and (K1) are useful for detecting enterovirus target sequences: (I), (M1) and
                                                                                                                                                                                                                                                                                                                                                                                                                      specifically and selectively recognizes the enterovirus genome. (I) sensitively and rapidly detects fewer than 500 copies of enteroviral genome and allows detection of broad range of enterovirus serotypes. The present sequence represents a viral 5' untranslated polynucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sequence given in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ch 93.6%; Score 23.4; DB 14; Length 238; l Similarity 96.0%; Pred. No. 0.29; 24; Conservative 0; Mismatches 1; Indels 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 238 BP; 53 A; 57 C; 61 G; 67 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA detection; enteroviral detection; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 TCCGCTGCAGAGTTGCCCGTTACGA 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22-SEP-2005 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
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US2005158710-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 AEB56866;
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                                                                                                                                                                                                                                                                                                                                                                                                                          target binding agequence of an observative of the carget binding agequence of an observative of the sequence of ABB5672 to ABB5671; and (b) a sequence required for selected amplification or detection reaction. Also described: (1) a kit (XI) comprising (I), and one or more container that contains (I); and (2) detecting (MI) an enterovirus target sequence, involving: (a) amplifying the target sequence using first amplification primer having a sequence consisting essentially of target binding sequence of any one of ABB56764 to ABB56771 and optionally a sequence required for selected amplification reaction, and (b) detecting the amplified target sequence. (I) (MI) and (XI) are useful for detecting enterovirus target sequence. (I) specifically and selectively recognizes the enterovirus genome. (I) sensitively and rapidly detects fewer than 500 copies of enteroviral companies. Genome and allows detection of broad range of enterovirus processor and present sequence sepresents a viral 5' untranslated polymuclectide sequence given in the exemplification of the present invention.
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                                                                                                                                                                       The invention relates to an oligonucleotide (I) consisting of: (a) the
                                                                                                                Novel oligonucleotide comprising sequences for binding and amplifying detecting target, useful for detecting enterovirus nucleic acids.
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                                                                                                                                                                                                                                                                                                                                                                                                Score 23.4; DB 14; Length 238; Pred, No. 0.29;
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                                                                                                                                                                                                                                                                                                                                                                                                                       1; Indels
                                                                                                                                                                                                                                                                                                                                                                         Sequence 238 BP; 59 A; 53 C; 53 G; 73 T; 0 U; 0 Other;
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Local Similarity 96.0%; Pred. No. 0.29
Nes 24; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA detection; enteroviral detection; ds.
                                                                                                                                                Disclosure; SEQ ID NO 33; 34pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                             1 TCCGCTGCAGAGTTGCCCGTTACGA 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   rcccriccagacriaccccriacca 51
                                                                   Hellyer TJ;
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16-JAN-2004; 2004US-00760048
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                   (TSAN/) TSANG S.
(PRIC/) PRICE J A.
(HELL/) HELLYER T J.
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(PRIC/) PRICE J A.
(HELL/) HELLYER T J.
                                                                   Price JA,
                                                                                         WPI; 2005-512251/52
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GENBANK; X79047.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human echovirus 12
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                                                                 Tsang S,
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Best Local S
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The invention relates to an oligonucleotide (I) consisting of: (a) the target binding sequence of an oligonucleotide chosen from any one of the 10 sequence of ABBS6771; and (b) a sequence required for cleated amplification or detection reaction. Also described: (I) a kit (KI) comprising (I), and one or more container that contains (I); and (2) detecting (MI) an enterovirus target sequence, involving: (a) amplifying the target sequence using first amplification primer having a sequence consisting essentially of target binding sequence of any one of ABBS6764 to ABBS6771 and optionally a sequence required for selected amplification reaction, and (b) detecting the amplified target sequence. (I) (MI) and (KI) are useful for detecting the amplified target sequence. (I) specifically and selectively recognizes the enterovirus genome. (I) specifically and selection of broad range of enterovirus connectived and allows detecting the amplification of broad range of enterovirus forms and allows detecting the aviral S' untranslated polymuclectide.
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Novel oligonucleotide comprising sequences for binding and amplifying or detecting target, useful for detecting enterovirus nucleic acids.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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Pred. No. 0.29;
0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human echovirus 12 5' untranslated polynucleotide sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 238 BP; 50 A; 55 C; 64 G; 69 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA detection; enteroviral detection; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      131 rccecrecaeaerreccarracea 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25
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                                                                                                                          Disclosure, Fig 1A-D; 34pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 TCCGCTGCAGAGTTGCCCGTTACGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tsang Ş, Price JA, Hellyer TJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ВР
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             93.6%;
96.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16-JAN-2004; 2004US-00760048.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16-JAN-2004; 2004US-00760048
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AEB56866 standard; DNA; 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22-SEP-2005 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 96.0
les 24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel oligonucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (TSAN/) TSANG S.
(PRIC/) PRICE J A.
(HELL/) HELLYER T J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2005-512251/52.
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                 (KI) comprising (I), and one or more container that contains (I); and (2) detecting (MI) an enterovirus target sequence, involving: (a) amplifying the target sequence, involving: (a) amplifying the target sequence involving sequence consisting essentially of target binding sequence of any one of ABBS6764 to ABBS6771 and optionally a sequence required for selected amplification exaction, and (b) detecting the amplified target sequence. (I), (MI) and specifically and selecting the amplified target sequences. (I) sensitively and rapidly detects fewer than 500 copies of enteroviral sensitively and alplay detects fewer than 500 copies of enteroviral genome and allows detection of broad range of enterovirus serotypes. The sequence given in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    quality of an aqueous environmental medium that potentially contains many different microorganisms. A reference set of at least three microorganisms is chosen that, separately or collectively, represent microorganisms is chosen that, separately or collectively, represent microorganisms, or their fragments, in the treated medium is contacted with a set of at least three probes for specific identification and wiltiple determination of selected microorganisms. This determination represents the level of microbiological quality. The method is useful for identifying and quantifying microorganisms in water and provides results that are used to control water purification/production processes. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Monitoring microbiological quality of water, useful particularly for controlling water purification, uses oligonucleotide probes to detect at least three representative microbes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention relates to a method for monitoring microbiological
selected amplification or detection reaction. Also described: (1) a kit
                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Vachon C, Lacroix B, Vernet G;
                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                 93.6%; Score 23.4; DB 14; Length 238;
llarity 96.0%; Pred. No. 0.29;
Conservative 0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Probe; microorganism detection; microbiological quality; water purification; ss.
                                                                                                                                                                                                                                                                                                                                     Sequence 238 BP; 50.A; 55 C; 64 G; 69 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 TCCGCTGCAGAGTTGCCCGTTACGA 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Micro-organism detection probe #55.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mabilat C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 24; Page 76; 85pp; French
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    06-JUL-2000; 2000FR-00008839.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     06-JUL-2001; 2001WO-FR002191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABL53113 standard; DNA; 525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Guillot E,
Laffaire P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (revised)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2002-148021/19.
                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
nes 24; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200202811-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Echovirus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                07-AUG-2003
25-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10-JAN-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Renaud P,
Armand M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABL53113;
                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABL53113/c
11D ABL53113/c
26 ABL53113/c
27 ABL53113/c
28 ABL53113/c
28 ABL53113/c
29 ABL53113/c
20 A
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Matches
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present sequence is a probe which was used to illustrate the invention. (Updated on 07-AUG-2003 to correct OS field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention provides an enterovirus genome (I) for use as a vector or
                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gene therapy; enterovirus; vaccine; diagnostic; RT-PCR; primer;
Coxsackievirus B3; CVB3; NTR; non-translated region; echo virus; ds.
                                                                                                                                        .;
                                                                                                Score 23.4; DB 6; Length 525; Pred. No. 0.32;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Echo virus (ECV12) 5' non-translated region (NTR) sequence.
                                                           Sequence 525 BP; 117 A; 142 C; 135 G; 131 T; 0 U; 0 Other;
                                                                                                                                        Indels
                                                                                                                                        0; Mismatches
                                                                                                                                                                                                      475 TCCGCTGCAGAGTTGCCCATTACGA 451
                                                                                                                                                                               1 TCCGCTGCAGAGTTGCCCGTTACGA 25
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note= "Domain III"
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/note= "Domain VII"
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note= "Domain IV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   '*tag= f
'note= "Domain VI"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /*tag= a
/note= "Domain I"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         *tag= e
note= "Domain V"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Fig 2; 49pp; English.
                                                                                                                                                                                                                                                                                                                    AAC85153 standard; RNA; 646 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   08-JUL-2000; 2000WO-US018681.
                                                                                                93.6%;
96.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              . 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .443
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .622
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .643
                                                                                                                    Best Local Similarity 96.0
Matches 24; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              *tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (UYNE-) UNIV NEBRASKA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        09-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18-JAN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Echo virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Romero JR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                stem_loop
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                                                                                                                                                                                                                                                                                                                                                           AAC85153;
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                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                AAC85153/
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                                                                                                                                                                                                                                                                             RESULT
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vaccine, modified to produce a virus (V1) having a restricted or altered species or tissue tropism, compared to an equivalent unmodified virus, or modified to produce an attenuated virus (V2), by replacing a part or all of the 5'non-translated region (5'NTR) of (I) with a 5'NTR of an enterovirus genome that encodes V1 or V2. (I) is useful as vaccine or vector in targeting genes of interest to specific cells or tissues. (I) is also useful for diagnostic purposes, e.g. to identify virulent, versus nonvirulent strains of an enterovirus. The present sequence, represents
                                                                                                                                                                                                                                                                5' NTR (non-translated region) sequence of echo virus (ECV12)
         8888888888888
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Sequence 646 BP; 145 A; 176 C; 163 G; 0 T; 162 U; 0 Other;

; ch 93.6%; Score 23.4; DB 4; Length 646; Similarity 96.0%; Pred. No. 0.33; 24; Conservative 0; Mismatches 1; Indels 1 TCCGCTGCAGAGTTGCCCGTTACGA 25 Best Local Similarity Query Match Matches ઠે

Gaps

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AAZ98719 standard; cDNA; 7400 BP. AAZ98719; RESULT 99 

(first entry) 20-JUN-2000

Swine vesicular disease virus (SVDV) N3 mutant strain gene sequence

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Swine vesicular disease virus; SVDV; swine vesicular disease; Taiwan Yu-Li strain; foot and mouth disease; coxsackie virus; differentiation; vaccine; prevent; ss.

Swine vesicular disease virus

Swine vesicular disease virus; SVDV; swine vesicular disease; Taiwan Yu-Li strain; foot and mouth disease; coxsackie virus; differentiation; vaccine; prevent; ss.

Swine vesicular disease virus

Location/Qualifiers 2693. .2710 misc\_feature

/\*tag= a /note= "Nucleotides in this position replace the wild-type nucleotide sequence of strain Taiwan Yu-Li (see 7AZ98717)

EP982403-A1

01-MAR-2000.

98EP-00306486 14-AUG-1998; 98EP-00306486. 14-AUG-1998; (BIOT-) DEV CENT BIOTECHNOLOGY

Lo C, Yang Y, Jeng K, ਹ ਹ Hwong

WPI; 2000-258616/23

Chang EL;

cant strains of swine vesicular disease virus (SVDV) used in vaccines prevent swine vesicular disease. Mutant 2

Claim 4; Page; 66pp; English.

(SDVD) gene sequence from the SVDV strain N3. SVDV is the causative agent of swine vesicular disease, which is very similar to foot and mouth disease. The invention relates to the wild-type Taivan Vu-Li strain cDNA sequence, and the gene sequences of the mutant SVDV strains N3, H21 and SP7. The mutant SVDV nucleotide sequence can be used in a vaccine for the prophylaxis of swine vesicular disease. The invention also includes a method for differentiating the mutant SVDV nucleotide sequences from the wild type strain of SVDV, coxsackie virus and foot-and-mouth disease virus through the use of polymerase chain reaction. Note: This sequence This sequence represents the full length Swine vesicular disease virus

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is not present in the specification, but has been derived from the wild-
type Taiwan Yu-Li strain SVDV gene sequence (see AAZ98717) shown on pages
34-38 of the specification
                                                           Gaps
                              Sequence 7400 BP; 2084 A; 1786 C; 1862 G; 1668 T; 0 U; 0 Other;
                                                           ö
                                            DB 3; Length 7400;
                                                           1; Indels
                                                                                                                                                                   Swine vesicular disease virus (SVDV) gene sequence.
                                            Score 23.4; DB Pred. No. 0.43;
                                                           0; Mismatches
                                                                                 538 TCCGCTGCAGAGTTGCCCATTACGA 514
                                                                         1 TCCGCTGCAGAGTTGCCCGTTACGA 25
                                                                                                                          BP
                                                                                                                          AAZ98717 standard; cDNA; 7400
                                            93.6%;
                                                                                                                                                     20-JUN-2000 (first entry)
                                                           24; Conservative
                                                   Local Similarity
                                                                                                                                        AAZ98717;
                                            Query Match
                                                           Matches
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Mutant strains of swine vesicular disease virus (SVDV) used in vaccines sequence represents the full length Swine vesicular disease virus to prevent swine vesicular disease. Claim 1; Page 34-38; 66pp; English.

E.

Chang

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Jeng

Lo C, Yang Y,

Hwong CL,

WPI; 2000-258616/23.

(BIOT-) DEV CENT BIOTECHNOLOGY,

98EP-00306486. 98EP-00306486.

14-AUG-1998; 14-AUG-1998;

01-MAR-2000. EP982403-A1

(SVDV) gene sequence from the SVDV strain Taiwan Yu-Li. SVDV is the causative agent of swine vesicular disease, which is very similar to foot and mouth disease. The invention relates to the wild-type Taiwan Yu-Li strain cDNA sequence, and the gene sequences of the mutant SVDV strains NJ, H21 and SP7. The mutant SVDV nucleotide sequence can be used in a vaccine for the prophylaxis of swine vesicular disease. The invention also includes a method for differentiating the mutant SVDV nucleotide sequences from the wild type strain of SVDV, coxsackievirus and mouth disease virus through the use of polymerase chain reaction

Sequence 7400 BP; 2082 A; 1786 C; 1862 G; 1670 T; 0 U; 0 Other;

TCGCTGCAGAGTTGCCCATTACGA 514 TCCGCTGCAGAGTTGCCCGTTACGA 25

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Gaps

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DB 3; Length 7400; 1; Indels

Score 23.4; DB Pred. No. 0.43; 0; Mismatches

Query Match 93.6%; Best Local Similarity 96.0%; Matches 24; Conservative C

Search completed: March 9, 2006, 00:30:40

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Job time : 264.485 secs